

Result No.	Score	Query Match	Length	DB	ID	Description
1	85.6	64.8	460	4	US-09-040-984-83	Sequence 83, Appl
2	85.6	64.8	460	4	US-09-123-912-83	Sequence 83, Appl
3	85.6	64.8	460	4	US-09-643-597-83	Sequence 83, Appl
4	43.4	32.9	556	3	US-09-058-489-25	Sequence 25, Appl
5	38.6	29.2	1161	3	US-09-058-489-26	Sequence 26, Appl
6	36.4	27.6	182	2	US-08-751-782-11	Sequence 11, Appl
7	36.4	27.6	182	2	US-08-925-171-11	Sequence 11, Appl
8	31.4	23.8	4117	4	US-09-484-9708-2	Sequence 2, Appl
9	31.2	23.6	2233	1	US-08-143-705A-1	Sequence 1, Appl
C 10	30.8	23.3	7218	1	US-08-232-463-14	Sequence 14, Appl
11	30.6	23.2	5394	3	US-08-688-376-1	Sequence 1, Appl
C 12	30.4	23.0	100	1	US-08-145-705A-3	Sequence 3, Appl
13	30	22.7	43795	3	US-08-742-185-101	Sequence 101, Appl
14	29.6	22.4	412	1	US-08-664-856A-1	Sequence 1, Appl
15	29.6	22.4	412	1	US-08-801-796-1	Sequence 1, Appl
16	29.6	22.4	412	2	US-08-931-877-1	Sequence 1, Appl
17	29.6	22.4	412	2	US-08-664-857A-1	Sequence 1, Appl
18	29.6	22.4	412	3	US-09-069-484-1	Sequence 1, Appl
19	29.6	22.4	412	3	US-09-133-599-1	Sequence 1, Appl
20	29.6	22.4	412	4	US-09-369-744-1	Sequence 1, Appl
21	29.6	22.4	2790	2	US-08-718-661-1	Sequence 1, Appl
C 22	29.2	22.1	1575	2	US-08-811-897A-34	Sequence 1, Appl
C 23	29.2	22.1	1575	2	US-08-855-213-34	Sequence 34, Appl
C 24	29.2	22.1	1575	4	US-09-201-474-34	Sequence 34, Appl
C 25	29.2	22.1	1656	2	US-08-811-897A-36	Sequence 36, Appl
C 26	29.2	22.1	1656	2	US-08-855-213-36	Sequence 36, Appl
C 27	29.2	22.1	1656	4	US-09-201-474-36	Sequence 36, Appl

QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACACAGAGCAGGAGAACTGG 117
Db 122 ACGGAGCAGCAGGAGAGACACCTCGCCGACCAAGAGACCATTTGAGCANGAGAAGCGG 181

QY 118 AGTGAATTTCTCTGA 132
Db 182 AGTGAATTTCTCTAA 196

RESULT 2
US-09-123-912-83
; Sequence 83, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (104)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (118)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (172)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (401)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (422)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (423)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (444)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (449)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-83

Query Match 64.8%; Score 85.6; DB 4; Length 460;
Best Local Similarity 81.5%; Pred. No. 6.9e-18;
Matches 110; Conservative 0; Mismatches 22; Indels 3; Caps 1;

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCAAGCTGAAGGCC 60
Db 62 ATGGCAGACAAACAGACATGCGGGAATCCGACGCTTCGATNAGGCCAAGCTGAANAAA 121

QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACACAGAGCAGGAGAACTGG 117
Db 122 ACGGAGCAGCAGGAGAGACACCTCGCCGACCAAGAGACCATTTGAGCANGAGAAGCGG 181

QY 118 AGTGAATTTCTCTGA 132
Db 182 AGTGAATTTCTCTAA 196

RESULT 3
US-09-123-912-83
; Sequence 83, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (104)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (118)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (172)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (401)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (422)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (423)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (444)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (449)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-83

Query Match 64.8%; Score 85.6; DB 4; Length 460;
Best Local Similarity 81.5%; Pred. No. 6.9e-18;
Matches 110; Conservative 0; Mismatches 22; Indels 3; Caps 1;

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCAAGCTGAAGGCC 60
Db 62 ATGGCAGACAAACAGACATGCGGGAATCCGACGCTTCGATNAGGCCAAGCTGAANAAA 121

QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACACAGAGCAGGAGAACTGG 117
Db 122 ACGGAGCAGCAGGAGAGACACCTCGCCGACCAAGAGACCATTTGAGCANGAGAAGCGG 181

QY 118 AGTGAATTTCTCTGA 132
Db 182 AGTGAATTTCTCTAA 196

US-09-643-597-83
; Sequence 83, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fauger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)--(460)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-83

Query Match 64.8%; Score 85.6; DB 4; Length 460;
Best Local Similarity 81.5%; Pred. No. 6.9e-18;
Matches 110; Conservative 0; Mismatches 22; Indels 3; Gaps 1;

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCAAGCTGAAGGCC 60
Db 62 ATGGCAGACAAACAGACATGCGGGAATCCGACGCTTCGATNAGGCCAAGCTGAANAAA 121

QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACACAGAGCAGGAGAACTGG 117
Db 122 ACGGAGCAGCAGGAGAGACACCTCGCCGACCAAGAGACCATTTGAGCANGAGAAGCGG 181

QY 118 AGTGAATTTCTCTGA 132
Db 182 AGTGAATTTCTCTAA 196

RESULT 4
US-09-058-489-25
; Sequence 25, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; FILE REFERENCE: WHI97-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Human
US-09-058-489-25

Query Match 32.9%; Score 43.4; DB 3; Length 556;


```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: 10.27
; US-08-925-171-11

Query Match 27.6%; Score 36.4; DB 2; Length 182;
Best Local Similarity 64.5%; Pred. No. 0.01;
Matches 71; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 8 ACAACTAGACTGGAGAAATTCCTGCTGATGACCAAGAGACACAGAGAGAGAG 67
Db 1 ACAAAACCGATGCTGCTGATGACCAAGAGAGAGAGAGAGAGAGAGAGAG 60

QY 68 TGC---AGAGAACACTCTGATGACCAAGAGAGAGAGAGAGAGAGAGAG 114
Db 61 CACAAGAGAAATCTCTGCTTCAAAAGAGAGAGAGAGAGAGAGAGAG 110

RESULT 8
US-09-484-970B-2
; Sequence 2, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484.970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 4117
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 344594 (1794154CBI)
US-09-484-970B-2

Query Match 23.8%; Score 31.4; DB 4; Length 4117;
Best Local Similarity 61.7%; Pred. No. 1.1;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 44 AGCCCACTGAGCCACAGATCCAGAACACTCTGATGACCAAGAGAGAGAG 103
Db 2558 ATGAAGCTTGAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2617

QY 104 AGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 124
Db 2618 ACAAGTACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2638

RESULT 9
US-08-145-705A-1/c
; Sequence 1, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: Lberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: 10.27
; US-08-925-171-11

CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: NEC PowerMate 1 plus
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: German P 42 36 708.5
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2233 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Candida albicans
US-08-145-705A-1

Query Match 23.6%; Score 31.2; DB 1; Length 2233;
Best Local Similarity 60.7%; Pred. No. 1;
Matches 51; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAGCCACAGAGATGCGAGAGAGAGAGAGAGAGAG 99
Db 264 GAAGAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 205

QY 100 ACAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db 204 GCAGAGAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181

RESULT 10
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```



```
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 23.3%; Score 30.8; DB 1; Length 7218;
Best Local Similarity 12.7%; Pred. No. 2;
Matches 14; Conservative 62; Mismatches 34; Indels 0; Gaps 0;

QY 15 AGACCTGGAGAAATGCCAGCTTGGATPAGCCCAAGCTGAAGCCACAGAGATGCAGAA 74
   ||| ||||| ||| | : : : : : : : : : : : : : : : : : :
DB 1455 AGATAGACGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1396

QY 75 GAACACTGTGATGACCAAGACAGACACAGCAGGAGGAAGTGGAGTGA 124
   : : : : : : : : : : : : : : : : : : : : : : : :
DB 1395 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1346

RESULT 11
US-08-688-376-1
; Sequence 1, Application US/08688376
; Patent No. 6018039
; GENERAL INFORMATION:
; APPLICANT: Satow, Hiroyasu
; TITLE OF INVENTION: NOVEL PROCESS FOR PRODUCING SUBSTANCES
; TITLE OF INVENTION: IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
; TITLE OF INVENTION: EXPRESSION-REGULATORY REGION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILWORTH & BARRESE
; STREET: 4350 LaJolla Village Drive, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688.376
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pepper, Frederick W.
; REGISTRATION NUMBER: 31,286
; REFERENCE/DOCKET NUMBER: 567-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4410
; TELEFAX: 619-453-2839
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CAAT_signal
; LOCATION: 2234..2243
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: 2275..2281
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 4607..4612
; US-08-688-376-1

Query Match 23.2%; Score 30.6; DB 3; Length 5394;
Best Local Similarity 58.1%; Pred. No. 2.1;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 39 GCATAGGCCCAAGCTGAAGCCACAGAGATGCAGAGAACACTCTGTATGACCAAGAGAC 98
   ||| ||||| ||| | : : : : : : : : : : : : : : : : : :
DB 1445 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1504

QY 99 CACAGAGCAGGAGAGAGTGGAGTGAAATTTCTCTG 131
   ||| ||||| ||| | : : : : : : : : : : : : : : : : : :
DB 1505 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1537

RESULT 12
US-08-145-705A-3/c
; Sequence 3, Application US/08145705A
; Patent No. 5489513
; GENERAL INFORMATION:
; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
; APPLICANT: L bberding, Antonius
; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
; TITLE OF INVENTION: ALBICANS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: NEC PowerMate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,705A
; FILING DATE: October 28, 1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: German P 42 36 708.5
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Candida albicans
US-08-145-705A-3

Query Match 23.0%; Score 30.4; DB 1; Length 100;

Best Local Similarity 61.2%; Pred. No. 0.61; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 0;

QY 44 AGCCAGAGCTGAAGGCCACAGAGATGCAGAGAACACTCTGTGACCAAGAGACACAG 103
||||| ||||| ||| ||||| | | ||||| |||
Db 97 AGCCAGAGAGAGGCGAGAGAGGCCCAAGAGAGGCGAGAGGCCCAAGAGAGGCGAG 38
||||| ||||| ||| ||||| | | ||||| |||
QY 104 AGCAGGAGAGTGGAGTGA 123
||| ||| ||| ||| |||
Db 37 AGGAGGCCAAGAGAGGCCA 18
||| ||| ||| ||| |||

RESULT 13

US-08-742-185-101

; Sequence 101, Application US/08742185

; Patent No. 6020476

; GENERAL INFORMATION:

; APPLICANT: Page, David C.

; APPLICANT: Reijo, Renee

; APPLICANT: Saxena, Richa

; APPLICANT: Hawkins, Trevor

; APPLICANT: Reeve, Mary Pat

; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA

; NUMBER OF SEQUENCES: 102

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/742.185

; FILING DATE: 30-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/690,734

; FILING DATE: 31-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/310,429

; FILING DATE: 22-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: WHI94-07A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 861-6240

; TELEFAX: (617) 861-9540

; INFORMATION FOR SEQ ID NO: 101:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43795 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-742-185-101

Query Match 22.7%; Score 30; DB 3; Length 43795;

Best Local Similarity 59.3%; Pred. No. 6.6;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 39 GGATAAGGCCAAGCTGAAGGCCACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGAC 98
||| ||| ||| ||||| | | ||||| |||
Db 38962 GAAGAGGAG 39021
||| ||| ||| ||||| | | ||||| |||

QY 99 CACAGACGAGAGAGAGTGGAGTGA 124
||| ||| ||| ||||| ||| |||||
Db 39022 GAGGAAGAAGAAGAAGAAGAGAGAAA 39047
||| ||| ||| ||||| ||| |||||

RESULT 14

US-08-664-856A-1

; Sequence 1, Application US/08664856A

; Patent No. 5663071

; GENERAL INFORMATION:

; APPLICANT: BRUCE R. ZETTER AND LERE BAO

; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02019

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/664,856A

; FILING DATE: 17 JUN 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 46507

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 412 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 98..232

; OTHER INFORMATION: Exon 1

US-08-664-856A-1

Query Match 22.4%; Score 29.6; DB 1; Length 412;

Best Local Similarity 59.5%; Pred. No. 1.8;

Matches 69; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 ATGGCACACAACACTGACCTGGAGAAATTCACGCTTGATAGAGCCACCTGAAGGCC 60
||| ||| ||||| ||| ||||| ||| ||||| |||

Db 98 ATGAGTGATAAACACCACTTATCAGAAAGTTGAACATTTGACAAATCAAGTTGAAGAG 157
||| ||| ||||| ||| ||||| ||| ||||| |||

0
0
0
0
-
0
0
0

THIS PAGE BLANK (13PT0)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 13:24:07 ; Search time 214 Seconds

(without alignments)
1389.083 Million cell updates/sec

Title: US-09-915-178-1

Perfect score: 132

Sequence: 1 atggcacacaaactagacct.....agtggagtgaaatttcctga 132

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	147	24	ABA92649 Human NOV2a encodi
2	132	100.0	147	24	ABA92650 Human NOV2b encodi
3	132	100.0	147	24	ABA92651 Human NOV2c encodi
4	88.6	67.1	243	24	ABK55047 Human colon cancer
5	88.6	67.1	353	24	ABK54754 Human colon cancer
6	88.6	67.1	395	24	ABK54737 Human colon cancer
7	88.6	67.1	428	24	ABK55033 Human colon cancer
8	88.6	67.1	429	24	ABK55163 Human colon cancer
9	88.6	67.1	434	24	ABK55157 Human colon cancer

10	88.6	67.1	438	24	ABK54988 Human colon cancer
11	88.6	67.1	438	24	ABK55113 Human colon cancer
12	88.6	67.1	439	24	ABK55440 Human colon cancer
13	88.6	67.1	443	24	ABK55189 Human colon cancer
14	88.6	67.1	445	24	ABK53257 Human colon cancer
15	88.6	67.1	446	24	ABK55421 Human colon cancer
16	88.6	67.1	451	24	ABK55083 Human colon cancer
17	88.6	67.1	452	24	ABK54878 Human colon cancer
18	88.6	67.1	453	24	ABN96522 Gene #3020 used to
19	88.6	67.1	453	24	ABK54804 Human colon cancer
20	88.6	67.1	455	24	ABK54803 Human colon cancer
21	88.6	67.1	456	24	ABK54749 Human colon cancer
22	88.6	67.1	465	24	ABK54586 Human colon cancer
23	88.6	67.1	488	21	AAC10524 Human thymosin b-1
24	88.6	67.1	491	22	AAD03640 Human colon cancer
25	88.6	67.1	517	24	ABK55404 Human prostate exp
26	88.6	67.1	534	23	ABV33875 Human prostate exp
27	88.6	67.1	534	23	ABV42758 Human colon cancer
28	88.6	67.1	693	24	ABK55328 Human prostate exp
29	88.6	67.1	836	23	ABV12746 Human prostate exp
30	88.6	67.1	1201	23	ABV21155 Human prostate exp
31	88.6	67.1	1201	23	ABV22339 Human prostate exp
32	88.6	67.1	1201	23	ABV28163 Human prostate exp
33	88	66.7	430	22	AAS00689 cDNA encoding thym
34	88	66.7	430	24	AAD38157 Thymosin-beta-10-1
35	85.6	64.8	460	20	AAC224583 Human lung tumor a
36	85.6	64.8	460	21	AAC65822 Human lung cancer-
37	85.6	64.8	460	24	ABL49041 Human lung tumour
38	82.2	62.3	446	24	ABK55170 Human colon cancer
39	80.8	61.2	267	21	AAC00908 Human secreted pro
40	77.8	58.9	449	24	ABK54652 Human colon cancer
41	77.8	58.9	451	24	ABK54720 Human colon cancer
42	73.2	55.5	792	23	ABV03577 Human prostate exp
43	70.2	53.2	263	20	AZ27510 Human ovarian tumo
44	63.4	48.0	453	21	AAC10525 Human secreted pro
45	63.2	47.9	724	24	AAS62054 Porcine muscular s

ALIGNMENTS

RESULT 1
ABA92649
ID ABA92649 standard; cDNA; 147 BP.
XX
AC ABA92649;
XX
DT 25-MAR-2002 (first entry)
XX
DE Human NOV2a encoding polynucleotide SEQ ID NO:3.
XX
KW Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;
KW fungicide; virucide; protozoacide; analgesic; antiparkinsonian;
KW antilasthmatic; hypotensive; osteopathic; antiinflammatory; antiulcer;
KW neuroprotective; cardiatic; antiallergic; antidepressant; nootropic;
KW anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;
KW developmental disease; taste and scent detectability disorder; infection;
KW Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;
KW retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;
KW noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;
KW hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
KW multiple sclerosis; angina pectoris; myocardial infarction; delirium;
KW benign prostatic hypertrophy; manic depression; dementia; dyslexia;
KW severe mental retardation; Huntington's disease; gene; chromosome 9;
KW Gilles de la Tourette syndrome; ss.

Homo sapiens.
Key Location/Qualifiers
CDS 6..137
/*tag= a
/product= "NOV2a"

Wed Jun 4 11:04:57 2003

us-09-915-178-1.rng

125

Db	66	ACAGAGATCCAGAAGACACTCTGTGATGACCAAGAGACCAAGAGAGAGAGTGGAGT	122
QY	121	GAATTTCTCTGA	132
Db	126	GAATTTCTCTGA	137

RESULT 2
ABA92650
ID ABA92650 standard; cDNA; 147 BP.
XX
XX
ABA92650;
AC
XX
XX
DT
25-MAR-2002 (first entry)
XX
XX
XXXXXX encoding polynucleotide SEQ ID NO:5.

XX Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;
KW fungicide; virucide; protozoacide; analgesic; antiparkinsonian;
KW antihypertensive; osteopathic; antiinflammatory; antulcer;
KW neuroprotective; antiasthmatic; antipruritic; antipressant; nootropic;
KW anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;
KW developmental disease; taste and scent detectability disorder; infection;
KW Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;
KW retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;
KW noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;
KW hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
KW multiple sclerosis; angina pectoris; myocardial infarction; delirium;
KW benign prostatic hypertrophy; manic depression; dementia; dyskinesia;
KW severe mental retardation; Huntington's disease; gene;
KW Gilles de la Tourette syndrome; ss.

[illegible]

XX	WO2000190155-A2.
PN	
XX	
XX	29-NOV-2001.
PD	
XX	
PF	24-MAY-2001; 2001WO-US17073.
XX	
XX	24-MAY-2000; 2000US-206679P.
PR	24-MAY-2000; 2000US-206688P.
PR	24-MAY-2000; 2000US-206829P.
PR	30-MAY-2000; 2000US-207748P.
PR	30-MAY-2000; 2000US-207798P.
PR	31-MAY-2000; 2000US-208263P.
PR	02-JUN-2000; 2000US-208831P.
PR	05-JUN-2000; 2000US-209451P.
PR	07-JUN-2000; 2000US-210060P.
PR	20-JUL-2000; 2000US-219507P.
PR	26-JUL-2000; 2000US-221337P.
PR	31-JUL-2000; 2000US-221927P.
PR	19-JAN-2001; 2001US-263135P.
PR	24-JAN-2001; 2001US-263688P.
PR	24-JAN-2001; 2001US-263694P.
PR	23-MAY-2001; 2001US-0863776.

xx
xx PA (CURA-) CURAGEN CORP.
xx
xx PI Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigar M;
xx PI Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
xx WPI: 2002-106174/14.
xx
xx DR P-PSDB: ABB05035.
xx

xx Novel polypeptide, useful for treating pain, cancer, urinary retention,
pt osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
pt

PN	WO2001190155-A2.
XX	
PD	29 - NOV - 2001.
PF	
XX	
XX	24 - MAY - 2001; 2001WO-US17073.
XX	
PR	24 - MAY - 2000; 2000US-206679P.
PR	24 - MAY - 2000; 2000US-206688P.
PR	24 - MAY - 2000; 2000US-206829P.
PR	30 - MAY - 2000; 2000US-207748P.
PR	30 - MAY - 2000; 2000US-207798P.
PR	31 - MAY - 2000; 2000US-208263P.
PR	02 - JUN - 2000; 2000US-208631P.
PR	05 - JUN - 2000; 2000US-209451P.
PR	07 - JUN - 2000; 2000US-210060P.
PR	20 - JUL - 2000; 2000US-219507P.
PR	26 - JUL - 2000; 2000US-221337P.
PR	31 - JUL - 2000; 2000US-221927P.
PR	19 - JAN - 2001; 2001US-263135P.
PR	24 - JAN - 2001; 2001US-263688P.
PR	24 - JAN - 2001; 2001US-263694P.
PR	23 - MAY - 2001; 2001US-0863776.

(CURA-) CURAGEN CORP.
PA
XX
XX
PI Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
PI Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangollil E;
XX
XX WPI: 2002-106174/14.
DR P-PSDB: ABB05034.
DR

XX Novel polypeptide, useful for treating pain, cancer, urinary retention,
PT
PT osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
PT asthma, ulcer, allergy and Huntington's disease, comprises isolated
PT polypeptide NOVX -
PT

XX
XX
ps
claim 8: page 20: 266pp: English.

The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial, fungicide, virucide, protozoacide, analgesic, antiparkinsonian, antiasthmatic, hypotensive, osteopathic, antiinflammatory, antitumor, neuroprotective, cardiant, antiallergic, antidepressant, neurotropic, anticonvulsant and neuroleptic activities. (I) and polynucleotides (II) can be used in gene therapy and vaccine production. (I) and (II) can be used for treating or preventing a NOVX-associated disorder such as cardiomyopathy, atherosclerosis and diabetes in a human, where the disorder is related to cell signal processing and metabolic path way modulation, in a subject, preferably human. (I) and (II) can be used for diagnosing, preventing or treating developmental diseases, immune diseases, taste and scent detectability disorder, Burkitt's lymphoma, signal transduction pathway disorders, retinal diseases including those involving photoreception, cell growth rate disorders, feeding disorders, parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, Crohn's disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial infarction, allergies, benign prostatic hypertrophy, manic depression, delirium, dementia, severe metal retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette syndrome. The present invention also describes NOV2a which is isolated to chromosome 9.

	SQ	Sequence 147 BP; 56 A; 30 C; 41 G; 20 T; 0 other;		
XX				
		Query Match	100.0%; Score 132; DB 24; Length 147;	
		Best Local Similarity	100.0%; Pred. No. 4.5e-29;	
		Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0		

QY		1	ATGGCACAAACTAGACCTTGGAGAANAATTGCCAGTTGGATTAAGCCCAAGCTGAAGGCC	60
D8		6	ATGGCACAAACTAGACCTTGGAGAANAATTGCCAGTTGGATTAAGCCCAAGCTGAAGGCC	65
QY		61	ACAGAGATGCGAAGAACACTGTATGCACCAAGAGACCACAGACGAGGAGAAGTGAGCT	120

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
|||||
Db 6 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 65
|||||

QY 61 ACAGAGATGCAGAGACACTCTGATCACCACAAAGACACAGAGCAGGAGAACTGGAGT 120
|||||
Db 66 ACAGAGATGCAGAGACACTCTGATCACCACAAAGACACAGAGCAGGAGAACTGGAGT 125
|||||

QY 121 GAAATTTCTCTGA 132
|||||
Db 126 GAAATTTCTCTGA 137
|||||

RESULT 4
ABK55047
ID ABK55047 standard; cDNA; 243 BP.
XX AC ABK55047;
XX DT
XX DE 18-JUN-2002 (first entry)
XX KW Human colon cancer-associated cDNA, SEQ ID No 517.
XX OS Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX PN Homo sapiens.
XX PD WO200212280-A2.
XX PF 14-FEB-2002.
XX PR 30-JUL-2001; 2001WO-US23826.
XX PR 03-AUG-2000; 2000US-223265P.
XX PR 02-OCT-2000; 2000US-237406P.
XX PR 20-MAR-2001; 2001US-277495P.
XX PR 03-JUL-2001; 2001US-302702P.
XX PA (CORI-) CORIXA CORP.
XX PI Pyle RA, Xu J, Secrlist H;
XX PS WPI; 2002-257462/30.
XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
XX PT vaccines for treating colon cancers
XX PS Claim 1; Page 297; 425pp; English.
XX CC The invention relates to isolated polynucleotides (I) encoding colon
XX CC tumour polypeptides (II). (I) is useful for stimulating an immune
XX CC response in a patient and treating colon cancer in a patient.
XX CC Oligonucleotides derived from (I) are useful for determining the presence
XX CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
XX CC and treatment of colon cancer. A composition comprising a first component
XX CC selected from physiologically acceptable carriers and immunostimulants,
XX CC and an antigen-presenting cell expressing (II) is useful for inhibiting
XX CC development of cancer in a patient. (I) is useful in the design and
XX CC preparation of ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
XX CC sequences of the invention.
XX SQ Sequence 243 BP; 73 A; 64 C; 68 G; 37 T; 1 other;

Query Match 67.1%; Score 88.6; DB 24; Length 243;
Best Local Similarity 83.7%; Pred. No. 2e-16;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
|||||
Db 37 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 96
|||||

QY 61 ACAGAGATGC---AGAGACACTCTGATCACCACAAAGACACAGAGCAGGAGAACTGG 117
|||||

Db 63 ATGGCAGACAAACCAGACATGGGGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGAAA 122
QY 61 ACAGAGATGC---AGAGACACTCTGATCACCACAAAGACACAGAGCAGGAGAACTGG 117
|||||
Db 123 ACGGAGACCGCAGGAGAGAACACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 182
|||||

QY 118 AGTGAATTTCTCTGA 132
|||||
Db 183 AGTGAATTTCTCTGA 197
|||||

RESULT 5
ABK54754
ID ABK54754 standard; cDNA; 353 BP.
XX AC ABK54754;
XX DT
XX DE 18-JUN-2002 (first entry)
XX KW Human colon cancer-associated cDNA, SEQ ID No 224.
XX OS Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX PN Homo sapiens.
XX PD WO200212280-A2.
XX PF 14-FEB-2002.
XX PR 30-JUL-2001; 2001WO-US23826.
XX PR 03-AUG-2000; 2000US-223265P.
XX PR 02-OCT-2000; 2000US-237406P.
XX PR 20-MAR-2001; 2001US-277495P.
XX PR 03-JUL-2001; 2001US-302702P.
XX PA (CORI-) CORIXA CORP.
XX PI Pyle RA, Xu J, Secrlist H;
XX PS WPI; 2002-257462/30.
XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
XX PT vaccines for treating colon cancers
XX PS Claim 1; Page 214; 425pp; English.
XX CC The invention relates to isolated polynucleotides (I) encoding colon
XX CC tumour polypeptides (II). (I) is useful for stimulating an immune
XX CC response in a patient and treating colon cancer in a patient.
XX CC Oligonucleotides derived from (I) are useful for determining the presence
XX CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
XX CC and treatment of colon cancer. A composition comprising a first component
XX CC selected from physiologically acceptable carriers and immunostimulants,
XX CC and an antigen-presenting cell expressing (II) is useful for inhibiting
XX CC development of cancer in a patient. (I) is useful in the design and
XX CC preparation of ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
XX CC sequences of the invention.
XX SQ Sequence 353 BP; 97 A; 103 C; 98 G; 55 T; 0 other;

Query Match 67.1%; Score 88.6; DB 24; Length 353;
Best Local Similarity 83.7%; Pred. No. 2.3e-16;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
|||||
Db 37 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 96
|||||

QY 61 ACAGAGATGC---AGAGACACTCTGATCACCACAAAGACACAGAGCAGGAGAACTGG 117
|||||


```
Db 97 ACGGACGACGAGGAGAACACACCTCGCGACCAAGAGACCATTTGAGCAGGAGAGCGG 156
QY 118 AGTGAATTTCTCTGA 132
    |||||
Db 157 AGTGAATTTCTCTAA 171

RESULT 6
ABK54737
ID ABK54737 standard; cDNA; 395 BP.
XX
AC ABK54737;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human colon cancer-associated cDNA, SEQ ID No 207.
XX
DE Human colon cancer; immunogenic; vaccine; tumour; gene; ss.
KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212280-A2.
XX
PD 14-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US23826.
XX
PR 03-AUG-2000; 2000US-223265P.
XX
PR 02-OCT-2000; 2000US-237406P.
XX
PR 20-MAR-2001; 2001US-277495P.
XX
PR 03-JUL-2001; 2001US-302702P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Pyle RA, Xu J, Secrist H;
XX
XX WPI; 2002-257462/30.
XX
PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers
XX
PS Claim 1; Page 209; 425pp; English.
XX
CC The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK5464 represent human colon cancer cDNA
CC sequences of the invention.
XX
SQ Sequence 395 BP; 105 A; 113 C; 115 G; 62 T; 0 other;

Query Match 67.1%; Score 88.6; DB 24; Length 395;
Best Local Similarity 83.7%; Pred. No. 2.3e-16;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCAGACAACTAGACCTGGAGAAATTCGACGTTGGATAGGCCAAGCTGAAGGCC 60
    |||||
Db 72 ATGGCAGACAAACAGACATCGGGGAAATTCGACGTTGGATAGGCCAAGCTGAAGAAA 131
    |||||

QY 61 ACAGAGATGC---AGAAGACACTCTGTATGACCAAGAGACACAGAGAGGAGAGTGG 117
    |||||
Db 132 ACGGACGCGAGGAGAGAGACACCTCGCGACCAAGAGACCATTTGAGCAGGAGAGCGG 191
    |||||

QY 118 AGTGAATTTCTCTGA 132
    |||||
```

```
Db 192 AGTGAATTTCTCTAA 206

RESULT 7
ABK55033
ID ABK55033 standard; cDNA; 428 BP.
XX
AC ABK55033;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human colon cancer-associated cDNA, SEQ ID No 503.
XX
DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212280-A2.
XX
PD 14-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US23826.
XX
PR 03-AUG-2000; 2000US-223265P.
XX
PR 02-OCT-2000; 2000US-237406P.
XX
PR 20-MAR-2001; 2001US-277495P.
XX
PR 03-JUL-2001; 2001US-302702P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Pyle RA, Xu J, Secrist H;
XX
XX WPI; 2002-257462/30.
XX
PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers
XX
PS Claim 1; Page 294; 425pp; English.
XX
CC The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK5464 represent human colon cancer cDNA
CC sequences of the invention.
XX
SQ Sequence 428 BP; 124 A; 114 C; 115 G; 75 T; 0 other;

Query Match 67.1%; Score 88.6; DB 24; Length 428;
Best Local Similarity 83.7%; Pred. No. 2.4e-16;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCAGACAACTAGACCTGGAGAAATTCGACGTTGGATAGGCCAAGCTGAAGGCC 60
    |||||
Db 50 ATGGCAGACAAACAGACATCGGGGAAATTCGACGTTGGATAGGCCAAGCTGAAGAAA 109
    |||||

QY 61 ACAGAGATGC---AGAAGACACTCTGTATGACCAAGAGACACAGAGAGGAGAGTGG 117
    |||||
Db 110 ACGGACGCGAGGAGAGAGACACCTCGCGACCAAGAGACCATTTGAGCAGGAGAGCGG 169
    |||||

QY 118 AGTGAATTTCTCTGA 132
    |||||
Db 170 AGTGAATTTCTCTAA 184

RESULT 8
```

ABK55163
ID ABK55163 standard; cDNA; 429 BP.

XX AC
XX ABK55163;

XX DT 18-JUN-2002 (first entry)

XX DE Human colon cancer-associated cDNA, SEQ ID No 633.

XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200212280-A2.

XX PD 14-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23826.

XX PR 03-AUG-2000; 2000US-223265P.

XX PR 02-OCT-2000; 2000US-237406P.

XX PR 20-MAR-2001; 2001US-277495P.

XX PR 03-JUL-2001; 2001US-302702P.

XX PA (CORI-) CORIXA CORP.

XX PI Pyle RA, Xu J, Secrlist H;

XX DR WPI; 2002-257462/30.

XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
vaccines for treating colon cancers

XX PS Claim 1; Page 329; 425pp; English.

XX CC The invention relates to isolated polynucleotides (I) encoding colon
tumour polypeptides (II). (I) is useful for stimulating an immune
response in a patient and treating colon cancer in a patient.

XX CC Oligonucleotides derived from (I) are useful for determining the presence
of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
and treatment of colon cancer. A composition comprising a first component

XX CC selected from physiologically acceptable carriers and immunostimulants,
and an antigen-presenting cell expressing (II) is useful for inhibiting

XX CC development of cancer in a patient. (I) is useful in the design and
preparation of ribozyme molecules for inhibiting expression of tumour

XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
sequences of the invention.

XX SQ Sequence 429 BP; 124 A; 115 C; 115 G; 75 T; 0 other;

Query Match 67.1%; Score 88.6; DB 24; Length 429;

Best Local Similarity 83.7%; Pred. No. 2.4e-16;

Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCGACCTTGGATAGGCCCAAGCTGAAGGCC 60

DB 51 ATGGCACAACAAACAGACATGGGGGAAATTCGACCTTGGATAGGCCCAAGCTGAAGAAA 110

QY 61 ACAGAGATGTC---AGAGAACTCTGTATGACCAAAAGAGACCACAGAGAGAGAGTGG 117

DB 111 ACGGAGACGAGGAGAGACACCTCGCCCAACAGACCATTTGAGCAGGAGAGCGG 170

QY 118 AGTGAATTTCTCTGA 132

DB 171 AGTGAATTTCTCTAA 185

RESULT 9

ABK55157

ID ABK55157 standard; cDNA; 434 BP.

XX AC

ABK55157;

XX DT 18-JUN-2002 (first entry)

XX DE Human colon cancer-associated cDNA, SEQ ID No 627.

XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200212280-A2.

XX PD 14-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23826.

XX PR 03-AUG-2000; 2000US-223265P.

XX PR 02-OCT-2000; 2000US-237406P.

XX PR 20-MAR-2001; 2001US-277495P.

XX PR 03-JUL-2001; 2001US-302702P.

XX PA (CORI-) CORIXA CORP.

XX PI Pyle RA, Xu J, Secrlist H;

XX DR WPI; 2002-257462/30.

XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
vaccines for treating colon cancers

XX PS Claim 1; Page 328; 425pp; English.

XX CC The invention relates to isolated polynucleotides (I) encoding colon
tumour polypeptides (II). (I) is useful for stimulating an immune
response in a patient and treating colon cancer in a patient.

XX CC Oligonucleotides derived from (I) are useful for determining the presence
of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
and treatment of colon cancer. A composition comprising a first component

XX CC selected from physiologically acceptable carriers and immunostimulants,
and an antigen-presenting cell expressing (II) is useful for inhibiting

XX CC development of cancer in a patient. (I) is useful in the design and
preparation of ribozyme molecules for inhibiting expression of tumour

XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
sequences of the invention.

XX SQ Sequence 434 BP; 124 A; 116 C; 117 G; 77 T; 0 other;

Query Match 67.1%; Score 88.6; DB 24; Length 434;

Best Local Similarity 83.7%; Pred. No. 2.4e-16;

Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCGACCTTGGATAGGCCCAAGCTGAAGGCC 60

DB 54 ATGGCACAACAAACAGACATGGGGGAAATTCGACCTTGGATAGGCCCAAGCTGAAGAAA 113

QY 61 ACAGAGATGTC---AGAGAACTCTGTATGACCAAAAGAGACCACAGAGAGAGTGG 117

DB 114 ACGGAGACGAGGAGAGACACCTCGCCCAACAGACCATTTGAGCAGGAGAGCGG 173

QY 118 AGTGAATTTCTCTGA 132

DB 174 AGTGAATTTCTCTAA 188

RESULT 10

ABK54988

ID ABK54988 standard; cDNA; 438 BP.

XX AC

ABK54988;

XX DT

18-JUN-2002 (first entry)

XX DE

Human colon cancer-associated cDNA, SEQ ID No 458.

XX 30-JUL-2001; 2001WO-US23826.
 PF 03-AUG-2000; 2000US-223265P.
 PR 02-OCT-2000; 2000US-237406P.
 PR 20-MAR-2001; 2001US-277495P.
 PR 03-JUL-2001; 2001US-302702P.
 XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secrist H;
 XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX vaccines for treating colon cancers -
 XX Claim 1; Page 415; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK5464 represent human colon cancer CDNA
 CC sequences of the invention.

XX Sequence 439 BP; 127 A; 116 C; 115 G; 78 T; 3 other;
 SQ Query Match 67.1%; Score 88.6; DB 24; Length 439;
 Best Local Similarity 83.7%; Pred. No. 2.4e-16;
 Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

XX 1 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGATAGGCCAAGCTGAAGGCC 60
 Db 55 ATGGCAGACAAACACAGACATGGGGGAAATCGCCAGCTTCGATAGGCCAAGCTGAAGAAA 114

XX 61 ACAGAGATGC--AGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGTGG 117
 Db 115 ACGGAGACGAGGAGAGAACACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 174
 XX 118 AGTGAATTTCTTGA 132
 Db 175 AGTGAATTTCTTAA 189

XX RESULT 13
 XX ABK55189
 XX ID ABK55189 standard; CDNA; 443 BP.

XX AC ABK55189;
 XX DT 18-JUN-2002 (first entry)

XX Human colon cancer-associated CDNA, SEQ ID NO 659.

XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

PR 02-OCT-2000; 2000US-237406P.
 PR 20-MAR-2001; 2001US-277495P.
 PR 03-JUL-2001; 2001US-302702P.
 XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secrist H;
 XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX vaccines for treating colon cancers -
 XX Claim 1; Page 337; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK5464 represent human colon cancer CDNA
 CC sequences of the invention.

XX Sequence 443 BP; 128 A; 119 C; 119 G; 77 T; 0 other;

XX Query Match 67.1%; Score 88.6; DB 24; Length 443;
 XX Best Local Similarity 83.7%; Pred. No. 2.4e-16;
 XX Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

XX 1 ATGGCACACAACTAGACCTGGAGAAATTCGCCAGCTTGATAGGCCAAGCTGAAGGCC 60
 Db 65 ATGGCAGACAAACACAGACATGGGGGAAATCGCCAGCTTCGATAGGCCAAGCTGAAGAAA 124
 XX 61 ACAGAGATGC--AGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGTGG 117
 Db 125 ACGGAGACGAGGAGAGAACACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 184
 XX 118 AGTGAATTTCTTGA 132
 Db 185 AGTGAATTTCTTAA 199

XX RESULT 14
 XX ABK55257
 XX ID ABK55257 standard; CDNA; 445 BP.

XX AC ABK55257;
 XX DT 18-JUN-2002 (first entry)

XX Human colon cancer-associated CDNA, SEQ ID NO 727.

XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

XX 02-OCT-2000; 2000US-237406P.

XX 20-MAR-2001; 2001US-277495P.

XX 03-JUL-2001; 2001US-302702P.

THIS PAGE BLANK (38PT0)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 2, 2003, 14:18:32 ; Search time 106 Seconds
(without alignments)
1679.096 Million cell updates/sec

Title: US-09-915-178-1
Perfect score: 132
Sequence: 1 atggcacacaaactagacct.....agtggagtgaatttcctga 132

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues
Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/FCI_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/FCIUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.6	67.1	243	10	US-09-919-580-517
2	88.6	67.1	353	10	US-09-919-580-224
3	88.6	67.1	395	10	US-09-919-580-207
4	88.6	67.1	426	10	US-09-998-598-71
5	88.6	67.1	428	10	US-09-919-580-503
6	88.6	67.1	429	10	US-09-919-580-633
7	88.6	67.1	434	10	US-09-919-580-627
8	88.6	67.1	438	10	US-09-919-580-458
9	88.6	67.1	438	10	US-09-919-580-583
10	88.6	67.1	439	10	US-09-919-580-910
11	88.6	67.1	443	10	US-09-919-580-659
12	88.6	67.1	445	10	US-09-919-580-727
13	88.6	67.1	446	10	US-09-919-580-891
14	88.6	67.1	449	9	US-09-918-995-15768
15	88.6	67.1	451	10	US-09-919-580-553
16	88.6	67.1	452	10	US-09-919-580-348
17	88.6	67.1	453	10	US-09-919-580-274
18	88.6	67.1	453	10	US-09-880-107-3019
19	88.6	67.1	455	10	US-09-919-580-273

20	88.6	67.1	456	10	US-09-919-580-219
21	88.6	67.1	465	10	US-09-919-580-56
22	88.6	67.1	468	9	US-09-918-995-21161
23	88.6	67.1	469	9	US-09-918-995-24062
24	88.6	67.1	473	9	US-09-918-995-15273
25	88.6	67.1	483	9	US-09-918-995-19906
26	88.6	67.1	517	10	US-09-919-580-874
27	88.6	67.1	593	10	US-09-919-580-798
28	85.6	64.8	460	10	US-09-735-705-83
29	85.6	64.8	460	10	US-09-850-716A-83
30	85.6	64.8	460	10	US-09-897-778-83
31	83.8	63.5	461	9	US-09-918-995-22450
32	82.2	62.3	446	10	US-09-919-580-640
33	80.6	61.1	465	9	US-09-918-995-23067
34	80.2	60.8	494	9	US-09-918-995-24178
35	77.8	58.9	449	10	US-09-919-580-122
36	77.8	58.9	451	10	US-09-919-580-190
37	77.8	58.9	474	9	US-09-918-995-22477
38	57.4	43.5	559	10	US-09-919-580-159
39	54.4	41.2	446	10	US-09-880-107-3158
40	50.2	38.0	404	10	US-09-960-352-10885
41	50.2	38.0	405	10	US-09-960-352-6906
42	50.2	38.0	408	10	US-09-960-352-12808
43	50.2	38.0	461	10	US-09-960-352-2605
44	46.6	35.3	468	9	US-09-918-995-13407
45	45.4	34.4	377	10	US-09-960-352-6901

ALIGNMENTS

RESULT 1
US-09-919-580-517
; Sequence 517, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 243
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-517

Query Match 67.1%; Score 88.6; DB 10; Length 243;
Best Local Similarity 83.7%; Pred. No. 4.6e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAAACTAGACCTGGAGAAATTCACAGTTCGATAGGCCAAGCTGAAGGCC 60
Db 63 ATGGCACAAACCACATCGGGGAAATTCGATAGGCCAAGCTGAAGAAA 122
QY 61 ACAGAGATGC---AGAAGACACCTGTGATGACCAAGAGACACACAGCAGAGATGG 117
Db 123 ACGGACGACGAGGAGAGACACCCCTGCCGACCAAGAGACCATTTGACGAGGAGCGG 182
QY 118 AGTGAATTTTCCTGA 132
Db 183 AGTGAATTTTCCTAA 197

Db 192 AGTGAATTCCTAA 206

RESULT 4

US-09-998-598-71

; Sequence 71, Application US/09998598

; Patent No. US20020150922A1

; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Chenault, Ruth A.

; APPLICANT: Meagher, Madelein Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.561

; CURRENT APPLICATION NUMBER: US/09/998,598

; CURRENT FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 2605

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 71

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-998-598-71

Query Match 67.1%; Score 88.6; DB 10; Length 426;

Best Local Similarity 83.7%; Pred. No. 5.3e-19;

Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACACAACTAGACCTGGGAAGAATTGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60

Db 48 ATGGCAGACAAACCAGACATCGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 107

QY 61 ACAGAGATGC---AGAGAACACTCTGATGACCACCAAGAGACCACAGACGAGGAGAAGTGG 117

Db 108 ACGGAGACGAGGAGGAAGAACCCTCGCCGACCAAGAGACCATTTGACGAGGAGANGCGG 167

QY 118 AGTGAATTCCTGA 132

Db 168 AGTGAATTCCTAA 182

RESULT 5

US-09-919-580-503

; Sequence 503, Application US/09919580

; Patent No. US20020110832A1

; GENERAL INFORMATION:

; APPLICANT: Pyle, Ruth

; APPLICANT: Xu, Jiangchun

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.552

; CURRENT APPLICATION NUMBER: US/09/919,580

; CURRENT FILING DATE: 2001-07-30

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 503

; LENGTH: 428

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-580-503

Query Match 67.1%; Score 88.6; DB 10; Length 428;

Best Local Similarity 83.7%; Pred. No. 5.3e-19;

Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCACACAACTAGACCTGGGAAGAATTGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60

Db 50 ATGGCAGACAAACCAGACATCGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 109

QY 61 ACAGAGATGC---AGAGAACACTCTGATGACCACCAAGAGACCACAGACGAGGAGAAGTGG 117


```
Db 110 ACGGAGCGCAGGAGAAACACCCCTGCCGACCAAGAGACCACTTGCAGCAGGAGAAAGCGG 169
QY 118 AGTGAATTTCTCTGA 132
Db 170 AGTGAATTTCTCTAA 184

RESULT 6
US-09-919-580-633
; Sequence 633, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-633

Query Match 67.1%; Score 88.6; DB 10; Length 429;
Best Local Similarity 83.7%; Pred. No. 5.3e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCAGACAACTAGACCTGGAAGAAATTCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 51 ATGGCAGACAAACACAGACATGGGGAAATCGCAGCTTCGATAAGGCCAAGCTGAAGAAA 110
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACCAACAGAGAGAGAGAGTGG 117
Db 111 ACGGAGCGCAGGAGAAAGAACCCCTGCCGACCAAGAGACCACTTGCAGCAGGAGAGCGG 170
QY 118 AGTGAATTTCTCTGA 132
Db 171 AGTGAATTTCTCTAA 185

RESULT 7
US-09-919-580-627
; Sequence 627, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-627

Query Match 67.1%; Score 88.6; DB 10; Length 434;
Best Local Similarity 83.7%; Pred. No. 5.3e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCAGACAACTAGACCTGGAAGAAATTCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 54 ATGGCAGACAAACACAGACATGGGGAAATCGCAGCTTCGATAAGGCCAAGCTGAAGAAA 113
```

```
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACCAACAGAGAGAGAGTGG 117
Db 114 ACGGAGCGCAGGAGAAAGAACCCCTGCCGACCAAGAGACCACTTGCAGCAGGAGAGCGG 173
QY 118 AGTGAATTTCTCTGA 132
Db 174 AGTGAATTTCTCTAA 188

RESULT 8
US-09-919-580-458
; Sequence 458, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-458

Query Match 67.1%; Score 88.6; DB 10; Length 438;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 1 ATGGCAGACAACTAGACCTGGAAGAAATTCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 60 ATGGCAGACAAACACAGACATGGGGAAATCGCAGCTTCGATAAGGCCAAGCTGAAGAAA 119
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAGAGACCAACAGAGAGAGAGTGG 117
Db 120 ACGGAGCGCAGGAGAAAGAACCCCTGCCGACCAAGAGACCACTTGCAGCAGGAGAGCGG 179
QY 118 AGTGAATTTCTCTGA 132
Db 180 AGTGAATTTCTCTAA 194

RESULT 9
US-09-919-580-583
; Sequence 583, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 583
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-583

Query Match 67.1%; Score 88.6; DB 10; Length 438;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
```

QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCGCAAGCTGAAGGCC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 ATGGCAGACAAACACAGACATGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACAGAGATGC---AGAAGACACTCTGTGATGACCAAGAGACACAGAGCAGGAGAAATGG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 ACGGAGACGAGCAGGAGAGACACCCCTGCCACCAAGAGACCAATTCGAGCAGGAGAGCGG 179
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 118 AGTGAATTTCTCTGA 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 AGTGAATTTCTCTAA 194
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 10
US-09-919-580-910
; Sequence 910, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 910
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 438, 439
; OTHER INFORMATION: n - A,T,C or G
US-09-919-580-910

Query Match 67.1%; Score 88.6; DB 10; Length 439;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCGCAAGCTGAAGGCC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 55 ATGGCAGACAAACACAGACATGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 114
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACAGAGATGC---AGAAGACACTCTGTGATGACCAAGAGACACAGAGCAGGAGAAATGG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 115 ACGGAGACGAGCAGGAGAGACACCCCTGCCACCAAGAGACCAATTCGAGCAGGAGAGCGG 174
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 118 AGTGAATTTCTCTGA 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 AGTGAATTTCTCTAA 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-919-580-659
; Sequence 659, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 659
; LENGTH: 443
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-919-580-659
Query Match 67.1%; Score 88.6; DB 10; Length 443;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCGCAAGCTGAAGGCC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 ATGGCAGACAAACACAGACATGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 124
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACAGAGATGC---AGAAGACACTCTGTGATGACCAAGAGACACAGAGCAGGAGAAATGG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 ACGGAGACGAGCAGGAGAGACACCCCTGCCACCAAGAGACCAATTCGAGCAGGAGAGCGG 184
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 118 AGTGAATTTCTCTGA 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 AGTGAATTTCTCTAA 199
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-919-580-727
; Sequence 727, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 727
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-727

Query Match 67.1%; Score 88.6; DB 10; Length 445;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACACTAGACCTGGAGAAATTCAGCTTGGATAGGCGCAAGCTGAAGGCC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 ATGGCAGACAAACACAGACATGGGGAAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAAA 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACAGAGATGC---AGAAGACACTCTGTGATGACCAAGAGACACAGAGCAGGAGAAATGG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 ACGGAGACGAGCAGGAGAGACACCCCTGCCACCAAGAGACCAATTCGAGCAGGAGAGCGG 179
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 118 AGTGAATTTCTCTGA 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 AGTGAATTTCTCTAA 194
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-919-580-891
; Sequence 891, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 891
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 427, 444
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-891

Query Match 67.1%; Score 88.6; DB 10; Length 446;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACAACTAGACCTGGAAGAAATTCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 44 ATGGCAGACAACCAACAGACATGGGGAATTCGCCAGCTTCGATAGGCCAAGCTGAAGAAA 103
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAAAGAGACACACAGAGCAGGAGAAGTGG 117
Db 104 ACGGAGCGCAGGAGAGAAGAACACCTCGCCGACCAAAAGAGACCATTTGAGCAGGAGAAGCGG 163
QY 118 AGTGAATTTCTCTGA 132
Db 164 AGTGAATTTCTCTAA 178

RESULT 14

US-09-918-995-15768
; Sequence 15768, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 1999-01-20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15768
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-15768

Query Match 67.1%; Score 88.6; DB 9; Length 449;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACAACTAGACCTGGAAGAAATTCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 107 ATGGCAGACAACCAACAGACATGGGGAATTCGCCAGCTTCGATAGGCCAAGCTGAAGAAA 166
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAAAGAGACACACAGAGCAGGAGAAGTGG 117
Db 167 ACGGAGCGCAGGAGAGAAGAACACCTCGCCGACCAAAAGAGACCATTTGAGCAGGAGAAGCGG 226
QY 118 AGTGAATTTCTCTGA 132
Db 227 AGTGAATTTCTCTAA 241

RESULT 15

US-09-919-580-553
; Sequence 553, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jjiangchun
; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-553

Query Match 67.1%; Score 88.6; DB 10; Length 451;
Best Local Similarity 83.7%; Pred. No. 5.4e-19;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACAACTAGACCTGGAAGAAATTCGCCAGCTTGGATAAGGCCAAGCTGAAGGCC 60
Db 73 ATGGCAGACAACCAACAGACATGGGGAATTCGCCAGCTTCGATAGGCCAAGCTGAAGAAA 132
QY 61 ACAGAGATGC---AGAAGAACACTCTGATGACCAAAAGAGACACACAGAGCAGGAGAAGTGG 117
Db 133 ACGGAGCGCAGGAGAGAAGAACACCTCGCCGACCAAAAGAGACCATTTGAGCAGGAGAAGCGG 192
QY 118 AGTGAATTTCTCTGA 132
Db 193 AGTGAATTTCTCTAA 207

Search completed: June 2, 2003, 15:41:27
Job time : 107 secs

THIS PAGE BLANK (10PT0)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 2, 2003, 14:12:12 ; Search time 1421 Seconds

(without alignments)

1504.436 Million cell updates/sec

Title: US-09-915-178-1

Perfect score: 132

Sequence: 1 atggcacacaaactagacct.....agtggagtgaatttcctga 132

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	90.4	68.5	210	10	AW240381	AW240381 up31e02.y
c	2	90.2	68.3	299	14	BM855208	BM855208 K-EST0138
c	3	90.2	68.3	475	9	AA525997	AA525997 nt58b07.s
c	4	89.2	67.6	403	9	AI708863	AI708863 as27h03.x
c	5	89.2	67.6	867	12	BG831864	BG831864 602765514
c	6	88.6	67.1	174	14	T27818	T27818 EST17484 Hu

88.6	67.1	182	9	AA316715	AA316715 EST188545
88.6	67.1	207	9	AA312784	AA312784 EST183467
88.6	67.1	213	14	F26549	F26549 HSPD14071 H
88.6	67.1	215	10	AW365977	AW365977 IL0-BT023
88.6	67.1	217	14	D53771	D53771 HOM119F07B
88.6	67.1	227	14	T60895	T60895 YB72F05.r1
88.6	67.1	239	9	AA340512	AA340512 EST45729
88.6	67.1	239	9	AA366141	AA366141 EST77049
88.6	67.1	240	14	T25985	T25985 ATH467 HTCD
88.6	67.1	241	9	AA302528	AA302528 EST15689
88.6	67.1	247	9	AA362157	AA362157 EST17636
88.6	67.1	251	9	AA301772	AA301772 EST14827
88.6	67.1	254	14	N85477	N85477 J3657F Huma
88.6	67.1	257	9	AA354418	AA354418 EST62702
88.6	67.1	257	10	AW800885	AW800885 MR3-UM006
88.6	67.1	258	9	AA339727	AA339727 EST44841
88.6	67.1	258	13	BG994832	BG994832 PM0-HT116
88.6	67.1	260	9	AA365696	AA365696 EST76526
88.6	67.1	260	10	AW998455	AW998455 PM2-BN006
88.6	67.1	264	12	BF378584	BF378584 CM0-UM004
88.6	67.1	270	9	AA304229	AA304229 EST16960
88.6	67.1	271	9	AA354636	AA354636 EST62927
88.6	67.1	273	10	AW797766	AW797766 CM2-UM004
88.6	67.1	273	10	AW800972	AW800972 MR3-UM006
88.6	67.1	274	9	AA308404	AA308404 EST179234
88.6	67.1	274	10	AW797701	AW797701 CM0-UM004
88.6	67.1	276	9	AA365522	AA365522 EST76310
88.6	67.1	276	14	BM855353	BM855353 K-EST0138
88.6	67.1	279	9	AA362030	AA362030 EST71374
88.6	67.1	280	10	AW797700	AW797700 CM0-UM004
88.6	67.1	282	9	AA301934	AA301934 EST15013
88.6	67.1	285	12	BE714668	BE714668 PM2-HT072
88.6	67.1	288	9	AA338821	AA338821 EST43818
88.6	67.1	289	9	AA374209	AA374209 EST86338
88.6	67.1	290	9	AA070672	AA070672 Zm53g03.r
88.6	67.1	290	9	AA380802	AA380802 EST93797
88.6	67.1	292	9	AA304555	AA304555 EST17331
88.6	67.1	293	9	AA301999	AA301999 EST15069
88.6	67.1	295	9	AA384610	AA384610 EST98393

ALIGNMENTS

RESULT 1
AW240381/c
LOCUS
DEFINITION
up31e02.y1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:2655962 5', similar to gb:SS4005 THYMOSIN BETA-10 (HUMAN);, mRNA sequence.
ACCESSION
AW240381
VERSION
AW240381.1 GI:6574067
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 210)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
JOURNAL
Tumor Gene Index
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
MGI:1034110
Seq primer: -40RP from Gibco

210 bp mRNA linear EST 14-DEC-1999
AW240381
up31e02.y1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:2655962 5', similar to gb:SS4005 THYMOSIN BETA-10 (HUMAN);, mRNA sequence.
ACCESSION
AW240381
VERSION
AW240381.1 GI:6574067
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 210)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
JOURNAL
Tumor Gene Index
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
MGI:1034110
Seq primer: -40RP from Gibco

/note="Vector: pAMP10; mRNA made from invasive ovarian

```
/lab_host="DH10B"
```

```
/lab_host="DH10B"
```


	Location/Qualifiers				
source	1..207				
	/organism="Homo sapiens"				
	/db_xref="ATCC (inhost):160014"				
	/db_xref="taxon:9606"				
	/clone_lib="Jurkat T-cells VI"				
	/cell_type="T-lymphocyte"				
	/note=Vector: phluescript SK-				
	XhoI"				
BASE COUNT	67 a	50 c	58 g	31 t	1 others
ORIGIN					
Query Match		67.1%	Score 88.6;	DB 9;	Length 207;
Best Local Similarity		83.7%;	Pred. No. 8.4e-15;		

[illegible]

```

QY 118 ACTGAATTTCTCTGA 132
Db 138 AGTGAATTTCTCTAA 152

RESULT 10
LOCUS AW369977
DEFINITION ILO-BT0234-221099-116-h09 BT0234 Homo sapiens CDNA, mRNA sequence. EST 04-FEB-2000
ACCESSION AW369977
VERSION AW369977.1 GI:6874631
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 215)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-BT0234-
221099-116-h09&t3=1999-10-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 215.
Location/Qualifiers
1..215
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0234"
/dev_stage="Adult"
/note="Organ: breast; Vector: pUC18; Site: 1; SmaI; Site: 2;
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 69 a 53 c 59 g 34 t
ORIGIN
Query Match 67.1%; Score 88.6; DB 10; Length 215;
Best Local Similarity 83.7%; Pred. No. 8.5e-15;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCAGCTTGGATAGGCCAAGCTGAAGGCC 60
Db 37 ATGGCAGACAAACACAGATGGGGAAATCCGAGCTTCGATAGGCCAAGCTGAAGAAA 96
QY 61 ACAGAGATGC---AGAGAACTCTGATGACCAAGAGACACACAGCAGGAGAGATGG 117
Db 97 ACGGAGACGCGAGGAGAGAACACCCCTGCCACCAAGAGACCATTTGAGCAGGAGAGCGG 156
QY 118 AGTGAATTTCTCTGA 132
Db 157 AGTGAATTTCTCTAA 171

RESULT 11
LOCUS D53771
DEFINITION HUM119F07B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens CDNA clone GEN-119F07 5', mRNA sequence.
QY 118 ACTGAATTTCTCTGA 132
Db 138 AGTGAATTTCTCTAA 152

RESULT 10
LOCUS AW369977
DEFINITION ILO-BT0234-221099-116-h09 BT0234 Homo sapiens CDNA, mRNA sequence. EST 04-FEB-2000
ACCESSION AW369977
VERSION AW369977.1 GI:6874631
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 215)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-BT0234-
221099-116-h09&t3=1999-10-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 215.
Location/Qualifiers
1..215
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0234"
/dev_stage="Adult"
/note="Organ: breast; Vector: pUC18; Site: 1; SmaI; Site: 2;
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 69 a 53 c 59 g 34 t
ORIGIN
Query Match 67.1%; Score 88.6; DB 10; Length 215;
Best Local Similarity 83.7%; Pred. No. 8.5e-15;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCAGCTTGGATAGGCCAAGCTGAAGGCC 60
Db 37 ATGGCAGACAAACACAGATGGGGAAATCCGAGCTTCGATAGGCCAAGCTGAAGAAA 96
QY 61 ACAGAGATGC---AGAGAACTCTGATGACCAAGAGACACACAGCAGGAGAGATGG 117
Db 97 ACGGAGACGCGAGGAGAGAACACCCCTGCCACCAAGAGACCATTTGAGCAGGAGAGCGG 156
QY 118 AGTGAATTTCTCTGA 132
Db 157 AGTGAATTTCTCTAA 171

RESULT 11
LOCUS D53771
DEFINITION HUM119F07B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens CDNA clone GEN-119F07 5', mRNA sequence.
QY 118 ACTGAATTTCTCTGA 132
Db 138 AGTGAATTTCTCTAA 152

```

```

ACCESSION D53771
VERSION D53771.1 GI:955668
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 217)
AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi,
A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,
Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Unpublished (1995)
COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers
1..217
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GEN-119F07"
/clone_lib="Clontech human fetal brain polyA+ mRNA (#6535)"
/note="Male adult, hematopoietic tissue, stem cell"
BASE COUNT 71 a 53 c 60 g 33 t
ORIGIN
Query Match 67.1%; Score 88.6; DB 14; Length 217;
Best Local Similarity 83.7%; Pred. No. 8.5e-15;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACACAACTAGACCTGGAGAAATTCGCAGCTTGGATAGGCCAAGCTGAAGGCC 60
Db 53 ATGGCAGACAAACACAGATGGGGAAATCCGAGCTTCGATAGGCCAAGCTGAAGAAA 112
QY 61 ACAGAGATGC---AGAGAACTCTGATGACCAAGAGACACACAGCAGGAGAGATGG 117
Db 113 ACGGAGACGCGAGGAGAGAACACCCCTGCCACCAAGAGACCATTTGAGCAGGAGAGCGG 172
QY 118 AGTGAATTTCTCTGA 132
Db 173 AGTGAATTTCTCTAA 187

RESULT 12
LOCUS T60895
DEFINITION YB72f05.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGE:76737 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);, mRNA
sequence.
ACCESSION T60895
VERSION T60895.1 GI:663932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 227)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
QY 118 ACTGAATTTCTCTGA 132
Db 157 AGTGAATTTCTCTAA 171

RESULT 11
LOCUS D53771
DEFINITION HUM119F07B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens CDNA clone GEN-119F07 5', mRNA sequence.
QY 118 ACTGAATTTCTCTGA 132
Db 138 AGTGAATTTCTCTAA 152

```


Tel: 82-053-950-5382
Fax: 82-053-955-5327
Email: usohn@bh.kyungpook.ac.kr
EST is putatively homologous to thymosin beta-10 (PIR, A27266) in human with 100% (35 amino acids overlapped) identity.

```

FEATURES
  source      Location/Qualifiers
              1..240
              seq primer; map reverse; or primer.

```

```
/db_xref="taxon:9606"  
/clone_lib="HTCDL1"  
/lab_host="XL1-Blue"
```

BASE COUNT	74 a	53 c	68 g	45 t
PRESCRIPT (carotene)				

Query Match 67.1%; Score 88.6; DB 14; Length 240;
Best Local Similarity 83.7%;
Pred. No. 8.9e-15;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

1 ATGGGCACACAACTAGCACTGGGAAGAAATGCCAGCTTGGTATAGGCCCAAGCTGAAGCC 60
 |||||
 85 ATGGCAGACAAACCGACATCGGGGGAATCGCCAGCTTCGATAGGCCCAAGCTGAAGAA 144
 |||||
 61 ACAGAGATGC---AAGAAGACACTCTGTATGCCAAAGAGACCACAGCAGGAGGAATGG 117
 |||||
 145 ACGGAGACCGGAGGAAGAAACCCCTGCCGACCAAGAGACCATTTAGCAGGAGGAAGCGG 204
 |||||

```
Db      205 AGTGAATTCCTAA 219
|||||
Search completed: June  2, 2003, 15:01:46
Job time : 1426 secs
```

```

Search completed: June 2, 2003, 15:01:46
Job time : 1426 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 13:25:22 ; Search time 1074 Seconds
(without alignments)
3576.881 Million cell updates/sec

Title: US-09-915-178-1
Perfect score: 132
Sequence: 1 atggcacacaaactagacct.....agtggagtgaattctctga 132

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	132	100.0	147	6	AX399230	Sequence
2	132	100.0	147	6	AX399232	Sequence
3	132	100.0	147	6	AX399234	Sequence
4	132	100.0	170536	9	HS18K17	Sequence
c 5	90.4	68.5	154265	2	AC127915	Homo sapi
6	90.4	68.5	158286	2	AC111338	Rattus no
c 7	90.4	68.5	194568	2	AC129614	Rattus no
8	88.8	67.3	183583	2	AC131114	Rattus no
9	88.8	67.3	186744	2	AC131561	Mus muscu
10	88.8	67.3	336512	2	AC126029	Rattus no
11	88.6	67.1	174	11	G06175	Mus muscu
12	88.6	67.1	243	6	AX381579	G06175 human STS W
13	88.6	67.1	353	6	AX381286	Sequence
14	88.6	67.1	395	6	AX381269	Sequence
15	88.6	67.1	400	9	HUMTHMBX	Sequence
16	88.6	67.1	428	6	AX381565	Human thymo
17	88.6	67.1	429	6	AX381695	Sequence
18	88.6	67.1	434	6	AX381689	Sequence
19	88.6	67.1	438	6	AX381520	Sequence
20	88.6	67.1	438	6	AX381645	Sequence
21	88.6	67.1	439	6	AX381972	Sequence
22	88.6	67.1	439	9	HUMTHYB10	Sequence
23	88.6	67.1	443	6	AX381721	Human thymo
24	88.6	67.1	445	6	AX381789	Sequence
25	88.6	67.1	446	6	AX381953	Sequence
26	88.6	67.1	451	6	AX381615	Sequence
27	88.6	67.1	452	6	AX381410	Sequence
28	88.6	67.1	453	6	AX381336	Sequence
29	88.6	67.1	453	6	AX410373	Sequence
30	88.6	67.1	453	9	S54005	thymosin be
31	88.6	67.1	455	6	AX381335	Sequence
32	88.6	67.1	456	6	AX381281	Sequence
33	88.6	67.1	465	6	AX381118	Sequence
34	88.6	67.1	491	6	AX107107	Sequence
35	88.6	67.1	500	9	BC016731	Homo sapi
36	88.6	67.1	511	9	BC016025	Homo sapi
37	88.6	67.1	517	6	AX381936	Sequence
38	88.6	67.1	693	6	AX381860	Sequence
39	88	66.7	430	6	AX119979	Sequence
c 40	88	66.7	107467	9	HS95883	Sequence
41	85.6	64.8	460	6	ARI44218	Homo sapien
42	85.6	64.8	460	6	ARI76405	Sequence
43	85.6	64.8	460	6	AX365690	Sequence
44	85.6	64.8	155930	2	AC109106	Rattus no
45	85.4	64.7	465	4	AF506973	Equus cab

ALIGNMENTS

RESULT 1	AX399230	AX399230	Sequence 3 from Patent WO0190155.	147 bp	DNA	linear	PAT 28-MAY-2002
LOCUS	AX399230	Sequence 3 from Patent WO0190155.					
DEFINITION	AX399230	Sequence 3 from Patent WO0190155.					
ACCESSION	AX399230	Sequence 3 from Patent WO0190155.					
VERSION	AX399230.1	GI:21261549					
KEYWORDS	human.						
SOURCE	human.						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1						
AUTHORS	Spytek, K.A., Majumder, K., Tchernev, V.T., Mishra, V., Padigar, M., Spaderna, S.K., Shenoy, S., Rastelli, L., Li, L., Taupier, R.J. and Gangolli, E.						

TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0190155-A 3 29-NOV-2001;
Curagen Corporation (US)

FEATURES
source
1..147
Location/Qualifiers

BASE COUNT 56 a 30 c 41 g 20 t
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 60
|||||
Db 6 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 65
|||||
QY 61 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGAGTGGAGT 120
|||||
Db 66 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGTGGAGT 125
|||||
QY 121 GAAATTTCTCTGA 132
|||||
Db 126 GAAATTTCTCTGA 137
|||||

RESULT 2
AX399232
LOCUS Sequence 5 from Patent WO0190155. 147 bp DNA linear PAT 28-MAY-2002
DEFINITION
ACCESSION AX399232
VERSION AX399232.1 GI:21261550
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE
AUTHORS Spytek,K.A., Majumder,K., Tchernev,V.T., Mishra,V., Padigar,M.,
Spaderna,S.K., Shenoy,S., Rastelli,L., Li,L., Taupier,R.J. and
Gangolli,E.

TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0190155-A 5 29-NOV-2001;
Curagen Corporation (US)

FEATURES
source
1..147
Location/Qualifiers

BASE COUNT 56 a 30 c 41 g 20 t
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 60
|||||
Db 6 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 65
|||||
QY 61 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGTGGAGT 120
|||||
Db 66 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGAGTGGAGT 125
|||||
QY 121 GAAATTTCTCTGA 132
|||||
Db 126 GAAATTTCTCTGA 137
|||||

RESULT 3
AX399234
LOCUS Sequence. 7 from Patent WO0190155. 147 bp DNA linear PAT 03-JUN-2002
DEFINITION

ACCESSION AX399234
VERSION AX399234.1 GI:21261551
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0190155-A 7 29-NOV-2001;
Curagen Corporation (US)

FEATURES
source
1..147
Location/Qualifiers

BASE COUNT 56 a 30 c 41 g 20 t
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 60
|||||
Db 6 ATGGCACAAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 65
|||||
QY 61 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGTGGAGT 120
|||||
Db 66 ACAGAGATGCAGAGAACACTCTGTGATGACCAAGAGACACAGAGAGAGTGGAGT 125
|||||
QY 121 GAAATTTCTCTGA 132
|||||
Db 126 GAAATTTCTCTGA 137
|||||

RESULT 4
AX399234
LOCUS Homo sapiens chromosome 9 BAC RP11-518K17, complete sequence. 170536 bp DNA linear PRI 04-FEB-2002
DEFINITION
ACCESSION AL513423 AL353720
VERSION AL513423.2 GI:18539155
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

REFERENCE
AUTHORS Plumb,B.

TITLE Direct Submission
JOURNAL Submitted (09-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

REFERENCE
AUTHORS 2 (bases 1 to 170536)
Scharfe,M., Conrad,A., Hornischer,K., Loehner,T.H., Thies,S. and
Bloeker,H.

TITLE Direct Submission
JOURNAL Submitted (07-FEB-2001) GBF, Dept. of Genome Analysis, Mascheroder
Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
On Feb 5, 2002 this sequence version replaced gi:12718191.

COMMENT All annotations in this database entry are developed by
computational tools. It is therefore not explicitly noted in the
feature lines that evidence is not experimental.
Mapping was performed at The Sanger Centre
(cf. <http://www.sanger.ac.uk/HGP/Chr9>)
Mapping information is available via
<http://webase.sanger.ac.uk/cgi-bin/display?db=acedb9&rep=518K17>

Center: GBF, Braunschweig
Center code: GBF

Web site: <http://genome.gbf.de/>


```

satellite      12927..12937
               /note="CG repeat"
               complement(12989..13135)
exon            /note="GRAIL, score = 90%, comment = excellent
               MZEF prediction, score = 0.97"
exon            /note="GRAIL, score = 90%, comment = excellent
               complement(13577..13664)
repeat_region  /note="GRAIL, score = 66%, comment = good"
               complement(14120..14818)
               /note="82% identity: matches 399..1100 of consensus"
               /rpt_family="L1"
exon            14916..15001
               /note="GRAIL, score = 91%, comment = excellent shadow"
               complement(15145..15418)
repeat_region  /note="81% identity: matches 312..587 of consensus"
               /rpt_family="L1"
repeat_region  15147..15418
               /note="84% identity: matches 11..281 of consensus"
               /rpt_family="ALU"
satellite      15421..15435
               /note="AAAT repeat"
exon            complement(15473..15595)

Query Match      100.0%; Score 132; DB 9; Length 170536;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACAAACTAGACCTGGGAAGAAATTCAGCTGATGAAGCCAGCTGAAGGCC 60
Db 111695 ATGGCACAAACTAGACCTGGGAAGAAATTCAGCTGATGAAGCCAGCTGAAGGCC 111754

QY 61 ACAGAGATGACAGAGACACTGTGATGACCAAGACACACAGAGAGAGTGGAGT 120
Db 111755 ACAGAGATGACAGAGACACTGTGATGACCAAGACACACAGAGAGAGTGGAGT 111814

QY 121 GAAATTCCTGA 132
Db 111815 GAAATTCCTGA 111826

RESULT 5
AC127915/c
LOCUS          154265 bp DNA linear HTG 19-JUL-2002
DEFINITION    Rattus norvegicus clone CH230-236P17, *** SEQUENCING IN PROGRESS
               Rattus norvegicus
AC127915
VERSION       AC127915.1 GI:21908439
KEYWORDS      HTGS PHASE1
SOURCE        Rattus norvegicus
ORGANISM      Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1 (bases 1 to 154265)
AUTHORS       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
               Alsbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
               Barbieri,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
               Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
               BuhaY,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
               Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
               Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
               Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
               Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
               Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
               Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,H.J.,
               Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
               Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
               Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
               Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
               Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
               Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
               Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
               Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
               Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

```

```

Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,J., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mahoney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shookhtari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-More,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleciyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 154265)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAAM
Center clone name: CH230-236P17
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115969 bases at least Q40
Consensus quality: 121810 bases at least Q30
Consensus quality: 127454 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
* 1
* 1224: contig of 1224 bp in length
* 1225
* 1235: gap of unknown length
* 1325
* 2862: contig of 1538 bp in length
* 2863
* 2962: gap of unknown length
* 2963
* 4039: contig of 1077 bp in length
* 4040
* 4139: gap of unknown length
* 4140
* 5220: contig of 1081 bp in length
* 5320: gap of unknown length
* 5321
* 6756: contig of 1436 bp in length
* 6757
* 6857: gap of unknown length
* 8352: contig of 1496 bp in length
* 8353
* 8452: gap of unknown length
* 8453
* 10449: contig of 1997 bp in length
* 10450
* 10549: gap of unknown length
* 12609: contig of 2060 bp in length
* 12610
* 12709: gap of unknown length
* 12710
* 14051: contig of 1342 bp in length
* 14052
* 14151: gap of unknown length
* 14152
* 15296: contig of 1145 bp in length

```


Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratochvil, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louise, H.,
 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
 Miner, G., Miner, Z., Mitchell, J., Mohabbat, K., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, S.,
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okuwonu, G.,
 Oreguene, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojebokan, I., Roife, M., Ruiz, S., Savary, G.,
 Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I.,
 Sodergren, E., Soraker, F., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

JOURNAL

REFERENCE
 2 (bases 1 to 158286)

AUTHORS

JOURNAL

REFERENCE
 3 (bases 1 to 158286)

AUTHORS

JOURNAL

COMMENT

Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 158286)

REFERENCE

AUTHORS

JOURNAL

COMMENT

On Jul 12, 2002 this sequence version replaced gi:18701102.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Center project name: GMBI

Center clone name: CH230-240A17

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 103746 bases at least Q40

Consensus quality: 108208 bases at least Q30

Consensus quality: 111376 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 68 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

be preserved.

1 1244: contig of 1244 bp in length

1345 1344: gap of unknown length

1345 2875: contig of 1531 bp in length

2876 2975: gap of unknown length

2976 4032: contig of 1057 bp in length

4033 4132: gap of unknown length

4133 5396: contig of 1264 bp in length

5397 5496: gap of unknown length

5497 6970: contig of 1473 bp in length

6970 7070: gap of unknown length

7070 8370: contig of 1301 bp in length

8371 8470: gap of unknown length

8471 9974: contig of 1504 bp in length

9975 10075: gap of unknown length

10076 12069: contig of 1895 bp in length

12070 13421: contig of 1352 bp in length

13422 13521: gap of unknown length

13523 14649: contig of 1128 bp in length

14650 16351: contig of 1602 bp in length

16352 17940: contig of 1489 bp in length

17941 19287: contig of 1247 bp in length

19288 20768: contig of 1381 bp in length

20769 22395: contig of 1527 bp in length

22396 23636: contig of 1141 bp in length

23637 25287: contig of 1551 bp in length

25288 26570: contig of 1183 bp in length

26571 28078: contig of 1408 bp in length

28079 29573: contig of 1395 bp in length

29574 31324: contig of 1651 bp in length

31325 32599: contig of 1175 bp in length

32600 34751: contig of 2052 bp in length

34752 36020: contig of 1169 bp in length

36021 37941: contig of 1821 bp in length

37942 39444: contig of 1103 bp in length

39445 41216: contig of 1971 bp in length

41217 43354: contig of 2039 bp in length

43355 45504: contig of 2050 bp in length

45505 47071: contig of 1466 bp in length

47072 48306: contig of 1136 bp in length

48307 49467: contig of 1061 bp in length

49468 51036: contig of 1469 bp in length

51037 53712: contig of 2576 bp in length

53713 55162: contig of 1350 bp in length

55163 57096: contig of 1834 bp in length

57097 58767: contig of 1571 bp in length

58768 60411: contig of 1544 bp in length

60412 62118: contig of 1607 bp in length

62119 63943: contig of 1725 bp in length

63944 66201: contig of 2158 bp in length

66202 68867: contig of 2566 bp in length

68868 68967: gap of unknown length

```

* 68968 71412: contig of 2445 bp in length
* 71413 71512: gap of unknown length
* 71513 74169: contig of 2657 bp in length
* 74170 74269: gap of unknown length
* 74270 78013: contig of 3744 bp in length
* 78014 78113: gap of unknown length
* 78114 80476: contig of 2363 bp in length
* 80477 80576: gap of unknown length
* 80577 83565: contig of 2989 bp in length
* 83566 83666: gap of unknown length
* 83667 85949: contig of 2284 bp in length
* 85950 86049: gap of unknown length
* 86050 89230: contig of 3201 bp in length
* 89231 89350: gap of unknown length
* 89351 91850: contig of 2500 bp in length
* 91851 91950: gap of unknown length
* 91951 93870: contig of 1920 bp in length
* 93871 93970: gap of unknown length
* 93971 96867: contig of 2897 bp in length
* 96868 96967: gap of unknown length
* 96968 99706: contig of 2739 bp in length
* 99707 99806: gap of unknown length
* 99807 101862: contig of 2056 bp in length

Query Match 68.5%; Score 90.4; DB 2; Length 158286;
Best Local Similarity 80.3%; Pred. No. 6.6e-15;
Matches 106; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 ATGGCACACAACTAGACCTGGAAGAAATGCCAGCTTGGATAGGCAAGCCAGTGAAGGCC 60
DB 76104 ATGGCAGACAGCAGCAGCATCGGAGAAATGCCAGCTTGGATAGGCAAGTCAAGTGAAGAAA 76163

QY 61 ACAGAGATGCGAGAGAACACTCTGATGACCAAGAGACACAGACAGAGAGAGAGTGGAGT 120
DB 76164 ACTGACACATAGACAGACACACCTGATGACCAAGAGACCATTTGAACAGAGAAAGAGAGT 76223

QY 121 GAAATTTCTCGA 132
DB 76224 GAAATCTCTTAA 76235

RESULT 7
AC129614/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-69C5, *** SEQUENCING IN PROGRESS ***,
75 unordered pieces.
ACCESSION
AC129614
VERSION
AC129614.2 GI:22091212
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 194568)
Muzny, D., Marle, J., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Chen, X., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., D'Souza, L.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Dalla, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

```

```

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Li, Z., Liu, J.,
Lorensuhera, L., Louised, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
Miner, G., Minja, E., Montanayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G.,
Olarunpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A.,
Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E.,
Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, J., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, R., Ruiz, S., Sanders, W., Savary, G., Scherer, S.,
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D.,
Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yan, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R.,
Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 194568)
Worley, K.C.
Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 194568)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 2, 2002 this sequence version replaced gi:22024297.

-----
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----
Project Information
Center project name: KBYZ
Center clone name: CH230-69C5
-----
Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 132737 bases at least Q40
Consensus quality: 140036 bases at least Q30
Consensus quality: 146272 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1169: contig of 1169 bp in length
* 1170 1269: gap of unknown length

```

```

1270 2371: contig of 1102 bp in length
1272 2471: gap of unknown length
2372 4053: contig of 1582 bp in length
2472 4153: gap of unknown length
4054 5159: contig of 1016 bp in length
4154 5259: gap of unknown length
5159 6322: contig of 1363 bp in length
5270 6732: gap of unknown length
6323 8018: contig of 1286 bp in length
6733 8118: gap of unknown length
8019 9402: contig of 1284 bp in length
8119 9502: gap of unknown length
9403 11015: contig of 1513 bp in length
9503 11116: gap of unknown length
11016 12367: contig of 1252 bp in length
12368 12468: gap of unknown length
12469 14348: gap of unknown length
14349 15769: contig of 1421 bp in length
15770 15869: gap of unknown length
15870 17323: contig of 1454 bp in length
17324 17423: gap of unknown length
17424 18642: contig of 1219 bp in length
18643 18742: gap of unknown length
18743 20469: contig of 1727 bp in length
20470 20569: gap of unknown length
20570 22186: contig of 1617 bp in length
22187 22286: gap of unknown length
22287 23424: contig of 1138 bp in length
23425 23524: gap of unknown length
23525 24789: contig of 1265 bp in length
24790 24889: gap of unknown length
24890 25910: contig of 1021 bp in length
25911 26010: gap of unknown length
26011 27562: contig of 1552 bp in length
27563 27662: gap of unknown length
27663 29775: contig of 2113 bp in length
29776 29875: gap of unknown length
29876 31070: contig of 1195 bp in length
31071 31170: gap of unknown length
31171 32563: contig of 1393 bp in length
32564 32663: gap of unknown length
32664 34201: contig of 1538 bp in length
34202 34301: gap of unknown length
34302 35650: contig of 1349 bp in length
35651 35750: gap of unknown length
35751 37335: contig of 1585 bp in length
37336 37435: gap of unknown length
37436 38621: contig of 1186 bp in length
38622 38721: gap of unknown length
38722 40075: contig of 1354 bp in length
40076 40175: gap of unknown length
40176 41658: contig of 1483 bp in length
41659 42864: contig of 1106 bp in length
42865 42964: gap of unknown length
42965 44914: contig of 1950 bp in length
44915 45014: gap of unknown length
45015 46766: contig of 1752 bp in length
46767 46866: gap of unknown length
46867 48110: contig of 1244 bp in length
48111 48210: gap of unknown length
48211 49776: contig of 1566 bp in length
49777 49876: gap of unknown length
49877 51418: contig of 1542 bp in length
51419 51518: gap of unknown length
51519 53046: contig of 1528 bp in length
53047 53146: gap of unknown length
53147 54638: contig of 1492 bp in length
54639 54738: gap of unknown length
54739 56322: contig of 1584 bp in length
56323 56422: gap of unknown length
56423 59603: contig of 3181 bp in length

59604 59703: gap of unknown length
59704 61605: contig of 1902 bp in length
61606 61705: gap of unknown length
61706 63104: contig of 1399 bp in length
63105 63204: gap of unknown length
63205 64728: contig of 1524 bp in length
64729 64828: gap of unknown length
64829 67139: contig of 2311 bp in length
67140 67239: gap of unknown length
67240 70126: contig of 2887 bp in length
70127 70226: gap of unknown length
70227 71406: contig of 1180 bp in length
71407 71506: gap of unknown length
71507 73165: contig of 1659 bp in length
73166 73265: gap of unknown length
73266 74712: contig of 1447 bp in length
74713 74812: gap of unknown length
74813 75932: contig of 1120 bp in length
75933 76032: gap of unknown length
76033 77652: contig of 1620 bp in length
77653 77752: gap of unknown length
77753 79810: contig of 2058 bp in length
79811 79910: gap of unknown length
79911 82473: contig of 2563 bp in length

Query Match 68.5%; Score 90.4; DB 2; Length 194568;
Best Local Similarity 80.3%; Pred. No. 6.7e-15;
Matches 106; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 ATGGGCACACAACTAGACCTGGAGAAATTCGACCTGGATGATGAGCCCAAGCTGAAGGCC 60
DB 74206 ATGGGCAGACAAAGCCAGACATGGGAGAAATTCGACCTGGATGATGAGCCCAAGCTGAAGAAA 74147
QY 61 ACAGAGATGCAGAGAAACACTCTGATGACCAAGAGACACAGACAGAGAGAGTGGAGT 120
DB 74146 ACTGAGACATAGAGACACACCTGATGACCAAGAGACACCTGATGACAGAGAGAGAGTGGAGT 74087
QY 121 GAAATTCCTGA 132
DB 74086 GAAATTCCTGA 74075

RESULT 8
AC131114 183583 bp DNA linear HTG 17-AUG-2002
LOCUS Mus musculus chromosome UNK clone RP24-212G16, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
ACCESSION AC131114.1 GI:22267918
VERSION AC131114
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 183583)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 183583)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 183583)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
```

```

Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M.BB0212G16
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182274 bases at least Q40
Consensus quality: 182633 bases at least Q30
Consensus quality: 182875 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 15774: contig of 15774 bp in length
* 15775 15874: gap of unknown length
* 15875 90246: contig of 74372 bp in length
* 90247 90346: gap of unknown length
* 90347 183583: contig of 93237 bp in length.
FEATURES             location/Qualifiers
source               1..183583
                    /organism="Mus musculus"
                    /db_xref="taxon:10090"
                    /chromosome="UNK"
                    /clone="RP24-212G16"
misc_feature         1..15774
                    /note="assembly_name:Contig13"
misc_feature         15875..90246
                    /note="assembly_name:Contig14"
misc_feature         90347..183583
                    /note="assembly_name:Contig15"
BASE COUNT          47220 a 44434 c 45182 g 46547 t 200 others
ORIGIN
Query Match          67.3%; Score 88.8; DB 2; Length 183583;
Best Local Similarity 79.5%; Pred. No. 1.9e-14;
Matches 105; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 ATGGCACACAACTGACCTGGAGAAATTCGACGCTGGATAGGCGCAAGCTCAAGGCC 60
Db 68234 ATGGCAGACACCGGACATAGGGGAAATTCGACGCTTCATTAAGGCGCAAGTGAAGAAA 68293
QY 61 ACAGAGATGCAGAGAACACTCTGATGACCAAGAGACACAGAGAGAGAGTGGAGT 120
Db 68294 ACCGAGCGCAGAGACACCTCGCGACCAAGAGACCACTGACACAGGAAGAGAGT 68353
QY 121 GAAATTTCTGTA 132
Db 68354 GAAATCTCTTAA 68365

RESULT 9
AC131561
LOCUS               186744 bp DNA linear HTG 24-AUG-2002
DEFINITION          Rattus norvegicus clone CH230-8p16, *** SEQUENCING IN PROGRESS ***,
72 unordered pieces.
ACCESSION           AC131561
VERSION             AC131561.1 GI:22474831
KEYWORDS            HTG; HTGS_PHASE1.
SOURCE              Norway rat.
ORGANISM            Rattus norvegicus
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                    Rattus.
REFERENCE            1 (bases 1 to 186744)

```

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anquiano, D., Anvaleschi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Burch, P., Burrell, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Carter, K., Cavazos, I., Cesar, H., Chen, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, J., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregorogis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Rulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhera, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Mallory, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Naif, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindest, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savory, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajd, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleczek, R., Wooten, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GCXJ

Center clone name: CH230-8p16

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 121943 bases at least Q40

Consensus quality: 127700 bases at least Q30

Consensus quality: 132440 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: this is a 'working draft' sequence. It currently
 * consists of 72 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1005: contig of 1005 bp in length
1105: gap of unknown length	
1106	2111: contig of 1006 bp in length
2112	2211: gap of unknown length
2212	3354: contig of 1143 bp in length
3355	3454: gap of unknown length
3455	4788: contig of 1334 bp in length
4789	4888: gap of unknown length
4889	5897: contig of 1009 bp in length
5898	5997: gap of unknown length
5998	7400: contig of 1403 bp in length
7401	7500: gap of unknown length
7501	8726: contig of 1226 bp in length
8727	8826: gap of unknown length
8827	9949: contig of 1123 bp in length
9950	10049: gap of unknown length
10050	11329: contig of 1280 bp in length
11330	11429: gap of unknown length
11430	12704: contig of 1275 bp in length
12705	12804: gap of unknown length
12805	13815: contig of 1011 bp in length
13816	13915: gap of unknown length
13916	15323: contig of 1408 bp in length
15324	15423: gap of unknown length
15424	16881: contig of 1458 bp in length
16882	16981: gap of unknown length
16982	18274: contig of 1293 bp in length
18275	18374: gap of unknown length
18375	19573: contig of 1199 bp in length
19574	19673: gap of unknown length
19674	21311: contig of 1638 bp in length
21312	21411: gap of unknown length
21412	23073: contig of 1662 bp in length
23074	23173: gap of unknown length
23174	24519: contig of 1346 bp in length
24520	24619: gap of unknown length
24620	25815: contig of 1196 bp in length
25816	25915: gap of unknown length
25916	27080: contig of 1165 bp in length
27081	27180: gap of unknown length
27181	28739: contig of 1559 bp in length
28740	28839: gap of unknown length
28840	30131: contig of 1292 bp in length
30132	30231: gap of unknown length
30232	31491: contig of 1260 bp in length
31492	31591: gap of unknown length
31592	33073: contig of 1482 bp in length
33074	33173: gap of unknown length
33174	34885: contig of 1712 bp in length
34886	34985: gap of unknown length
34988	36797: contig of 1812 bp in length
36798	36897: gap of unknown length
36898	37941: contig of 1044 bp in length
37942	38041: gap of unknown length
38042	39171: contig of 1130 bp in length
39172	39271: gap of unknown length
39272	42341: contig of 3070 bp in length
42342	42441: gap of unknown length
42442	43915: contig of 1474 bp in length
43916	44015: gap of unknown length
44016	45006: contig of 1491 bp in length
45007	45606: gap of unknown length
45607	47263: contig of 1657 bp in length
47264	47363: gap of unknown length

*	47364	49962:	contig	of 2599	bp in length
*	49963	50062:	gap of	unknown length	
*	50063	50162:	contig	of 1320	bp in length
*	51482:	51582:	gap of	unknown length	
*	51483	51482:	contig	of 2740	bp in length
*	54322:	54322:	gap of	unknown length	
*	54323	54322:	contig	of 1973	bp in length
*	56296	56395:	gap of	unknown length	
*	56396	56395:	contig	of 2236	bp in length
*	58632	58731:	gap of	unknown length	
*	58732	61246:	contig	of 2515	bp in length
*	61247	61346:	gap of	unknown length	
*	61347	63640:	contig	of 2294	bp in length
*	63641	63740:	gap of	unknown length	
*	63741	65684:	contig	of 1944	bp in length
*	65685	65784:	gap of	unknown length	
*	65785	68593:	contig	of 2811	bp in length
*	68594	68693:	gap of	unknown length	
*	68696	70643:	contig	of 1948	bp in length
*	70644	70743:	gap of	unknown length	
*	70744	72535:	contig	of 1792	bp in length
*	72536	72633:	gap of	unknown length	
*	72636	75700:	contig	of 3071	bp in length
*	75707	75806:	gap of	unknown length	
*	75807	78876:	contig	of 3070	bp in length
*	78877	78976:	gap of	unknown length	
*	78977	80826:	contig	of 1850	bp in length
*	80827	80926:	gap of	unknown length	
*	80927	82962:	contig	of 2036	bp in length
*	82963	83062:	gap of	unknown length	
*	83063	84768:	contig	of 1706	bp in length
*	84769	84868:	gap of	unknown length	
*	84869	87876:	contig	of 3008	bp in length
*	87877	87976:	gap of	unknown length	
*	87977	90977:	contig	of 3001	bp in length
*	90978	91077:	gap of	unknown length	
*	91078	94179:	contig	of 3102	bp in length
*	94180	94278:	gap of	unknown length	
*	94280	96823:	contig	of 2550	bp in length
*	96830	96929:	gap of	unknown length	
*	96930	99586:	contig	of 2657	bp in length
*	99587	99686:	gap of	unknown length	

Query Match 67.3%; Score 88.8; DB 2; Length 186744;
Best Local Similarity 79.5%; Pred. NO. 1.9e-14;

Qy	1	ATGCCACAAACTAGACCTTGGAGAAATTCGCAGCTTGGATAGGCCAAGCTGAAGGCC	50
Db	101164	ATGCAAAACAGCCGAGCTGGGGAAATCCGCCAGTTCAATAGGCCAAGCTGAAGAAA	101223
Qy	61	ACAGAGATGCAGAGAACAACACTCTGTATGACCAAGAGACCCAGAGCAGAGAGTGGAGT	120
Db	101224	ACCGAAACGAGAGAGAACACCCCTCCGACCAAGAGACCATTGAACAGGAAAGAGAGT	101283
Qy	121	GAATTTTCCTGA	132
Db	101284	GAATCTCCTAA	101295

RESULT 10

AC126029	336512 bp	DNA linear	HTG 04-JUL-2002
LOCUS			
DEFINITION	Mus musculus chromosome UNK clone RP23-389K5, WORKING DRAFT SEQUENCE, 14 unordered pieces.		

AC126029

VERSION AC126029.1 'GI:21672227

KEYWORDS HTG; HTGS_PH

SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CACGATGCTTTTAAAGAAATGG
Primer B: GAAATTCACCTCCGCTTCTCC
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from T27818 -- dbEST.
Location/Qualifiers
1. 174

/organism="Homo sapiens"
/db_xref="taxon:9606"

/map="808_E_1; 849_E_2; 931_E_8; (789-796)_C_5;
20..169
20..142

primer_bind
primer_bind
primer_bind
BASE COUNT 62 a 37 c 52 g 23 t
ORIGIN

Query Match
Best Local Similarity 67.1%; Score 88.6; DB 11; Length 174;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
Db 39 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
QY 61 ACAGAGATGC---AGAAGAACACTCTGTATGACCAAGAGACACAGAGCAGGAGAGTGG 98
Db 99 ACGGAGACGAGAGAGAGAACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 117
QY 118 AGTGAATTTCTCTGA 132
Db 159 AGTGAATTTCTCTAA 173

RESULT 12
AX381579
LOCUS
DEFINITION
Sequence 517 from Patent W00212280. 243 bp DNA linear PAT 18-MAR-2002
ACCESSION
AX381579
VERSION
AX381579.1 GI:19576398
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Pyle, R.A., Xu, J., and Secrist, H.
Compositions and methods for the therapy and diagnosis of colon cancer

REFERENCE
AUTHORS
TITLE

Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0212280-A 517 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..243
BASE COUNT 73 a 64 c 68 g 37 t 1 others
ORIGIN
Query Match
Best Local Similarity 67.1%; Score 88.6; DB 6; Length 243;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
Db 63 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
QY 61 ACAGAGATGC---AGAAGAACACTCTGTATGACCAAGAGACACACAGAGCAGGAGAGTGG 122
Db 123 ACGGAGACGAGAGAGAGAACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 117
QY 118 AGTGAATTTCTCTGA 132
Db 183 AGTGAATTTCTCTAA 197

RESULT 13
AX381286
LOCUS
DEFINITION
Sequence 224 from Patent W00212280. 353 bp DNA linear PAT 18-MAR-2002
ACCESSION
AX381286
VERSION
AX381286.1 GI:19576105
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Pyle, R.A., Xu, J., and Secrist, H.
Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0212280-A 224 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..353
BASE COUNT 97 a 103 c 98 g 55 t
ORIGIN
Query Match
Best Local Similarity 67.1%; Score 88.6; DB 6; Length 353;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
Db 37 ATGGCACAACCTAGACCTGGAGAAATTCGCCAGCTTGGATAGGCCCAAGCTGAAGGCC 60
QY 61 ACAGAGATGC---AGAAGAACACTCTGTATGACCAAGAGACACACAGAGCAGGAGAGTGG 96
Db 97 ACGGAGACGAGAGAGAGAACACCTCGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 117
QY 118 AGTGAATTTCTCTGA 132
Db 157 AGTGAATTTCTCTAA 171

RESULT 14
AX381269
LOCUS
DEFINITION
Sequence 207 from Patent W00212280. 395 bp DNA linear PAT 18-MAR-2002
ACCESSION
AX381269
VERSION
AX381269.1 GI:19576088
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Pyle, R.A., Xu, J., and Secrist, H.
Compositions and methods for the therapy and diagnosis of colon cancer

REFERENCE
AUTHORS
TITLE

Compositions and methods for the therapy and diagnosis of colon cancer

KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1
Pyle,R.A., Xu,J. and Secrist,H.
JOURNAL Compositions and methods for the therapy and diagnosis of colon
PATENT: WO 0212280-A 207 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
source
1. .395
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 105 a 113 c 115 g 62 t
ORIGIN

Query Match 67.1%; Score 88.6; DB 6; Length 395;
Best Local Similarity 83.7%; Pred. No. 1.4e-14;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCAGACAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 60
DB 72 ATGGCAGACAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGAAA 131
QY 61 ACAGAGATGC---AGAAGAACAACCTCTGATGACCAAGAGACCAAGAGAGAGAGAGTGG 117
DB 132 ACGGAGACGACGAGAGAAACACCTTGGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 191
QY 118 AGTGAATTTCTCTGA 132
DB 192 AGTGAATTTCTCTAA 206

RESULT 15

HUMTHMBX
LOCUS Human thymosin beta 10 mRNA, complete cds. PRI 03-AUG-1993
DEFINITION
ACCESSION M92381
VERSION M92381.1 GI:339660
KEYWORDS thymosin beta 10.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Hall,A.K., Hempstead,J. and Morgan,J.I.
TITLE Thymosin beta 10 levels in developing human brain and its
JOURNAL regulation by retinoic acid in the HTB-10 neuroblastoma
MEDLINE Brain Res. Mol. Brain Res. 8 (2), 129-135 (1990)
PUBMED 90384336
PUBMED 2169566

FEATURES

source
1. .400
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
36. .152
/codon_start=1
/product="thymosin beta 10"
/protein_id="AAC41691.1"
/db_xref="GI:339661"
/translation="MGEIASFDKAKLKKTETQKNTLPTKETIEQKRSEIS"
BASE COUNT 118 a 106 c 105 g 71 t
ORIGIN

Query Match 67.1%; Score 88.6; DB 9; Length 400;
Best Local Similarity 83.7%; Pred. No. 1.4e-14;
Matches 113; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
QY 1 ATGGCAGACAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGGCC 60
DB 18 ATGGCAGACAACTAGACCTGGAGAAATTCAGCTTGGATAGGCCAAGCTGAAGAAA 77

QY 61 ACAGAGATGC---AGAAGAACAACCTCTGATGACCAAGAGACCAAGAGAGAGAGTGG 117
DB 78 ACGGAGACGACGAGAGAAACACCTTGGCCGACCAAGAGACCATTTGAGCAGGAGAGCGG 137
QY 118 AGTGAATTTCTCTGA 132
DB 138 AGTGAATTTCTCTAA 152
Search completed: June 2, 2003, 14:36:33
Job time : 1077 secs

THIS PAGE BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:34:51 ; Search time 44 Seconds
(without alignments)
98.923 Million cell updates/sec

Title: US-09-915-178-2

Perfect score: 213

Sequence: 1 MAHKLDLEIASLDKAKLKA.....QKNTLMKTETQEKWSEIS 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	135.5	63.6	49	9 US-09-842-758-51	Sequence 51, Appl
2	130.5	61.3	43	9 US-09-772-445A-7	Sequence 7, Appl
3	116.5	54.7	41	9 US-09-772-445A-11	Sequence 11, Appl
4	112.5	52.8	41	9 US-09-772-445A-5	Sequence 5, Appl
5	110.5	51.9	41	9 US-09-772-445A-6	Sequence 6, Appl
6	106.5	50.0	41	9 US-09-772-445A-8	Sequence 8, Appl
7	104.5	49.1	40	9 US-09-772-445A-15	Sequence 15, Appl
8	99.5	46.7	40	9 US-09-772-445A-12	Sequence 12, Appl
9	99.5	46.7	42	9 US-09-772-445A-9	Sequence 9, Appl
10	97.5	45.8	43	9 US-09-772-445A-4	Sequence 4, Appl
11	97.5	45.8	44	9 US-10-171-311-220	Sequence 220, Appl
12	97.5	45.8	50	9 US-09-842-758-50	Sequence 50, Appl
13	97.5	45.8	56	9 US-09-925-299-1252	Sequence 1252, Appl
14	97.5	45.8	56	9 US-09-842-758-49	Sequence 49, Appl
15	97.5	45.8	56	10 US-09-925-299-1252	Sequence 1252, Appl
16	96.5	45.3	43	9 US-09-772-445A-10	Sequence 10, Appl
17	95.5	44.8	45	9 US-09-874-736-2	Sequence 2, Appl
18	95.5	44.8	45	9 US-09-842-758-52	Sequence 52, Appl
19	93.5	43.9	40	9 US-09-772-445A-14	Sequence 14, Appl

20	91.5	43.0	45	9 US-09-842-758-48	Sequence 48, Appl
21	90.5	42.5	43	9 US-09-772-445A-3	Sequence 3, Appl
22	90.5	42.5	44	9 US-09-772-445A-13	Sequence 13, Appl
23	89.5	42.0	38	10 US-09-879-666-6	Sequence 6, Appl
24	87.5	41.1	43	9 US-09-772-445A-2	Sequence 2, Appl
25	69	32.4	69	9 US-09-842-758-10	Sequence 10, Appl
26	64	30.0	120	9 US-09-746-783-190	Sequence 190, Appl
27	61	28.6	517	10 US-09-815-242-4970	Sequence 4970, Appl
28	61	28.6	518	10 US-09-815-242-10891	Sequence 10891, Appl
29	54	25.4	289	10 US-09-764-864-911	Sequence 911, Appl
30	54	25.4	388	10 US-09-764-864-931	Sequence 931, Appl
31	54	25.4	739	9 US-09-874-162A-8	Sequence 5, Appl
32	54	25.4	776	9 US-09-874-162A-5	Sequence 8, Appl
33	52	24.4	122	9 US-09-897-645-1	Sequence 1, Appl
34	52	24.4	122	10 US-09-815-242-13472	Sequence 13472, Appl
35	52	24.4	122	10 US-09-815-242-13649	Sequence 13649, Appl
36	52	24.4	418	9 US-09-893-519A-10	Sequence 10, Appl
37	52	24.4	1530	9 US-10-118-513A-6	Sequence 6, Appl
38	52	24.4	2266	9 US-10-118-513A-14	Sequence 14, Appl
39	51.5	24.2	174	10 US-09-864-761-48360	Sequence 48360, Appl
40	51.5	24.2	533	10 US-09-815-242-11612	Sequence 11612, Appl
41	51	23.9	488	9 US-10-033-297-141	Sequence 141, Appl
42	51	23.9	488	9 US-09-940-244-141	Sequence 141, Appl
43	51	23.9	888	9 US-10-231-035-3	Sequence 3, Appl
44	51	23.9	1207	10 US-09-927-112-2	Sequence 2, Appl
45	50.5	23.7	458	9 US-09-965-529-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-842-758-51

Sequence 51, Application US/09842758

Publication No. US20030083244A1

GENERAL INFORMATION:

APPLICANT: Vernet, Corine A. M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Gerlach, Valerie

APPLICANT: Shimkets, Richard A

APPLICANT: Malyanaka, Uriel M

APPLICANT: Boldog, Ferenc L

APPLICANT: Zerkhusen, Bryan D

APPLICANT: Spytek, Kimberly A

APPLICANT: Majumder, Kumud

APPLICANT: Tchernev, Velizar T

APPLICANT: Padigaru, Muralidhara

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E

APPLICANT: Gangolli, Esha A

APPLICANT: Smithson, Glennnda

APPLICANT: Rastelli, Luca

APPLICANT: MacDougall, John R

APPLICANT: Taupier, Raymond J

APPLICANT: Grosse, William M

APPLICANT: Edward, Szekeres S

APPLICANT: Alsobrook II, John P

TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Sa

FILE REFERENCE: 15966-783

CURRENT APPLICATION NUMBER: US/09/842,758

CURRENT FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/200,158

PRIOR FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: 60/200,613

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,780

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/201,006

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/201,007

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/201,236

PRIOR FILING DATE: 2000-05-01

```

; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-758-51

Query Match 63.6%; Score 135.5; DB 9; Length 49;
Best Local Similarity 75.0%; Pred. No. 4e-10;
Matches 33; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 MAHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEKWSEIS 43
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 6 MADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQKRSEIS 49

RESULT 2
US-09-772-445A-7
; Sequence 7, Application US/09772445A
; Publication No. US20030060405A1
; GENERAL INFORMATION:
; APPLICANT: Kleinman, Hynda K.
; APPLICANT: Goldstein, Allan L.
; APPLICANT: Malinda, Katherine M.
; APPLICANT: Sosne, Gabriel
; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
; FILE REFERENCE: 08830-056001
; CURRENT APPLICATION NUMBER: US/09/772,445A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/17282
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/094,690
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-772-445A-7

Query Match 61.3%; Score 130.5; DB 9; Length 43;
Best Local Similarity 74.4%; Pred. No. 1.4e-09;
Matches 32; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 2 AHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEKWSEIS 43
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 1 ADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQKRSEIS 43

RESULT 3
US-09-772-445A-11
; Sequence 11, Application US/09772445A
; Publication No. US20030060405A1
; GENERAL INFORMATION:
; APPLICANT: Kleinman, Hynda K.
; APPLICANT: Goldstein, Allan L.
; APPLICANT: Malinda, Katherine M.
; APPLICANT: Sosne, Gabriel
; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
; FILE REFERENCE: 08830-056001
; CURRENT APPLICATION NUMBER: US/09/772,445A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/17282
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/094,690
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Balaenoptera acutorostrata
US-09-772-445A-11

Query Match 54.7%; Score 116.5; DB 9; Length 41;
Best Local Similarity 73.7%; Pred. No. 7.5e-08;
Matches 28; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 AHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEK 38
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 1 ADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQEK 38

RESULT 4
US-09-772-445A-5
; Sequence 5, Application US/09772445A
; Publication No. US20030060405A1
; GENERAL INFORMATION:
; APPLICANT: Kleinman, Hynda K.
; APPLICANT: Goldstein, Allan L.
; APPLICANT: Malinda, Katherine M.
; APPLICANT: Sosne, Gabriel
; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
; FILE REFERENCE: 08830-056001
; CURRENT APPLICATION NUMBER: US/09/772,445A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/17282
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/094,690
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-772-445A-5

Query Match 52.8%; Score 112.5; DB 9; Length 41;
Best Local Similarity 73.7%; Pred. No. 2.3e-07;
Matches 28; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 2 AHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEK 38
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 1 ADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQEK 38

RESULT 5
US-09-772-445A-6
; Sequence 6, Application US/09772445A
; Publication No. US20030060405A1
; GENERAL INFORMATION:
; APPLICANT: Kleinman, Hynda K.
; APPLICANT: Goldstein, Allan L.
; APPLICANT: Malinda, Katherine M.
; APPLICANT: Sosne, Gabriel
; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
; FILE REFERENCE: 08830-056001
; CURRENT APPLICATION NUMBER: US/09/772,445A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/17282
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/094,690
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-772-445A-6

Query Match 61.3%; Score 130.5; DB 9; Length 43;
Best Local Similarity 74.4%; Pred. No. 1.4e-09;
Matches 32; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 2 AHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEKWSEIS 43
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 1 ADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQKRSEIS 43

RESULT 6
US-09-772-445A-11
; Sequence 11, Application US/09772445A
; Publication No. US20030060405A1
; GENERAL INFORMATION:
; APPLICANT: Kleinman, Hynda K.
; APPLICANT: Goldstein, Allan L.
; APPLICANT: Malinda, Katherine M.
; APPLICANT: Sosne, Gabriel
; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
; FILE REFERENCE: 08830-056001
; CURRENT APPLICATION NUMBER: US/09/772,445A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/17282
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/094,690
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Balaenoptera acutorostrata
US-09-772-445A-11

Query Match 54.7%; Score 116.5; DB 9; Length 41;
Best Local Similarity 73.7%; Pred. No. 7.5e-08;
Matches 28; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 AHKLDLEEIASLDRKAKLKATEMQ-KNTLMTKETTEQEK 38
    ||| : ||| ||||| ||| ||| ||| ||| ||| |||
DB 1 ADKPDGMEIASFDRAKLKKTETQEKNTLPTKETIEQEK 38
```

; APPLICANT: Sosne, Gabriel
 ; TITLE OF INVENTION: THYMOSIN BETA 4 PROMOTES WOUND REPAIR
 ; FILE REFERENCE: 08830-056001
 ; CURRENT APPLICATION NUMBER: US/09/772,445A
 ; CURRENT FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/17282
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: US 60/094,690

APPLICANT:	Venett, Corine A. M.
APPLICANT:	Fernandes, Elma R.
APPLICANT:	Gerlach, Valerie
APPLICANT:	Shimkets, Richard A
APPLICANT:	Malyankar, Uriel M
APPLICANT:	Boldog, Ferenc L
APPLICANT:	Zerhusen, Bryan D
APPLICANT:	Spytek, Kimberly A
APPLICANT:	Majumder, Kumud
APPLICANT:	Thernev, Velizar T
APPLICANT:	Padigaru, Muralidhara
APPLICANT:	Patturajan, Meera
APPLICANT:	Burgess, Catherine E
APPLICANT:	Gangolli, Esna A
APPLICANT:	Smithson, Glennnda
APPLICANT:	Rastelli, Luca
APPLICANT:	MacDougall, John R
APPLICANT:	Taupier, Raymond J
APPLICANT:	Grosse, William M

; ORGANISM: HOMO
US-09-925-299-1252

; ORGANISM: HOMO
US-09-925-299-1252

us-09-915-178-2.rapb

	Query Match	45.88;	Score: 97.5;	DB 10;	Length 56;
	Best Local Similarity	59.08;	Pred. No. 2.5e-05;		
	Matches	23;	Conservative	4;	Mismatches 11; Indels 1; Gaps 1;
Qy	1	MAHKLDLEETASDIAKAKL	KAT	EMQ-KNTLMTKETTEQEK	38
db	13	MSDKPDMAETKFDKSLK	AKTFTQ	ENKPLPSPKETIEQEK	51

Search completed:: May 30, 2003, 10:43:49
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:31:35 ; Search time 26 Seconds
(without alignments)
48.661 Million cell updates/sec

Title: US-09-915-178-2
Perfect score: 213
Sequence: 1 MAHKDLLEFIASLDKAKLKA.....QKNTLMTKETTEQKRWSEIS 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	45.8	44	3	US-09-058-489-27
2	95.5	44.8	45	1	US-08-664-856A-2
3	95.5	44.8	45	1	US-08-801-796-2
4	95.5	44.8	45	2	US-08-931-877-2
5	95.5	44.8	45	2	US-08-664-857A-2
6	95.5	44.8	45	3	US-09-069-484-2
7	95.5	44.8	45	4	US-09-135-599-2
8	95.5	44.8	45	4	US-09-369-744-2
9	88.5	41.5	44	3	US-09-058-489-28
10	54.5	25.6	245	1	US-08-317-707-2
11	54.5	25.6	245	2	US-08-514-921-2
12	54.5	25.6	245	2	US-08-514-921-4
13	54.5	25.6	245	2	US-08-514-921-6
14	54.5	25.6	245	2	US-08-514-921-8
15	53.5	25.1	210	4	US-08-858-207A-269
16	52.5	24.6	272	4	US-09-029-213B-27
17	52	24.4	122	3	US-08-987-144-2
18	52	24.4	131	4	US-08-765-012A-6
19	52	24.4	131	4	US-08-765-012A-7
20	52	24.4	131	4	US-08-765-012A-8
21	52	24.4	131	4	US-08-765-012A-9
22	52	24.4	131	4	US-08-765-012A-10
23	52	24.4	222	3	US-09-066-408-6
24	51	23.9	488	2	US-08-823-516-141
25	50	23.5	133	1	US-08-234-812-2
26	50	23.5	133	2	US-08-663-809-2
27	50	23.5	287	3	US-08-937-271-2

28	50	23.5	428	1	US-07-882-790-4	Sequence 4, Appli
29	50	23.5	613	2	US-08-915-207-2	Sequence 2, Appli
30	50	23.5	613	2	US-08-915-207-4	Sequence 4, Appli
31	50	23.5	613	4	US-09-238-555-2	Sequence 2, Appli
32	50	23.5	613	4	US-09-238-555-4	Sequence 4, Appli
33	50	23.5	1312	4	US-09-343-882-29	Sequence 29, Appli
34	49	23.0	139	4	US-08-559-896B-4	Sequence 4, Appli
35	49	23.0	451	4	US-09-134-001C-4461	Sequence 4461, Ap
36	49	23.0	652	4	US-08-559-896B-2	Sequence 2, Appli
37	49	23.0	1240	3	US-08-930-996A-4	Sequence 4, Appli
38	49	23.0	1388	4	US-09-572-191-2	Sequence 2, Appli
39	49	23.0	1388	4	US-09-723-262-2	Sequence 2, Appli
40	49	23.0	1388	4	US-09-723-219-2	Sequence 2, Appli
41	48.5	22.8	239	3	US-09-479-309-2	Sequence 2, Appli
42	48	22.5	46	1	US-08-214-770-11	Sequence 11, Appli
43	48	22.5	46	4	US-08-734-607B-20	Sequence 20, Appli
44	48	22.5	46	5	PCT-US95-02885-11	Sequence 11, Appli
45	48	22.5	223	3	US-09-066-408-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-058-489-27
; Sequence 27, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WHI97-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human
US-09-058-489-27

Query Match	45.8%	Score	97.5	DB 3	Length	44			
Best Local Similarity	59.0%	Pred. No.	4.2e-06						
Matches	23	Conservative	4	Mismatches	11	Indels	1	Gaps	1
QY	1	MAHKDLLEFIASLDKAKLKA	EMQ-KNTLMTKETTEQEK	38					
Db	1	MSDRPDMAIEKFKDKLKKTKETQKKNPLPSKETIQEK	39						

RESULT 2
US-08-664-856A-2
; Sequence 2, Application US/08664856A
; Patent No. 5663071
; GENERAL INFORMATION:
; APPLICANT: BRUCE R. ZETTER AND LERE BAO
; TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
; TITLE OF INVENTION: PROTEIN AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,856A
FILING DATE: 17 JUN 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-664-856A-2

Query Match 44.8%; Score 95.5; DB 1; Length 45;
Best Local Similarity 53.8%; Pred. No. 7.9e-06;
Matches 21; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
QY 1 MAHKLDLEETASLDKAKLKATEM-QKNTLMTKETEQEK 38
Db 1 MSKDPOLSEVETFDKSKLKKNTTEKNTLPSKETIQEK 39

RESULT 3
US-08-801-796-2
Sequence 2, Application US/08801796
Patent No. 5721337
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,796
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-801-796-2

Query Match 44.8%; Score 95.5; DB 1; Length 45;
Best Local Similarity 53.8%; Pred. No. 7.9e-06;
Matches 21; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATEM-QKNTLMTKETEQEK 38
Db 1 MSKDPOLSEVETFDKSKLKKNTTEKNTLPSKETIQEK 39

RESULT 4
US-08-931-877-2
Sequence 2, Application US/08931877
Patent No. 5831033
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,877
FILING DATE: 17-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE: 14-FEB-1997
APPLICATION NUMBER: 08/664,856
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

; Sequence 2, Application US/09069484

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,599
FILING DATE: 18 AUG 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/664,857
FILING DATE: 17 JUN 1996
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46403
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-135-599-2

Query Match 44.8%; Score 95.5; DB 4; Length 45;
Best Local Similarity 53.8%; Pred. No. 7.9e-06;
Matches 21; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MAHKDLDEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
| : | | | : | : | | | | : | | | : | | | : | | |
Db 1 MSDKPDLSVEVTFDKSKLKKTKNTTEKNTLPKSTIQEKK 39

RESULT 8
US-09-369-744-2
Sequence 2, Application US/09369744
Patent No. 6300479
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
TITLE OF INVENTION: PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/369,744
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-369-744-2

Query Match 44.8%; Score 95.5; DB 4; Length 45;
Best Local Similarity 53.8%; Pred. No. 7.9e-06;
Matches 21; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MAHKDLDEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
| : | | | : | : | | | | : | | | : | | | : | | |
Db 1 MSDKPDLSVEVTFDKSKLKKTKNTTEKNTLPKSTIQEKK 39

RESULT 9
US-09-058-489-28
Sequence 28, Application US/09058489
Patent No. 6103886
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
FILE REFERENCE: WHI97-08pa
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 44
TYPE: PRT
ORGANISM: Human
US-09-058-489-28

Query Match 41.5%; Score 88.5; DB 3; Length 44;
Best Local Similarity 53.8%; Pred. No. 6.1e-05;
Matches 21; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MAHKDLDEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
| : | : | | : | | | | | : | | | : | | | : | | |
Db 1 MSDKPGMAIEKFKDKSKLKKTKETQKNPLSKKETIQEQR 39

RESULT 10
US-08-317-707-2
Sequence 2, Application US/08317707
Patent No. 5470737
GENERAL INFORMATION:
APPLICANT: Weinshilbom, Richard M.
APPLICANT: Honchel, Ronald
APPLICANT: Otterness, Diane M.
APPLICANT: Wood, Thomas C.
APPLICANT: AKSOY, Ibrahim A.
APPLICANT: Szumianski, Carol L.
APPLICANT: Wieben, Eric D.
TITLE OF INVENTION: Stably-Transformed Cells Expressing
TITLE OF INVENTION: Human Thiopurine Methyltransferase

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,707
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,348
FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.103-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-707-2

Query Match 25.6%; Score 54.5; DB 1; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATMOKNTLMTKETTEQKW 39
||| : ||:|||| :|| :|||
Db 7 SLDIEYSDEVQKNQVLTLEEW-QDKW 33

RESULT 11
US-08-514-921-2
Sequence 2, Application US/08514921
Patent No. 5856095
GENERAL INFORMATION:
APPLICANT: Evans, William E.
TITLE OF INVENTION: Identification of Two No. 5856095el Mutant
TITLE OF INVENTION: Alleles of Human Thiopurine S-Methyltransferase, and
TITLE OF INVENTION: Diagnostic Uses Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,921
FILING DATE: 14-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0656.0580000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-921-4

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATMOKNTLMTKETTEQKW 39
||| : ||:|||| :|| :|||
Db 7 SLDIEYSDEVQKNQVLTLEEW-QDKW 33

REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0656.0580000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-921-2

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATMOKNTLMTKETTEQKW 39
||| : ||:|||| :|| :|||
Db 7 SLDIEYSDEVQKNQVLTLEEW-QDKW 33

RESULT 12
US-08-514-921-4
Sequence 4, Application US/08514921
Patent No. 5856095
GENERAL INFORMATION:
APPLICANT: Evans, William E.
TITLE OF INVENTION: Identification of Two No. 5856095el Mutant
TITLE OF INVENTION: Alleles of Human Thiopurine S-Methyltransferase, and
TITLE OF INVENTION: Diagnostic Uses Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,921
FILING DATE: 14-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0656.0580000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-921-4

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATMOKNTLMTKETTEQKW 39
||| : ||:|||| :|| :|||
Db 7 SLDIEYSDEVQKNQVLTLEEW-QDKW 33

```
RESULT 13
US-08-514-921-6
; Sequence 6, Application US/08514921
; Patent No. 5856095
; GENERAL INFORMATION:
; APPLICANT: Evans, William E.
; TITLE OF INVENTION: Identification of Two No. 5856095el Mutant
; TITLE OF INVENTION: Alleles of Human Thiopurine S-Methyltransferase, and
; TITLE OF INVENTION: Diagnostic Uses Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,921
; FILING DATE: 14-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleshner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 0656.0580000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-514-921-6

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATKEMOKNTLMTKETTEQEKW 39
Db 7 SLDIEEYSDTEVQKNQVLTLEW-QDKW 33

RESULT 14
US-08-514-921-8
; Sequence 6, Application US/08514921
; Patent No. 5856095
; GENERAL INFORMATION:
; APPLICANT: Evans, William E.
; TITLE OF INVENTION: Identification of Two No. 5856095el Mutant
; TITLE OF INVENTION: Alleles of Human Thiopurine S-Methyltransferase, and
; TITLE OF INVENTION: Diagnostic Uses Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,921
; FILING DATE: 14-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleshner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 0656.0580000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-514-921-8

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATKEMOKNTLMTKETTEQEKW 39
Db 7 SLDIEEYSDTEVQKNQVLTLEW-QDKW 33

RESULT 15
US-08-858-207A-269
; Sequence 269, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,921
; FILING DATE: 14-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleshner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 0656.0580000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-514-921-8

Query Match 25.6%; Score 54.5; DB 2; Length 245;
Best Local Similarity 46.4%; Pred. No. 11;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 12 SLDKAKLKATKEMOKNTLMTKETTEQEKW 39
Db 7 SLDIEEYSDTEVQKNQVLTLEW-QDKW 33

RESULT 15
US-08-858-207A-269
; Sequence 269, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```

Query Match      25.1% ; Score 53.5 ; DB 4 ; Length 210 ;
Best Local Similarity 30.0% ; Pred. No. 12 ;
Matches 15 ; Conservative 9 ; Mismatches 7 ; Indels 19 ; Gaps 2 ;

QY      5 LDLEETASLDKAKLKATEMQ-----NTLMTKTEEQEKWSE 41
||||: || |||: : ||| : |||
DB      90 LDDKLTPLD-----TELEETNYIKSIIISLDVLTSEKGEAKHWSE 133

```

Search completed: May 30, 2003, 10:36:05
Job time : 27 secs

THIS PAGE BLANK (1 of 1)


```

AC Q9D9W8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:1700026G08, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006383; BAB24560.1; -
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
SQ SEQUENCE 38 AA; 4418 MW; 42BCD4A0E30ED5AA CRC64;

Query Match 51.4%; Score 109.5; DB 11; Length 38;
Best Local Similarity 75.0%; Pred. No. 5,1e-06;
Matches 27; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 9 EIASLDRKLKATEMQ-KNTLMTKETTEQKWEIS 43
| | | | | | | | | | | | | | | | | | | | | |
DB 3 EIASFHAKLKKTKETQKNTLPTRETIEQKRSEIS 38
| | | | | | | | | | | | | | | | | | | | | |

RESULT 3
Q76538 ID Q76538 PRELIMINARY; PRT; 41 AA.
AC Q76538;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thymosin beta.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99328904; PubMed=10398804;
RA Pancer Z., Rast J.P., Davidson E.H.;
RT "Origins of immunity: transcription factors and homologues of effector
RT genes of the vertebrate immune system expressed in sea urchin
RT coelomocytes.";
RL Immunogenetics 49:773-786(1999).
DR EMBL; AF076515; AAC26833.1; -

```

```

DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; UNKNOWN1.
SQ SEQUENCE 41 AA; 4598 MW; B4A7838CE16915B8 CRC64;

Query Match 49.5%; Score 105.5; DB 5; Length 41;
Best Local Similarity 61.5%; Pred. No. 1,6e-05;
Matches 24; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
| | | | | | | | | | | | | | | | | | | | | |
DB 1 MADKPDVSAVSSFDKTKLKTKETTEKNTLPTKETIEQEK 39
| | | | | | | | | | | | | | | | | | | | | |

RESULT 4
Q9GUA6 ID Q9GUA6 PRELIMINARY; PRT; 42 AA.
AC Q9GUA6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-thymosin.
OS Sycon raphanus.
OC Eukaryota; Metazoa; Porifera; Calcarea; Leucosoleniida;
OC Sycettidae.
OX NCBI_TaxID=56443;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20496958; PubMed=11040289;
RA Manuel M., Kruse M., Muller W.E., Le Parco Y.;
RT "The comparison of beta-thymosin homologues Among Metazoa Supports an
RT Arthropod-Nematode Clade.";
RL J. Mol. Evol. 51:378-381(2000).
DR EMBL; AF155935; AAG08963.1; -
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR SMART; SM00152; THY; 1.
SQ SEQUENCE 42 AA; 4637 MW; BD9BF6EA8CE16C12 CRC64;

Query Match 49.1%; Score 104.5; DB 5; Length 42;
Best Local Similarity 61.5%; Pred. No. 2,2e-05;
Matches 24; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATE-MQKNTLMTKETTEQEK 38
| | | | | | | | | | | | | | | | | | | | | |
DB 1 MGDKPDVSEVAFDKTKLKTKETAEKKNPLPTKETIEQEK 39
| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
Q9GUA5 ID Q9GUA5 PRELIMINARY; PRT; 42 AA.
AC Q9GUA5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-thymosin.
OS Sycon raphanus.
OC Eukaryota; Metazoa; Porifera; Calcarea; Leucosoleniida;
OC Sycettidae.
OX NCBI_TaxID=56443;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20496958; PubMed=11040289;
RA Manuel M., Kruse M., Muller W.E., Le Parco Y.;
RT "The comparison of beta-thymosin homologues Among Metazoa Supports an
RT Arthropod-Nematode Clade.";
RL J. Mol. Evol. 51:378-381(2000).
DR EMBL; AF156177; AAG08964.1; -
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR SMART; SM00152; THY; 1.
SQ SEQUENCE 42 AA; 4706 MW; BD9BF75A8CE16C12 CRC64;

```



```

AC Q9D2B9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1700129115RIK protein.
GN 1700129115RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018998; BAB31502.1; -
DR MGD; MGI:1925728; 1700129115RIK.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
SQ SEQUENCE 45 AA; 5296 MW; 654354C0C7E2D556 CRC64;

Query Match 42.0%; Score 89.5; DB 11; Length 45;
Best Local Similarity 53.8%; Pred. NO. 0.0014;
Matches 21; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MAHKDLERIASDKAKLKATEMO-KNTLMTKETTEQEK 38
DB 1 MGRDPPDLSVEVFEKSKLAKTTVEKNTLPSKETIEQEK 39
- - - - - 11:11111 - - - - - 1111111111
- - - - - 1 MGRDPPDLSVEVFEKSKLAKTTVEKNTLPSKETIEQEK 39

RESULT 13
Q9UE55 PRELIMINARY; PRT; 37 AA.
AC Q9UE55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interferon-inducible mRNA (CDNA 6-26) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=85024867; PubMed=6548414;
Friedman R.L., Manly S.P., McMahon M., Kerr I.M., Stark G.R.;
RT "transcriptional and posttranscriptional regulation of the interferon-
induced gene expression in human cells.";
RL Cell 38:745-755(1984).
[2]
AC Q9UE55;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1700129115RIK protein.
GN 1700129115RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018998; BAB31502.1; -
DR MGD; MGI:1925728; 1700129115RIK.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
SQ SEQUENCE 45 AA; 5296 MW; 654354C0C7E2D556 CRC64;

```

(constant concentration) and

THIS PAGE BLANK (1-3PTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:31:31 ; Search time 21 Seconds
(without alignments)
84.928 Million cell updates/sec

Title: US-09-915-178-2

Perfect score: 213

Sequence: 1 MAHKLDLEIASLDAKLKA.....OKNTLMKTETQEKWSEIS 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130.5	61.3	43	1	TYB0_HUMAN
2	112.5	52.8	41	1	TYB9_BOVIN
3	110.5	51.9	41	1	TYB9_PIG
4	108.5	50.9	42	1	TYB8_CYPCA
5	106.5	50.0	41	1	TYBA_ONCMY
6	106.5	50.0	43	1	TYB0_TORMA
7	99.5	46.7	42	1	TYBB_ONCMY
8	97.5	45.8	50	1	TYB4_MOUSE
9	96.5	45.3	43	1	TYBB_LATJA
10	95.5	44.8	43	1	TYB4_RABIT
11	95.5	44.8	43	1	TYB4_XENLA
12	95.5	44.8	44	1	TYB_BRARE
13	92.5	43.4	43	1	TYB4_HUMAN
14	90.5	42.5	44	1	TYBN_COTJA
15	88.5	40.6	44	1	TYBN_HUMAN
16	85.5	40.1	43	1	TYB_GILMI
17	83.5	39.2	43	1	TYBY_HUMAN
18	70.5	33.1	45	1	TYBA_CYPCA
19	63	29.6	543	1	HMA1_ARATH
20	60	28.2	2869	1	RBP1_PLAVB
21	58	27.2	418	1	HEM1_ECOLI
22	57	26.8	467	1	P60_LISIN
23	56.5	26.5	161	1	Y0UD_CAEEL
24	56	26.3	327	1	ODBB_BACSU
25	56	26.3	3396	1	PGCV_HUMAN
26	55.5	26.1	757	1	PPE2_MOUSE
27	54.5	25.6	245	1	TPMT_MOUSE
28	54.5	25.6	432	1	ACDB_HUMAN
29	54.5	25.6	1433	1	REST_CHICK
30	54.5	25.6	4473	1	PLE1_CRIGR
31	54.5	25.6	4687	1	PLB1_RAT
32	54	25.4	742	1	KM55_YEAST
33	54	25.4	2663	1	CENE_HUMAN

RESULT 1

ID	TYB0_HUMAN	STANDARD;	PRT;	43 AA.
AC	P13472;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Thymosin beta-10.			
GN	TMSB10 OR PTMB10 OR THYB10.			
OS	Homo sapiens (Human).			
'OS	Rattus norvegicus (Rat), and			
'OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606, 10116, 9796;			
[1]	SEQUENCE FROM N.A.			
RP	SPECIES-Human; TISSUE-Kidney;			
RC	MEDLINE-8209071; PubMed-3365256;			
RA	McCreary V., Kartha S., Bell G.I., Toback F.G.;			
RT	"Sequence of a human kidney cDNA encoding thymosin beta 10.";			
RL	Biochem. Biophys. Res. Commun. 152:862-866(1988).			
[2]	SEQUENCE FROM N.A.			
RP	SPECIES-Human; TISSUE-Brain;			
RC	MEDLINE-90384336; PubMed-2169566;			
RA	Hall A.K., Hempstead J., Morgan J.I.;			
RT	"Thymosin beta 10 levels in developing human brain and its regulation			
RT	by retinoic acid in the HTB-10 neuroblastoma.";			
RL	Brain Res. Mol. Brain Res. 8:129-135(1990).			
[3]	SEQUENCE FROM N.A.			
RP	SPECIES-Human;			
RC	MEDLINE-93146649; PubMed-8425765;			
RA	Weterman M.A., van Muijen G.N., Ruiter D.J., Bloemers H.P.;			
RT	"Thymosin beta-10 expression in melanoma cell lines and melanocytic			
RT	lesions: a new progression marker for human cutaneous melanoma.";			
RL	Int. J. Cancer 53:278-284(1993).			
[4]	SEQUENCE FROM N.A.			
RP	SPECIES-Human;			
RA	Condon M.R., Hall A.K.;			
RT	Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.			
[5]	SEQUENCE FROM N.A.			
RP	SPECIES-Human; TISSUE-Brain, and Uterus;			
RC	Strausberg R.;			
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
[6]	SEQUENCE FROM N.A.			
RP	SPECIES-Rat;			
RC	MEDLINE-87269651; PubMed-3606131;			
RA	Goodall G.J., Horecker B.L.;			
RT	"Molecular cloning of the cDNA for rat spleen thymosin beta 10 and			
RT	the deduced amino acid sequence.";			
RL	Arch. Biochem. Biophys. 256:402-405(1987).			

34	53.5	25.1	178	1	SIGY_BACSU
35	53.5	25.1	816	1	NEL2_MOUSE
36	53.5	25.1	1005	1	Y321_MYCPN
37	53.5	25.1	4684	1	PLE1_HUMAN
38	53	24.9	220	1	Y231_RICPR
39	53	24.9	863	1	GLND_HAEN
40	53	24.9	1107	1	POL2_RRVS
41	52.5	24.6	205	1	AIAG_RAT
42	52.5	24.6	509	1	RA18_MOUSE
43	52	24.4	120	1	ACPS_STRPN
44	52	24.4	222	1	CAS2_BOVIN
45	52	24.4	398	1	SUCC_BRUME

ALIGNMENTS

P94370	bacillus su
O61220	mus musculus
P75327	mycoplasma
Q15149	homo sapien
Q9ZDU3	rickettsia
P43919	haemophilus
P36324	raspberry r
P02764	rattus norv
Q9QXK2	mus musculus
Q9F755	streptococc
P02663	bos taurus
Q8YJ66	brucella me

```

RN RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE-91108433; PubMed-1988550;
RA LUGO D.I., Chen S.C., Hall A.K., Ziai R., Hempstead J.L., Morgan J.I.;
RT "Developmental regulation of beta-thymosins in the rat central
RL nervous system.";
RN J. Neurochem. 56:457-461(1991).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat;
RX MEDLINE-92078211; PubMed-1744129;
RA Lin S.C., Morrison-Bogorad M.;
RT "Cloning and characterization of a testis-specific thymosin beta 10
RN cDNA. Expression in post-meiotic male germ cells.";
RN J. Biol. Chem. 266:23347-23353(1991).
RN [9]
RP SEQUENCE.
RC SPECIES-Horse; TISSUE-Spleen;
RA Hoerger S., Gallert B., Kellerman J., Voelter W.;
RT "Isolation and structural identification of beta-thymosins from equine
RN tissue: development of a specific ELISA against thymosin beta-10
RL (beta-10)";
RN (In) Schneider C.H., Eberles A.N. (eds.);
RA Peptides 1992, pp.749-750, Escom Science Publishers, Leiden (1993).
CC -1- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DEVELOPMENTAL STAGE: FOUND TO DECREASE DRAMATICALLY AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20259; AAA36744.1; -
DR EMBL; M92381; AAC41691.1; ALT_INIT.
DR EMBL; M54005; AAB25225.1; -
DR EMBL; M92383; AAA36746.1; ALT_INIT.
DR EMBL; BC016025; AAH16025.1; -
DR EMBL; BC016731; AAH16731.1; -
DR EMBL; M17698; AAA42244.1; -
DR EMBL; M58404; AAA42247.1; -
DR EMBL; M58405; AAA42248.1; -
DR PIR; A27704; A27704.
DR PIR; A27266; A27266.
DR PIR; A43757; A43757.
DR HSSP; P21752; LHJ0.
DR Genew; HGNC:11879; TMSB10.
DR MIM; 188399; -
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 43 AA; 4894 MW; 54852726E86B570 CRC64;
Query Match 61.3%; Score 130.5; DB 1; Length 43;
Best Local Similarity 74.4%; Pred. No. 7.5e-09;
Matches 32; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 2 AHKLDLEETASLQKAKLQTEMQ-KNTLMTKETTQEKWSEIS 43
DB 1 ADKPDGMEIASFDKAKLKKETQKNTLPTKETIEQEKRSSEIS 43

```

```

RESULT 2
ID TYB9_BOVIN STANDARD; PRT; 41 AA.
AC P21752; Q9GMC3;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-9 (Thymosin beta-10) [Contains: Thymosin beta-8].
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE-Thymus;
RX MEDLINE-82197566; PubMed-6952223;
RA Hannappel E., Davoust S., Horecker B.L.;
RT "Thymosins beta 8 and beta 9: two new peptides isolated from calf
RN thymus homologous to thymosin beta 4.";
RA Proc. Natl. Acad. Sci. U.S.A. 79:1708-1711(1982).
RN [2]
RP SEQUENCE FROM N.A.
RA Gutierrez-Pabello J.A., Adams L.G.;
RT "Bovine thymosin beta-10 full length cDNA sequence.";
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SYNTHESIS.
RX MEDLINE-87136392; PubMed-3818171;
RA Chandramouli N., Bhargava K.K., Incefy G.S., Modak M.J.,
RA Merrifield R.B.;
RT "Solid phase synthesis of thymosin beta 9.";
RN [4]
RP STRUCTURE BY NMR.
RA Gallert B., Zarbock J., Voelter W., Holak T.A.;
RT "A nuclear magnetic resonance and simulated annealing study of
RN thymosin beta-9 in solution.";
RA (In) Schneider C.H., Eberles A.N. (eds.);
RN Peptides 1992, pp.517-518, Escom Science Publishers, Leiden (1993).
RN [5]
RP STRUCTURE BY NMR.
RC TISSUE-Thymus;
RX MEDLINE-97262390; PubMed-9108730;
RA Stoll R., Voelter W., Holak T.A.;
RT "Conformation of thymosin beta 9 in water/fluoroalcohol solution
RN determined by NMR spectroscopy.";
CC -1- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DEVELOPMENTAL STAGE: DISTRIBUTED IN NUMEROUS TYPES OF TISSUES,
CC INCLUDING THYMUS, SPLEEN, LUNG, LIVER AND MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF294616; AAG03074.1; -
DR PIR; A19438; A19438.
DR PIR; B19438; B19438.
DR PDB; 1HJ0; 04-JAN-02.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.

```



```

DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation; 3D-structure.
FT INIT_MET 0 0
FT PEPTIDE 1 41 THYMOSIN BETA-9.
FT PEPTIDE 1 39 THYMOSIN BETA-8.
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 41 AA; 4674 MW; 268E1AB71E6A8909 CRC64;

Query Match
Best Local Similarity 52.8%; Score 112.5; DB 1; Length 41;
Matches 28; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 2 AHKLDLEIASLDKAKLKATQM-QNTLMKTKETQEK 38
Db 1 ADKPDGEGINSFDKAKLKATQKNTLPTKETIEQEK 38

RESULT 3
TYB9_PIG
ID TYB9_PIG STANDARD; PRT; 41 AA.
AC P21753;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-9.
OS Sus scrofa (Fig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=89372897; PubMed=2774558;
RA Hannappel E., Wartenberg F., Bustelo X.R.;
RT "Isolation and characterization of thymosin beta 9 Met from pork
  spleen.";
RL Arch. Biochem. Biophys. 273:396-402(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=91216695; PubMed=2090639;
RA Low T.L.K., Lin C.Y., Pan T.L., Chiou A.J., Tsugita A.;
RT "Structure and immunological properties of thymosin beta 9 Met, a new
  analog of thymosin beta 4 isolated from porcine thymus.";
RL Int. J. Pept. Protein Res. 36:481-488(1990).
CC Int. J. Pept. Protein Res. 36:481-488(1990).
CC FUNCTION: Plays an important role in the organization of the
  cytoskeleton. Binds to and sequesters actin monomers (G actin) and
  therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC PIR; S05644; S05644.
CC PIR; A60290; A60290.
DR HSSP; P21752; 1HQJ.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT MOD_RES 1 1
SQ SEQUENCE 41 AA; 4692 MW; 268E1AB6B5703909 CRC64;

Query Match
Best Local Similarity 51.9%; Score 110.5; DB 1; Length 41;
Matches 27; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

Qy 2 AHKLDLEIASLDKAKLKATQM-QNTLMKTKETQEK 38
Db 1 ADKPDGEGINSFDKAKLKATQKNTLPTKETIEQEK 38

RESULT 4
TYB_CYPCA

```

```

ID TYB_CYPCA STANDARD; PRT; 42 AA.
QY9154;
AC Q9154;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-b.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "Molecular cloning of carp (Cyprinus carpio) thymosin beta b.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Plays an important role in the organization of the
  cytoskeleton. Binds to and sequesters actin monomers (G actin) and
  therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation
  at the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB028457; BAA96493.1; -
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton.
FT INIT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 42 AA; 4838 MW; 47667BB96C9DDAFB CRC64;

Query Match
Best Local Similarity 50.9%; Score 108.5; DB 1; Length 42;
Matches 25; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

Qy 2 AHKLDLEIASLDKAKLKATQM-QNTLMKTKETQEKWSE 41
Db 1 ADKPDISEVSQFDKTKLKKTKETQKNTLPTKETIEQKCE 41

RESULT 5
TYBA_ONCMY
ID TYBA_ONCMY STANDARD; PRT; 41 AA.
AC P26351; Q9PT32;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-11.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=92245862; PubMed=1575682;
RA Yialouris P.P., Coles B., Tsitsiloni O., Schmid B., Howell S.;
RT "The complete sequences of trout (Salmo gairdneri) thymosin beta 11
  and its homologue thymosin beta 12.";
RL Biochem. J. 283:385-389(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;

```

RA Sakai M., Kono T.;
 RT "The cDNA sequence of rainbow trout thymosin beta-12";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SYNTHESIS.
 RA Echner H., Vialouris P.P., Haritos A.A., Gruebler G., Voelter W.;
 RT "Structure and syntheses of thymosin beta-11 and beta-12";
 RL (In) Schneider C.H., Eberles A.N. (eds.);
 RL Peptides 1992, pp.751-752, Escom Science Publishers, Leiden (1993).
 CC -1- FUNCTION: Plays an important role in the organization of the
 CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
 CC therefore inhibits actin polymerization (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB033770; BAA85772.1;
 DR HSSP; P21752; IHJ0.
 DR InterPro; IPR001152; Thymosin_b4.
 DR Pfam; PF01290; Thymosin; 1.
 DR SMART; SM00152; THY; 1.
 DR PROSITE; PS00500; THYMOSIN_B4; 1.
 KW Actin-binding; Cytoskeleton; Acetylation.
 FT INIT_MET 0
 FT MOD_RES 1
 FT SEQUENCE 41 AA; 4689 MW; AD907D5A60046CF2 CRC64;
 SQ
 Query Match 50.0%; Score 106.5; DB 1; Length 41;
 Best Local Similarity 69.4%; Pred. No. 4e-06;
 Matches 25; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 4 KLDLEEIASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
 DB 3 KPNLEEVASFDTKLKKTETQKKNPLTKETIEQEK 38
 RESULT 6
 TYBO_TORMA STANDARD; PRT; 43 AA.
 AC Q91980;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thymosin beta-10 (Thymio10).
 OS Torpedo marmorata (Marbled electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hyposquala; Pristiorajae; Batoidea;
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7788;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Electric lobe;
 RA O'Regan S., Matz V., Cha N., Meunier F.M.;
 RT "Torpedo electric lobe cDNAs that suppress a choline metabolism
 RL mutation in yeast";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Plays an important role in the organization of the
 CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
 CC therefore inhibits actin polymerization (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AJ276369; CAB76965.1;
 DR InterPro; IPR001152; Thymosin_b4.
 DR Pfam; PF01290; Thymosin; 1.
 DR PRODOM; PD005116; Thymosin_b4; 1.
 DR SMART; SM00152; THY; 1.
 DR PROSITE; PS00500; THYMOSIN_B4; 1.
 KW Actin-binding; Cytoskeleton.
 FT INIT_MET 0
 FT SEQUENCE 43 AA; 4785 MW; 63D5D49977A2E351 CRC64;
 SQ
 Query Match 50.0%; Score 106.5; DB 1; Length 43;
 Best Local Similarity 58.1%; Pred. No. 4.2e-06;
 Matches 25; Conservative 6; Mismatches 11; Indels 1; Gaps 1;
 QY 2 AHKLDLEEIASLDKAKLKATEMQ-KNTLMTKETTEQEKWSEIS 43
 DB 1 ADKPDFGEVASFDSKLLKTDTEYKNTLPTKETIDQEKKAESS 43
 RESULT 7
 TYBB_ONCMY STANDARD; PRT; 42 AA.
 AC P26352;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thymosin beta-12.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Profacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Spleen;
 RX MEDLINE=92246862; PubMed=1575682;
 RA Vialouris P.P., Coles B., Tsitsiloni O., Schmid B., Howell S.,
 RA Aitken A., Voelter W., Haritos A.A.;
 RT "The complete sequences of trout (Salmo gairdneri) thymosin beta 11
 RT and its homologue thymosin beta 12";
 RL Biochem. J. 283:385-389(1992).
 RN [2]
 RP SYNTHESIS.
 RA Echner H., Vialouris P.P., Haritos A.A., Gruebler G., Voelter W.;
 RT "Structure and syntheses of thymosin beta-11 and beta-12";
 RL (In) Schneider C.H., Eberles A.N. (eds.);
 RL Peptides 1992, pp.751-752, Escom Science Publishers, Leiden (1993).
 CC -1- FUNCTION: Plays an important role in the organization of the
 CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
 CC therefore inhibits actin polymerization (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
 CC HSSP; P21752; IHJ0.
 DR InterPro; IPR001152; Thymosin_b4.
 DR Pfam; PF01290; Thymosin; 1.
 DR SMART; SM00152; THY; 1.
 DR PROSITE; PS00500; THYMOSIN_B4; 1.
 KW Actin-binding; Cytoskeleton; Acetylation.
 FT MOD_RES 1
 FT SEQUENCE 42 AA; 4760 MW; C290EE1BF604CA90 CRC64;
 SQ
 Query Match 46.7%; Score 99.5; DB 1; Length 42;
 Best Local Similarity 63.9%; Pred. No. 2.6e-05;
 Matches 23; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
 QY 4 KLDLEEIASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
 DB 3 KPDLEAVSNFDTKLKKTETQKKNPLTKETIEQEK 38

```
RESULT 8
TYB4_MOUSE
ID TYB4_MOUSE STANDARD; PRT; 50 AA.
AC P20065;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-4 (T beta 4).
GN TMSB4 OR TMSB4X OR PTMB4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (LONG FORM).
RX MEDLINE=90278100; PubMed=2351831;
RA Rudin C.M., Engler P., Storb U.;
RT "Differential splicing of thymosin beta 4 mRNA.";
RL J. Immunol. 144:4857-4862(1990).
[2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=91032153; PubMed=2226839;
RA Low T.L.K., Pan T.L., Lin Y.S.;
RT "Depression of prothymosin alpha production in murine thymus
correlates with staphylococcal enterotoxin-B-induced
immunosuppression.";
RL FEBS Lett. 273:1-5(1990).
[3]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=96435916; PubMed=8838802;
RA Li X., Zimmerman A., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Yin H.L.;
RT "The mouse thymosin beta 4 gene: structure, promoter identification,
and chromosome localization.";
RL Genomics 32:388-394(1996).
CC -!- FUNCTION: Plays an important role in the organization of the
cytoskeleton. Binds to and sequesters actin monomers (G actin) and
therefore inhibits actin polymerization.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
short form; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: ORIGINALLY FOUND IN THYMUS BUT IT IS WIDELY
DISTRIBUTED IN MANY TISSUES.
CC -!- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; X16053; CAA34187.1; -
DR EMBL; X16053; CAA34188.1; -
DR EMBL; U38967; AAC52490.1; -
DR PIR; S08074; S08074.
DR PIR; S12884; S12884.
DR PIR; A37217; A37217.
DR HSSP; P21752; 1HJ0.
DR MGD; MGI:99510; Tmsb4x.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
DR Actin-binding; Cytoskeleton; Acetylation; Alternative splicing.
FT CHAIN 1 50 THYMOSIN BETA-4, LONG FORM.
FT CHAIN 8 50 THYMOSIN BETA-4, SHORT FORM.
FT MOD_RES 8 8 ACETYLATION (BY SIMILARITY).
FT VARSPLIC 1 6 MISSING (IN SHORT ISOFORM).
```

```
SQ SEQUENCE 50 AA; 5679 MW; 9A289F60EE48EB8A CRC64;
Query Match 45.8%; Score 97.5; DB 1; Length 50;
Best Local Similarity 59.0%; Pred. No. 5.2e-05;
Matches 23; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAHKDLEETASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
I: | | | | | | | | | | | | | | | | | | | |
D: | | | | | | | | | | | | | | | | | | | |
7 MSKDPDMAEIEKFDKSLKKTETQEKNPSPSKETIEQEK 45

RESULT 9
TYBB_LATJA
ID TYBB_LATJA STANDARD; PRT; 43 AA.
AC P33248;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-12.
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92117698; PubMed=1731637;
RA Low T.L.K., Liu D.T.-W., Jou J.-H.;
RT "Primary structure of thymosin beta 12, a new member of the beta-
thymosin family isolated from perch liver.";
RL Arch. Biochem. Biophys. 293:32-39(1992).
CC -!- FUNCTION: Plays an important role in the organization of the
cytoskeleton. Binds to and sequesters actin monomers (G actin) and
therefore inhibits actin polymerization (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
DR PIR; S21694; S21694.
DR HSSP; P21752; 1HJ0.
DR InterPro; IPR001152; Thymosin_b4.
DR Pfam; PF01290; Thymosin; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 43 AA; 4779 MW; E7E4A32B091046DA CRC64;
Query Match 45.3%; Score 96.5; DB 1; Length 43;
Best Local Similarity 61.1%; Pred. No. 5.8e-05;
Matches 22; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 4 KLDLEETASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
I: | | | | | | | | | | | | | | | | | | | |
D: | | | | | | | | | | | | | | | | | | | |
3 KPDISEVTSPDKTLKKTETQEKNPSPSKETIEQEK 38

RESULT 10
TYB4_RABIT
ID TYB4_RABIT STANDARD; PRT; 43 AA.
AC P34032;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-4 (T beta 4).
GN TMSB4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=83177074; PubMed=6838210;
```

RA Erickson-Viitanen S., Ruggieri S., Natalini P., Horecker B.L.;
RL "Distribution of thymosin beta 4 in vertebrate classes.";
RR Arch. Biochem. Biophys. 221:570-576(1983).
CC -1- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: ORIGINATING IN THYMUS BUT IT IS WIDELY
CC DISTRIBUTED IN MANY TISSUES.
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
DR HSP: P21752: 1HJ0.
DR InterPro: IPR001152; Thymosin_b4.
DR Pfam: PF01290; Thymosin; 1.
DR ProDom: PD005116; Thymosin_b4; 1.
DR SMART: SM00152; THY; 1.
DR PROSITE: PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 43 AA; 4905 MW; 440C76B45C6B03D0 CRC64;

Query Match 44.8%; Score 95.5; DB 1; Length 43;
Best Local Similarity 60.5%; Pred. No. 7.5e-05;
Matches 23; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 2 AHKLEETASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
Db 1 AKPDMAEIEKFDKSLKKTETQEKNPSPKETIEQEK 38

RESULT 11
TYB4_XENLA
ID TYB4_XENLA STANDARD; PRT; 43 AA.
AC P18758;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta-4 (T beta 4) (Thymosin beta 4Xen).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92231989; PubMed=1567461;
RA Yamamoto M., Shoda A., Minamino N., Matsuo H., Nishimatsu S., Ueno N.,
RA Murakami K.;
RT "Expression of thymosin beta 4 gene during Xenopus laevis
RT embryogenesis.";
RL Biochem. Biophys. Res. Commun. 184:93-99(1992).
RN [2]
RP SEQUENCE.
RC TISSUE=Oocyte;
RX MEDLINE=88132867; PubMed=3124756;
RA Hannappel E., Kalbacher H., Voelter W.;
RT "Thymosin beta 4Xen: a new thymosin beta 4-like peptide in oocytes of
RT Xenopus laevis.";
RL Arch. Biochem. Biophys. 260:546-551(1988).
CC -1- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: SPLEEN, KIDNEY, HEART, AND OOCYTES.
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; D10692; BAA01534.1; -
DR PIR; S06344; S06344.
DR PIR; JQ1489; JQ1489.
DR HSP: P21752: 1HJ0.
DR InterPro: IPR001152; Thymosin_b4.
DR Pfam: PF01290; Thymosin; 1.
DR ProDom: PD005116; Thymosin_b4; 1.
DR SMART: SM00152; THY; 1.
DR PROSITE: PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 40 41 TS -> ST (in ref. 1).
SQ SEQUENCE 43 AA; 4965 MW; 440C7CDEE4301D0 CRC64;

Query Match 44.8%; Score 95.5; DB 1; Length 43;
Best Local Similarity 63.9%; Pred. No. 7.5e-05;
Matches 23; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 4 KLDLEEIASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
Db 3 KPDMAEIEKFDKSLKKTETQEKNPSPKETIEQEK 38

RESULT 12
TYB_BRARE
ID TYB_BRARE STANDARD; PRT; 44 AA.
AC Q9W7M8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thymosin beta.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169080; PubMed=10068630;
RA Roth L.W., Bormann P., Bonnet A., Reinhard E.;
RT "Beta-thymosin is required for axonal tract formation in developing
RT zebrafish brain.";
RL Development 126:1365-1374(1999).
CC -1- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

QY 2 AHKLEETASLDKAKLKATEMQ-KNTLMTKETTEQEK 41


```

DR ProDom; PD005116; Thymosin_b4; 1.
DR SMART; SM00152; THY; 1.
DR PROSITE; PS00500; THYMOSIN_B4; 1.
KW Actin-binding; Cytoskeleton; Acetylation.
FT INIT_MET 0 0
FT PEPTIDE 1 4 HEMATOPOIETIC SYSTEM REGULATORY PEPTIDE.
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 7 7 A -> V (IN REF. 5).
SQ SEQUENCE 43 AA; 4921 MW; 440C6102871103D0 CRC64;

Query Match
Best Local Similarity 43.4%; Score 92.5; DB 1; Length 43;
Matches 22; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 4 KLDLEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
DB 3 KPDMAETKFDKSKLTKTETQEKPLPSKETIEQEK 38

RESULT 14
TYBN_COTJA
ID TYBN_COTJA STANDARD; PRT; 44 AA.
AC Q9DET5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Thymosin beta.
OS Coturnix coturnix japonica (Japanese quail)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RA Dathe V.E., Prols F., Brand-Saberi B.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AJ301650; CAC17010.1;
CC InterPro; IPR001152; Thymosin_b4.
CC Pfam; PF01290; Thymosin; 1.
CC SMART; SM00152; THY; 1.
CC PROSITE; PS00500; THYMOSIN_B4; 1.
CC Actin-binding; Cytoskeleton.
CC INIT_MET 0 0 BY SIMILARITY.
CC SEQUENCE 44 AA; 5114 MW; 653D099D1D9AAC62 CRC64;

Query Match
Best Local Similarity 42.5%; Score 90.5; DB 1; Length 44;
Matches 21; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 4 KLDLEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
DB 3 KPDLESEKFDKSKLTKTETQEKPLPSKETIEQEK 38

RESULT 15
TYBN_HUMAN
ID TYBN_HUMAN STANDARD; PRT; 44 AA.
AC Q99406;
DT 15-DEC-1998 (Rel. 37, Created)

```

```

DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE NB Thymosin beta.
GN TMSNB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97191543; PubMed=9039501;
RA Yokoyama M., Nishi Y., Yoshii J., Okubo K., Matsubara K.;
RT Identification and cloning of neuroblastoma-specific and nerve
RL tissue-specific genes through compiled expression profiles.;
RN [2]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the organization of the
CC cytoskeleton. Binds to and sequesters actin monomers (G actin) and
CC therefore inhibits actin polymerization (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: NEUROBLASTOMA-SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; D82345; BAA11556.1;
CC EMBL; AL035609; CAC18959.1;
CC HSSP; BC000183; AAH00183.1;
CC InterPro; IPR001152; Thymosin_b4.
CC Pfam; PF01290; Thymosin; 1.
CC SMART; SM00152; THY; 1.
CC PROSITE; PS00500; THYMOSIN_B4; 1.
CC Actin-binding; Cytoskeleton; Acetylation.
CC INIT_MET 0 0 BY SIMILARITY.
CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC SEQUENCE 44 AA; 5098 MW; B118286809C2656B CRC64;

Query Match
Best Local Similarity 40.6%; Score 86.5; DB 1; Length 44;
Matches 19; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 4 KLDLEETASLDKAKLKATEM-QKNTLMTKETTEQEK 38
DB 3 KPDLESEKFDKSKLTKTETQEKPLPSKETIEQEK 38

Search completed: May 30, 2003, 10:32:03
Job time : 23 secs

```

R;McCreary, V.; Kartha, S.; Bell, G.I.; Toback, F.G.

A:Accession: A60290
A:Molecule type: protein
A:Residues: 1-41 <LOW>
R:Hannappel, E.; Wartenberg, F.; Bustelo, X.R.
Arch. Biochem. Biophys. 273, 396-402, 1989
A:Title: Isolation and characterization of thymosin beta(9)(Met) from pork spleen
C:Keywords: acetylated amino end
A:Reference number: S05644; MUID:89372897; PMID:2774558
A:Accession: S05644
A:Molecule type: protein
A:Residues: 1-41 <HAN>
C:Superfamily: thymosin beta
C:Keywords: acetylated amino end
F:1/Modified site: acetylated amino end (Ala) #status predicted

Query Match 51.9%; Score 110.5; DB 1; Length 41;
Best Local Similarity 71.1%; Pred. No. 1.6e-06;
Matches 27; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 2 AHKLDLEETASLDKAKLKATEMO-KNTLMTKETTEQEK 38
| | : | : | | | | | | | | | | | | | | |
DB 1 ADKPDMGEINSDKALKKTETQEKNLPLPKETIEQEK 38

RESULT 5
S21282
thymosin beta-11 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S21282
R:Vialouris, P.P.; Coles, B.; Tsitsiloni, O.; Schmid, B.; Howell, S.; Aitken, A.;
Biochem. J. 283, 385-389, 1992
A:Title: The complete sequences of trout (Salmo gairdneri) thymosin beta(11) and
C:Keywords: acetylated amino end
A:Reference number: S21282; MUID:92246862; PMID:1575562
A:Accession: S21282
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-43 <YIA>
C:Superfamily: thymosin beta

Query Match 50.0%; Score 106.5; DB 2; Length 43;
Best Local Similarity 69.4%; Pred. No. 5e-06;
Matches 25; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 4 KLDLEETASLDKAKLKATEMO-KNTLMTKETTEQEK 38
| : | | : | | | | | | | | | | | | | | |
DB 5 KPNLEEAVSFDTKLKKTETQEKNLPLPKETIEQEK 40

RESULT 6
A59005
thymosin beta - sea urchin (Arbacia punctulata)
C:Species: Arbacia punctulata (punctureate urchin)
C:Date: 01-Aug-1997 #sequence_revision 01-Aug-1997 #text_change 24-Nov-1999
C:Accession: A59005
R:Safer, D.; Chowrashi, P.K.
submitted to the Protein Sequence Database, July 1997
A:Reference number: A59005
A:Accession: A59005
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-40 <SAF>
C:Superfamily: thymosin beta
C:Keywords: acetylated amino end; actin binding
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 49.1%; Score 104.5; DB 2; Length 40;
Best Local Similarity 60.5%; Pred. No. 7.9e-06;
Matches 23; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 2 AHKLDLEETASLDKAKLKATEMQ-KNTLMTKETTEQEK 38
| | : | : | | | | | | | | | | | | | | |
pb 1 ADKPPVSVMVFDFSKLKKTTQEQNKTLPLTKDITQEK 38

thymosin beta-12 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

RESULT 11
A37217

thymosin beta-4 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A37217; S08074; S12884
R:Rudin, C.M.; Engler, P.; Storb, U.

A:Title: Differential splicing of thymosin beta-4 mRNA.
A:Reference number: A37217; MUID:90278100; PMID:2351831
A:Accession: A37217

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-50 <RUD>

A:Cross-references: GB:X16053; GB:M54991; NID:954793; PIDN:CAA34187.1; PID:g54794; GB:M54991

R:Rudin, C.; Engler, P.; Provost, S.; Storb, U.
submitted to the EMBL Data Library, August 1989

A:Reference number: S08074

A:Accession: S08074

A:Molecule type: mRNA

A:Residues: 1-50 <RUD>

A:Cross-references: EMBL:X16053; NID:954793; PIDN:CAA34187.1; PID:g54794

R:Low, T.L.K.; Pan, T.L.; Lin, Y.S.
FEBS Lett. 273, 1-5, 1990

A:Title: Depression of prothymosin-alpha production in murine thymus correlates with sta

A:Reference number: S12884

A:Accession: S12884

A:Molecule type: protein

A:Residues: 8-50 <LOW>

A:Superfamily: thymosin beta

C:Keywords: actin binding; alternative splicing

F:1-50/Product: thymosin beta-4 precursor, long splice form #status predicted <LFO>

F:7-50/Product: thymosin beta-4 precursor, short splice form #status predicted <SFO>

F:8-50/Product: thymosin beta-4 #status experimental <MAT>

Query Match

Best Local Similarity 45.8%; Score 97.5; DB 1; Length 50;

Matches 23; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATEMQ-KNTLMKTEETQEK 38

Db 7 MSKPDMAETEKEDKSLKKTETQEKNPPLPSKETIEQEK 45

RESULT 12

I52084

thymosin beta-4 precursor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999

C:Accession: I52084

R:Goodall, G.J.; Richardson, M.; Furuichi, Y.; Wodnar-Fillipowicz, A.; Horecker, B.L.

A:Title: Sequence of a cloned 523-bp cDNA for thymosin beta-4.

A:Reference number: I52084; MUID:85095883; PMID:3838131

A:Accession: I52084

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-56 <RES>

A:Cross-references: GB:M26759; NID:g207317; PIDN:AAA42246.1; PID:g207318

C:Superfamily: thymosin beta

Query Match

Best Local Similarity 45.8%; Score 97.5; DB 2; Length 56;

Matches 23; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATEMQ-KNTLMKTEETQEK 38

Db 13 MSKPDMAETEKEDKSLKKTETQEKNPPLPSKETIEQEK 51

RESULT 13

S21694

thymosin beta-12 - Japanese seaperch

C:Species: Lateolabrax japonicus (Japanese seaperch)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S21694

R:Low, T.L.K.; Liu, D.T.; Jou, J.

Arch. Biochem. Biophys. 293, 32-39, 1992

A:Title: Primary structure of thymosin beta(12), a new member of the beta-thymosin

A:Reference number: S21694; MUID:92117698; PMID:1731637

A:Accession: S21694

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-43 <LOW>

C:Superfamily: thymosin beta

Query Match

Best Local Similarity 45.3%; Score 96.5; DB 2; Length 43;

Matches 22; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 4 KIDLEEIASLDKAKLKATEMQ-KNTLMKTEETQEK 38

Db 3 KPDISEVTSFDKTKLKKTETQEKNPPLPSKETIEQEK 38

RESULT 14

TNRTB4

thymosin beta-4 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 18-Jun-1999

C:Accession: A01522; A36123

R:Wodnar-Fillipowicz, A.; Gubler, U.; Furuichi, Y.; Richardson, M.; Nowoswiat, E.F.;

Proc. Natl. Acad. Sci. U.S.A. 81, 2295-2297, 1984

A:Title: Cloning and sequence analysis of cDNA for rat spleen thymosin beta-4.

A:Reference number: A01522; MUID:84193997; PMID:6201851

A:Accession: A01522

A:Molecule type: mRNA

A:Residues: 1-44 <WOD>

A:Cross-references: GB:K01334; NID:g207315; PIDN:AAA42245.1; PID:g207316

A>Note: the authors translated the codon GUC for residue 8 as Ala

R:Atkinson, M.J.; Freeman, M.W.; Kronenberg, H.M.

Mol. Endocrinol. 4, 69-74, 1990

A:Title: Thymosin beta-4 is expressed in ROS 17/2.8 osteosarcoma cells in a regulated

A:Reference number: A36123; MUID:90220652; PMID:2325669

A:Accession: A36123

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-7, 'A', '9-44 <ATR>

A:Cross-references: GB:M34043; NID:g206707; PIDN:AAA42062.1; PID:g206708

C:Comment: This protein does not have the typical amino-terminal hydrophobic region u

C:Superfamily: thymosin beta

C:Keywords: actin binding

Query Match

Best Local Similarity 45.3%; Score 96.5; DB 1; Length 44;

Matches 23; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAHKLDLEETASLDKAKLKATEMQ-KNTLMKTEETQEK 38

Db 1 MSKPDMAETEKEDKSLKKTETQEKNPPLPSKETIEQEK 39

RESULT 15

TNBOB4

thymosin beta-4 - bovine

N:Alternate names: hematopoietic stem cell proliferation inhibitor

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 24-Feb-1995

C:Accession: A01521; A31451; S13193

R:Low, T.L.K.; Hu, S.K.; Goldstein, A.L.

Proc. Natl. Acad. Sci. U.S.A. 78, 1162-1166, 1981

A:Title: Complete amino acid sequence of bovine thymosin beta-4: a thymic hormone tha

A:Reference number: A01521; MUID:81199361; PMID:6940133

A:Accession: A01521

A:Molecule type: protein

A:Residues: 1-43 <LOW>

R:Lenfant, M.; Wdziecizak-Bakala, J.; Guittet, E.; Prome, J.C.; Sotty, D.; Frindel, E.

Query Match 43.4%; Score 92.5; DB 1; Length 43;
Best Local Similarity 61.1%; Pred. No. 0.00022;
Matches 22; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Search completed: May 30, 2003, 10:35:32
Job time : 42 secs

THIS PAGE BLANK (3870)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:31:31 ; Search time 70 Seconds
(without alignments)
81.854 Million cell updates/sec

Title: US-09-915-178-2

Perfect score: 213
Sequence: 1 MAHKLDLEETASLDKAKLKA.....QKNTLMRTKETTEQKWSBIS 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID52/qcgcdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/qcgcdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/qcgcdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/qcgcdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	100.0	43	ABB05034	Human NOV2a protei
2	213	100.0	43	ABB05035	Human NOV2b protei
3	213	100.0	43	ABB05036	Human NOV2c protei
4	130.5	61.3	43	AA196932	Thymosin beta 10.
5	130.5	61.3	43	AA196932	Thymosin beta 10.
6	128	60.1	58	AAU00689	Thymosin-beta-10-1
7	128	60.1	58	AAU00689	Thymosin-beta-10-1
8	127.5	59.9	43	AA196932	Thymosin-beta-10-1
9	116.5	54.7	41	AA196935	N-Terminus of thym
10	116.5	54.7	41	AA196935	Thymosin beta 13.
			21	AA196935	Thymosin beta 4 pe

11	112.5	52.8	39	13	AA196935	N-Terminus of thym
12	112.5	52.8	41	13	AA196935	N-Terminus of thym
13	112.5	52.8	41	17	AA196930	Thymosin beta 9.
14	112.5	52.8	41	21	AA196930	Thymosin beta 9.
15	110.5	51.9	41	17	AA196931	Thymosin beta 4 pe
16	110.5	51.9	41	21	AA196931	Thymosin beta 4 pe
17	108.5	50.9	41	13	AA196932	Thymosin beta 4 pe
18	106.5	50.0	41	17	AA196933	N-Terminus of thym
19	106.5	50.0	41	17	AA196933	Thymosin beta 11.
20	104.5	49.1	40	21	AA196936	Thymosin beta 4 pe
21	104.5	49.1	40	17	AA196936	Thymosin beta 14.
22	103.5	48.6	44	23	ABP60994	Novel human protei
23	103.5	48.6	74	22	ABG23079	Novel human diagno
24	99.5	46.7	40	21	AA196934	Thymosin beta 4 pe
25	99.5	46.7	42	17	AA196934	Thymosin beta 12.
26	99.5	46.7	42	21	AA196934	Thymosin beta 4 pe
27	98.5	46.2	58	21	AA196934	Human secreted pro
28	97.5	45.8	43	21	AA196934	Thymosin beta 4 pe
29	97.5	45.8	44	19	AA196934	Thymosin beta 4 pe
30	97.5	45.8	56	21	AA196934	Human colon cancer
31	97.5	45.8	57	21	AA196934	Human cytoskeleton
32	97.5	45.8	68	9	AA196934	Protein produced i
33	96.5	45.3	43	21	AA196934	Thymosin beta 4 pe
34	95.5	44.8	43	17	AA196934	Thymosin beta 4 pe
35	95.5	44.8	43	17	AA196934	Thymosin beta 4-Xe
36	95.5	44.8	45	18	AA196934	Human thymosin bet
37	95.5	44.8	45	19	AA196934	Rat thymosin-beta1
38	95.5	44.8	45	19	AA196934	Human thymosin bet
39	95.5	44.8	45	19	AA196934	Human thymosin bet
40	95.5	44.8	45	21	AA196934	Human thymosin bet
41	95.5	44.8	45	23	AA196934	Human thymosin bet
42	93.5	43.9	40	21	AA196934	Thymosin beta 4 pe
43	92.5	43.4	43	2	AA196934	Thymosin beta-4.
44	92.5	43.4	43	17	AA196934	Thymosin beta 4.
45	92.5	43.4	43	21	AA196934	Thymosin beta 4 pe

ALIGNMENTS

RESULT 1	ABB05034	standard; Protein; 43 AA.
ID	ABB05034	standard; Protein; 43 AA.
XX	AC	ABB05034;
XX	AC	ABB05034;
DT	25-MAR-2002	(first entry)
XX	Human NOV2a protein	SEQ ID NO:4.
DE	Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;	
KW	fungicide; virucide; protozoacide; analgesic; antiparkinsonian;	
KW	antidiabetic; hypotensive; cardiatic; antileptotic; antitumor;	
KW	neuroprotective; cardiatic; antileptotic; antitumor;	
KW	anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;	
KW	developmental disease; taste and scent detectability disorder; infection;	
KW	Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;	
KW	retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;	
KW	noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;	
KW	hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;	
KW	multiple sclerosis; angina pectoris; myocardial infarction; delirium;	
KW	benign prostatic hypertrophy; manic depression; dementia; dyskinesia;	
KW	severe mental retardation; Huntington's disease; chromosome 9;	
KW	Gilles de la Tourette syndrome.	
XX	Homo sapiens.	
OS	WO200190155-A2.	
XX	29-NOV-2001.	
PD	24-MAY-2001; 2001WO-US17073.	
XX		

PR 24-MAY-2000; 2000US-206679P.
 PR 24-MAY-2000; 2000US-206688P.
 PR 24-MAY-2000; 2000US-206829P.
 PR 30-MAY-2000; 2000US-207748P.
 PR 30-MAY-2000; 2000US-207798P.
 PR 31-MAY-2000; 2000US-208263P.
 PR 02-JUN-2000; 2000US-20831P.
 PR 05-JUN-2000; 2000US-209451P.
 PR 07-JUN-2000; 2000US-210060P.
 PR 20-JUL-2000; 2000US-219507P.
 PR 26-JUL-2000; 2000US-221337P.
 PR 31-JUL-2000; 2000US-221927P.
 PR 19-JAN-2001; 2001US-263135P.
 PR 24-JAN-2001; 2001US-263688P.
 PR 24-JAN-2001; 2001US-263694P.
 PR 23-MAY-2001; 2001US-0863776.
 XX (CURA-) CURAGEN CORP.
 XX Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
 PI Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
 XX WPI: 2002-106174/14.
 DR N-PSDB; ABA92649.
 XX Novel polypeptide, useful for treating pain, cancer, urinary retention,
 PT osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
 PT asthma, ulcer, allergy and Huntington's disease, comprises isolated
 PT polypeptide NOVX -
 XX Claim 1; page 20; 266pp; English.
 XX The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
 CC proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
 CC fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
 CC antiasthmatic, hypotensive, osteopathic, antiinflammatory, antiulcer,
 CC neuroprotective, cardiant, antiallergic, antidepressant, nootropic,
 CC anticonvulsant and neuroleptic activities. (I) and (II) can be
 CC used in gene therapy and vaccine production. (I) and (II) can be
 CC used for treating or preventing a NOVX-associated disorder such as
 CC cardiomyopathy, atherosclerosis and diabetes in a human, where the
 CC disorder is related to cell signal processing and metabolic path way
 CC modulation, in a subject, preferably human. (I) and (II) can be used for
 CC diagnosing, preventing or treating developmental diseases, immune
 CC diseases, taste and scent detectability disorder, Burkitt's lymphoma,
 CC signal transduction pathway disorders, retinal diseases including those
 CC involving photoreception, cell growth rate disorders, feeding disorders,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
 CC infarction, allergies, benign prostatic hypertrophy, manic depression,
 CC delirium, dementia, severe metal retardation and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome. The present
 CC sequence represents the human NOV2a protein from the present invention.
 CC Human NOV2a is isolated to chromosome 9.
 XX
 XX Sequence 43 AA:
 Query Match 100.0%; Score 213; DB 23; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2.7e-19;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAHKLDLEETASLDKAKLKATEMKQNTLMTKETTTQEKWSEIS 43
 DB 1 MAHKLDLEETASLDKAKLKATEMKQNTLMTKETTTQEKWSEIS 43
 RESULT 2
 ABB05035
 ID ABB05035 standard; Protein; 43 AA.
 XX
 AC ABB05035;

XX 25-MAR-2002 (first entry)
 XX Human NOV2b protein SEQ ID NO:6.
 DE
 XX Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;
 KW fungicide; virucide; protozoacide; analgesic; antiparkinsonian;
 KW antiasthmatic; hypotensive; osteopathic; antiinflammatory; antiulcer;
 KW neuroprotective; cardiant; antiallergic; antidepressant; nootropic;
 KW anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;
 KW developmental disease; taste and scent detectability disorder; infection;
 KW Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;
 KW retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;
 KW noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;
 KW hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
 KW multiple sclerosis; angina pectoris; myocardial infarction; delirium;
 KW benign prostatic hypertrophy; manic depression; dementia; dyskinesia;
 KW severe metal retardation; Huntington's disease;
 KW Gilles de la Tourette syndrome.
 XX Homo sapiens.
 OS
 XX WO200190155-A2.
 PN
 XX 29-NOV-2001.
 XX
 PD
 XX 24-MAY-2001; 2001WO-US17073.
 XX
 PF
 XX 24-MAY-2000; 2000US-206679P.
 XX
 XX 24-MAY-2000; 2000US-206688P.
 PR
 XX 24-MAY-2000; 2000US-206829P.
 PR
 XX 30-MAY-2000; 2000US-207748P.
 PR
 XX 30-MAY-2000; 2000US-207798P.
 PR
 XX 31-MAY-2000; 2000US-208263P.
 PR
 XX 02-JUN-2000; 2000US-20831P.
 PR
 XX 05-JUN-2000; 2000US-209451P.
 PR
 XX 07-JUN-2000; 2000US-210060P.
 PR
 XX 20-JUL-2000; 2000US-219507P.
 PR
 XX 26-JUL-2000; 2000US-221337P.
 PR
 XX 31-JUL-2000; 2000US-221927P.
 PR
 XX 19-JAN-2001; 2001US-263135P.
 PR
 XX 24-JAN-2001; 2001US-263688P.
 PR
 XX 24-JAN-2001; 2001US-263694P.
 PR
 XX 23-MAY-2001; 2001US-0863776.
 XX (CURA-) CURAGEN CORP.
 XX Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
 PI Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
 XX WPI: 2002-106174/14.
 DR N-PSDB; ABA92650.
 XX Novel polypeptide, useful for treating pain, cancer, urinary retention,
 PT osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
 PT asthma, ulcer, allergy and Huntington's disease, comprises isolated
 PT polypeptide NOVX -
 XX Claim 1; page 22; 266pp; English.
 XX The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
 CC proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
 CC fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
 CC antiasthmatic, hypotensive, osteopathic, antiinflammatory, antiulcer,
 CC neuroprotective, cardiant, antiallergic, antidepressant, nootropic,
 CC anticonvulsant and neuroleptic activities. (I) and (II) can be
 CC used in gene therapy and vaccine production. (I) and (II) can be
 CC used for treating or preventing a NOVX-associated disorder such as
 CC cardiomyopathy, atherosclerosis and diabetes in a human, where the
 CC disorder is related to cell signal processing and metabolic path way
 CC modulation, in a subject, preferably human. (I) and (II) can be used for
 CC diagnosing, preventing or treating developmental diseases, immune
 CC diseases, taste and scent detectability disorder, Burkitt's lymphoma,
 CC signal transduction pathway disorders, retinal diseases including those
 CC involving photoreception, cell growth rate disorders, feeding disorders,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
 CC infarction, allergies, benign prostatic hypertrophy, manic depression,
 CC delirium, dementia, severe metal retardation and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome. The present
 CC sequence represents the human NOV2a protein from the present invention.
 CC Human NOV2a is isolated to chromosome 9.
 XX

CC signal transduction pathway disorders, retinal diseases including those
 CC involving photoreception, cell growth rate disorders, feeding disorders,
 CC noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
 CC infarction, allergies, benign prostatic hypertrophy, manic depression,
 CC delirium, dementia, severe metal retardation and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome. The present
 CC sequence represents the human NOV2b protein from the present invention.
 XX
 SQ Sequence 43 AA;

Query Match 100.0%; Score 213; DB 23; Length 43;

Best Local Similarity 100.0%; Pred. No. 2.7e-19;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHKLDLEEIASLDKAKLKATEMOKNTLMTKETTEQEKWSEIS 43

DB 1 MAHKLDLEEIASLDKAKLKATEMOKNTLMTKETTEQEKWSEIS 43

RESULT 3

ABB05036

ID ABB05036 standard; Protein; 43 AA.

XX AC ABB05036;

DT 25-MAR-2002 (first entry)

XX Human NOV2c protein SEQ ID NO:8.

Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;
 KW fungicide; virucide; protozoacide; analgesic; antiparkinsonian;
 KW antiasthmatic; hypotensive; osteopathic; antiinflammatory; antiulcer;
 KW neuroprotective; cardiant; antiallergic; antidepressant; nootropic;
 KW anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;
 KW developmental disease; taste and scent detectability disorder; infection;
 KW Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;
 KW retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;
 KW noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;
 KW hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
 KW multiple sclerosis; angina pectoris; myocardial infarction; delirium;
 KW benign prostatic hypertrophy; manic depression; dementia; dyskinesia;
 KW severe metal retardation; Huntington's disease;
 KW Gilles de la Tourette syndrome.

XX Homo sapiens.

XX WO200190155-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17073.

XX 24-MAY-2000; 2000US-206679P.

XX 24-MAY-2000; 2000US-206688P.

XX 24-MAY-2000; 2000US-206829P.

XX 30-MAY-2000; 2000US-207748P.

XX 30-MAY-2000; 2000US-207798P.

XX 31-MAY-2000; 2000US-208263P.

XX 02-JUN-2000; 2000US-208831P.

XX 05-JUN-2000; 2000US-209451P.

XX 07-JUN-2000; 2000US-210060P.

XX 20-JUL-2000; 2000US-219507P.

XX 26-JUL-2000; 2000US-221337P.

XX 31-JUL-2000; 2000US-221927P.

XX 19-JAN-2001; 2001US-263135P.

XX 24-JAN-2001; 2001US-263688P.

XX 24-JAN-2001; 2001US-263694P.

XX 23-MAY-2001; 2001US-0863776.

XX (CURA-) CURAGEN CORP.

XX

PI

XX

XX

DR

DR

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 43 AA;

Query Match 100.0%; Score 213; DB 23; Length 43;

Best Local Similarity 100.0%; Pred. No. 2.7e-19;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHKLDLEEIASLDKAKLKATEMOKNTLMTKETTEQEKWSEIS 43

DB 1 MAHKLDLEEIASLDKAKLKATEMOKNTLMTKETTEQEKWSEIS 43

RESULT 4

AAR96932

ID AAR96932 standard; protein; 43 AA.

XX AC AAR96932;

XX 17-OCT-1996 (first entry)

XX Thymosin beta 10.

XX Thymosin beta 4; OAD; obstructive airway disease; sputum;

KW viscoelasticity; respiratory disorder; respiratory distress syndrome;

KW chronic bronchitis; asthma; emphysema; cystic fibrosis; actin;

KW polymerisation.

XX Synthetic.

XX WO9611016-A1.

XX 18-APR-1996.

XX 06-OCT-1995; 95WO-US12543.

XX 07-JUN-1995; 95US-0483572.

XX

PR

Spyttek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
 Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
 WPI: 2002-106174/14.
 N-PSDB; ABA92651.

Novel polypeptide, useful for treating pain, cancer, urinary retention,
 osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
 asthma, ulcer, allergy and Huntington's disease, comprises isolated
 polypeptide NOVX -

Claim 1; page 23; 266pp; English.

The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
 proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
 fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
 antiasthmatic, hypotensive, osteopathic, antiinflammatory, antiulcer,
 neuroprotective, cardiant, antiallergic, antidepressant, nootropic,
 anticonvulsant and neuroleptic activities. (I) and polynucleotides (II)
 can be used in gene therapy and vaccine production. (I) and (II) can be
 used for treating or preventing a NOVX-associated disorder such as
 cardiomyopathy, atherosclerosis and diabetes in a human, where the
 disorder is related to cell signal processing and diabetes in a human, where the
 modulation, in a subject, preferably human. (I) and (II) can be used for
 diagnosing, preventing or treating developmental diseases, immune
 diseases, taste and scent detectability disorder, Burkitt's lymphoma,
 signal transduction pathway disorders, retinal diseases including those
 involving photoreception, cell growth rate disorders, feeding disorders,
 noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
 Parkinson's disease, acute heart failure, hypotension, hypertension,
 urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
 infarction, allergies, benign prostatic hypertrophy, manic depression,
 delirium, dementia, severe metal retardation and dyskinesias, such as
 Huntington's disease or Gilles de la Tourette syndrome. The present
 sequence represents the human NOV2c protein from the present invention.

PR 06-OCT-1994; 94US-0318994.
 PA (ALPH-) ALPHA 1 BIOMEDICALS INC.
 PA (UTWA-) UNIV WASHINGTON MEDICAL CENT GEORGE.
 PI Bauman C, Berman ML, Crockford DR, Goldstein AL;
 PI Kater A, Rubin BK;
 XX WPI; 1996-209656/21.
 XX Reduction of viscoelasticity of sputum of obstructive airway disease
 PT - for use in treating, e.g. cystic fibrosis.
 PT Disclosure; Figure 1B; 45pp; English.
 PS
 CC Thymosin beta 4 may be used in a composition alongside DNaseI to
 CC reduce the viscoelasticity of sputum causing obstructive airway
 CC disease (OAD). Such disease includes disorders such as acute and
 CC chronic respiratory distress syndrome, chronic bronchitis, asthma,
 CC emphysema and cystic fibrosis associated with excess actin
 CC polymerisation (polymerisation of G-actin into F-actin).
 XX Sequence 43 AA;
 SQ

Query Match 61.3%; Score 130.5; DB 17; Length 43;
 Best Local Similarity 74.4%; Pred. No. 4e-09;
 Matches 32; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
 QY 2 AHKLDLEETASLDKAKLKATEMO-KNTLMTKETTEQEKWSEIS 43
 DB 1 ADKPDGMEIASFDKAKLKKTETQKNTLPTKETIEQEKSEIS 43
 RESULT 5
 ID AAY80267
 XX AAY80267 standard; peptide: 43 AA.
 AC AAY80267;
 DT 26-MAY-2000 (first entry)
 DE Thymosin beta 4 peptide isoform Tbeta10.
 KW Thymosin beta 4; Tbeta4; tissue repair; angiogenesis; wound repair;
 KW cell migration; vulnery; antiatherosclerotic; cytostatic; diagnosis;
 KW healing disorder; fibrotic disease; ischaemia; atherosclerosis;
 KW cell proliferative disorder.
 XX Unidentified.
 OS
 XX WO200006190-A1.
 PN 10-FEB-2000.
 PD
 XX 29-JUL-1999; 99WO-US17282.
 PF
 XX 30-JUL-1998; 98US-0094690.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Kleinman HK, Goldstein A, Malinda KM, Sosne G;
 PI WPI; 2000-195195/17.
 DR
 XX A novel method to promote wound healing comprises administering
 PT thymosin beta 4, useful for promoting tissue repair, angiogenesis and
 PT cell migration
 XX
 PS Claim 10; Fig 11; 61pp; English.
 CC A method has been developed for promoting wound healing in a subject
 CC comprising administering a composition containing a wound healing
 CC polypeptide comprising the amino acid sequence Leu-Lys-Thr-Glu-Thr

CC and conservative variants, which have wound healing activity. The wound
 CC healing polypeptide is preferably thymosin beta 4 (Tbeta4) or an isoform
 CC of Tbeta4. The polypeptide has vulnery, antiatherosclerotic and
 CC cytostatic activities. It is useful for promoting wound healing, in vivo
 CC in a subject, especially humans, or ex vivo in tissues (e.g. urogenital,
 CC gastro-intestinal, cardiovascular, muscle, connective and neural,
 CC to inhibit/ameliorate wound healing. The level of Tbeta4 can be used
 CC can be used to diagnose a pathological state characterised by a wound
 CC healing disorder, such as fibrotic disease, ischaemia, atherosclerosis
 CC and cell proliferative disorders. Tbeta4 or its isoforms can also be
 CC used to promote epithelial cell (e.g. skin cells, especially
 CC keratinocytes, corneal cells) migration and angiogenesis. The polypeptide
 CC is able to promote wound repair without any side effects, unlike prior
 CC art growth and angiogenic factors used for such treatment. The present
 CC sequence represents a thymosin beta 4 peptide isoform from the present
 CC invention.
 XX
 XX Sequence 43 AA;
 SQ

Query Match 61.3%; Score 130.5; DB 21; Length 43;
 Best Local Similarity 74.4%; Pred. No. 4e-09;
 Matches 32; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
 QY 2 AHKLDLEETASLDKAKLKATEMO-KNTLMTKETTEQEKWSEIS 43
 DB 1 ADKPDGMEIASFDKAKLKKTETQKNTLPTKETIEQEKSEIS 43
 RESULT 6
 ID AAU00689
 XX AAU00689 standard; Protein: 58 AA.
 AC AAU00689;
 DT 07-SEP-2001 (first entry)
 DE Thymosin-beta-10-like protein.
 XX
 KW Thymosin-beta-10-like protein; ephrin type-A receptor 8-like protein;
 KW proteoglycan-like protein; fibromodulin; fibronectin; thymic immune cell;
 KW spermatogenesis; male infertility; neoplasia; red blood cell; platelet;
 KW small cell lung cancer; GPI-anchored ephrin-A ligand; prostate cancer;
 KW neurological disorder; cardiac disorder; vascular disorder; orthopaedic;
 KW inflammatory disease; rheumatoid arthritis; connective tissue;
 KW congenital muscular dystrophy; chemotherapy; immunotherapy.
 XX Homo sapiens.
 OS
 XX WO200129217-A2.
 PN
 XX 26-APR-2001.
 PD
 XX 13-OCT-2000; 2000WO-US28474.
 PF
 XX 15-OCT-1999; 99US-0159805.
 PR 18-OCT-1999; 99US-0159992.
 PR 22-OCT-1999; 99US-0160952.
 PR 12-OCT-2000; 2000US-0159805.
 XX (CURA-) CURAGEN CORP.
 PA Prayaga SK, Taupier RJ, Bandaru R;
 PI WPI; 2001-308489/32.
 DR N-PSDB; AAS00689.
 XX
 PT New isolated polypeptides, NOV 1-3, having identity to
 PT thymosin-beta-10, ephrin type-A receptor 8 and proteoglycans, and
 PT polynucleotides, useful for treating male infertility, neurological or
 PT cardiac disease or rheumatoid arthritis -
 XX
 PS Claim 1; Page 8; 102pp; English.

us-09-915-178-2.rag

Wed Jun 4 11:04:59 2003

WPI: 2002-452341/48.
N-PSDB; AAD38157.

DR DR Novel membrane bound and secreted NOV polypeptides, for treating,
XX XX diagnosing and preventing male infertility, neurological, cardiac and
PT PT vascular pathologies, and inflammatory diseases e.g. rheumatoid
PT PT arthritis -
XX XX

Claim 1; Page 12; 180pp; English.

XX The present invention relates to novel membrane bound and secreted NOV
XX proteins and polynucleotides encoding such proteins. Sequences of the
CC invention are useful for treating or preventing NOV-associated disorders
CC in humans and for manufacturing a medicament for treating a syndrome
CC associated with human disease. They are useful for determining the
CC presence of or predisposition to lung cancer. NOV1 compounds are useful
CC for development, differentiation and activation of thymic immune cells,
CC pathologies related to spermatogenesis and male infertility. NOV1 nucleic
CC acids are useful for detecting specific cell types and as specific
CC marker for cancers in tissues. NOV2 and NOV4 compounds are useful to
CC direct the development of nervous system and angiogenesis and for
CC treating neurological, cardiac and vascular pathologies. NOV3 and NOV5
CC compounds are useful for treating various orthopaedic disorders and/or
CC injuries, inflammatory diseases of connective tissue e.g. rheumatoid
CC arthritis, congenital muscular dystrophies, various muscular disorders,
CC fixed deformities (arthrogryposis) and abnormal white matter. They are
CC useful for treating atopy, dysprothrombinaemia, hyperparathyroidism, Leigh
CC centrocyclic lymphoma, cervical carcinoma, hyperparathyroidism, leukaemia,
CC syndrome, hypokalaemic period paralysis, acute promyelocytic leukaemia,
CC NUNA/RARA type, macular dystrophy, vitelliform type, Mcardie myeloma,
CC type 2 Meckel syndrome, multiple endocrine neoplasia I, multiple myeloma,
CC parathyroid adenomatosis 1, prolactinoma, hyperparathyroidism, carcinoma
CC inflammatory vitreoretinopathy, arthritis and tendonitis. Sequences of
CC the invention are also used in gene therapy and as vaccines. The present
CC sequence is thymosin-beta-10-like (NOV1) protein.

XX Sequence 58 AA;

Query Match 60.1%; Score 128; DB 23; Length 58;

Best Local Similarity 71.1%; Pred. No. 1,1e-08;

Matches 27; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAHKLDEETASLDKAKLKATEMKNLTMTKETTEQEK 38

DB 1 MADKPDIGEIASFNKAKLKATEMKNLTMTKETTEQEK 38

RESULT 8

AAR27109

ID AAR27109 standard; peptide: 43 AA.

XX AAR27109;

XX AAR27109;

XX 26-FEB-1993 (first entry)

XX N-terminus of thymosin beta peptide.

XX Neuropathic; encephalopathy; cerebro-degenerative; neuro-;

XX degenerative.

XX Synthetic.

XX OS

XX JP04234325-A.

XX 24-AUG-1992.

XX 27-DEC-1990;

XX 90JP-0418312.

XX 27-DEC-1990;

XX 90JP-0418312.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX The sequence represents a thymosin-beta-10-like protein (NOV1).
CC Thymosin-beta-10-like protein, ephrin type-A receptor 8-like protein
CC (NOV2) and proteoglycan-like proteins (NOV3) may be used in the
CC diagnosis, treatment and prevention of disorders caused by abnormal
CC expression or activity of thymosin-beta-10, ephrin type-A receptor 8 and
CC proteoglycans such as fibronectin and fibronectin. The polypeptides of
CC the invention are useful in screening for agents that modulate their
CC activity, and in determining predispositions to disorders. NOV1 is useful
CC for treating conditions involving development, differentiation, and
CC activation of thymic immune cells, in pathologies of neoplasias, in
CC diseases or pathologies of red blood cells or platelets, in detection of
CC small cell lung cancer. NOV1 nucleic acids can be combined in
CC chemo-immunotherapeutic anti-cancer treatments. NOV2 is useful for
CC detecting cells expressing GPI-anchored ephrin-A ligands, as a marker for
CC prostate cancer, and in treating neurological, cardiac and vascular
CC disorders. NOV3 (proteoglycan) nucleic acids and proteins are useful for
CC treating orthopaedic disorders and/or injuries, and inflammatory diseases
CC of connective tissues e.g. rheumatoid arthritis, congenital muscular
CC dystrophies.

XX Sequence 58 AA;

Query Match 60.1%; Score 128; DB 22; Length 58;

Best Local Similarity 71.1%; Pred. No. 1,1e-08;

Matches 27; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAHKLDEETASLDKAKLKATEMKNLTMTKETTEQEK 38

DB 1 MADKPDIGEIASFNKAKLKATEMKNLTMTKETTEQEK 38

RESULT 7

AAR23797

ID AAR23797 standard; Protein: 58 AA.

XX AAR23797;

XX 10-SEP-2002 (first entry)

XX Thymosin-beta-10-like (NOV1) protein.

XX Membrane bound protein; secreted NOV protein; spermatogenesis; neoplasia;
XX male infertility; angiogenesis; vascular pathology; orthopaedic disorder;
XX inflammatory disease; congenital muscular dystrophy; muscular disorder;
XX rheumatoid arthritis; fixed deformity; dysprothrombinaemia; cancer;
XX arthrogryposis; hypokalaemic period paralysis;
XX Smith-Lemli-Opitz syndrome; carcinoma; cervical carcinoma; leukaemia;
XX hyperparathyroidism; Leigh syndrome; cervical carcinoma; Meckel syndrome;
XX macular dystrophy; vitelliform type; Mcardie disease; hyperparathyroidism;
XX multiple endocrine neoplasia I; multiple myeloma; hyperparathyroidism;
XX parathyroid adenomatosis 1; prolactinoma; digenic retinitis pigmentosa;
XX somatotrophinoma; neovascular inflammatory vitreoretinopathy; arthritis;
XX carcinoma syndrome; atopy; tendonitis; gene therapy; vaccines;
XX thymosin-beta-10-like protein.

XX Unidentified.

XX WO200230979-A2.

XX 18-APR-2002.

XX 10-OCT-2001; 2001WO-US31498.

XX 12-OCT-2000; 2000US-0689486.

XX 13-OCT-2000; 2000US-0687276.

XX 09-OCT-2001; 2001US-0973424.

XX (CURA-) CURAGEN CORP.

XX Prayaga SK, Taupier RJ, Bandaru R;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX
PA (FARH) HOECHST JAPAN LTD.
DR WPI; 1992-327505/40.
XX
PT Neuropathic agent containing thymosin B4, B8, B10 or B11
PT peptide(s) - for treatment and prevention of cerebro- and
XX neuro-degenerative diseases
PS Claim 1; Page 6; 7pp; Japanese.
XX
CC The thymosin beta peptide was used in an agent for the treatment
CC of encephalopathy and neuropathy. The agent may be used for the
CC treatment or prevention of cerebro- or neuro-degenerative diseases.
XX See also AAR27106-10.
SQ Sequence 43 AA;

Query Match
Best Local Similarity 59.9%; Score 127.5; DB 13; Length 43;
Matches 31; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 2 AHKLDLEIASLDRKAKLKATPMQ-KNTLMTKETTEQKWEIS 43
Db 1 ADKPDGMEIASFDKAKLKKTETQKNTLPTKETIEQK 38

RESULT 9
AAR96935
ID AAR96935 standard; protein; 41 AA.
AC AAR96935;
XX
DT 17-OCT-1996 (first entry)
DE Thymosin beta 13.
XX
KW Thymosin beta 4; OAD; obstructive airway disease; sputum;
KW viscoelasticity; respiratory disorder; respiratory distress syndrome;
KW chronic bronchitis; asthma; emphysema; cystic fibrosis; actin;
XX polymerisation.
OS Synthetic.
XX
PN WO9611016-A1.
XX
PD 18-APR-1996.
XX
PF 06-OCT-1995; 95WO-US12543.
XX
PR 07-JUN-1995; 95US-0483572.
XX
PS 06-OCT-1994; 94US-0318994.
XX
PA (ALPH-) ALPHA 1 BIOMEDICALS INC.
XX (UYWA-) UNIV WASHINGTON MEDICAL CENT GEORGE.
XX
PI Bauman C, Berman ML, Crockford DR, Goldstein AL;
XX Kater A, Rubin BK;
XX WPI; 1996-209656/21.
XX
PT Reduction of viscoelasticity of sputum of obstructive airway disease
PT - for use in treating, e.g. cystic fibrosis.
PS Disclosure; Figure 1C; 45pp; English.
XX
CC Thymosin beta 4 may be used in a composition alongside DNase1 to
CC reduce the viscoelasticity of sputum causing obstructive airway
CC disease (OAD). Such disease includes obstructive airway
CC chronic respiratory distress syndrome, chronic bronchitis, asthma,
CC emphysema and cystic fibrosis associated with excess actin,
CC polymerisation (polymerisation of G-actin into F-actin).
XX

SQ Sequence 41 AA;

Query Match
Best Local Similarity 54.7%; Score 116.5; DB 17; Length 41;
Matches 28; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 AHKLDLEIASLDRKAKLKATPMQ-KNTLMTKETTEQK 38
Db 1 ADKPDGMEIASFDKAKLKKTETQKNTLPTKETIEQK 38

RESULT 10
AAY80270
ID AAY80270 standard; peptide; 41 AA.
XX
AC AAY80270;
XX
DT 26-MAY-2000 (first entry)
DE Thymosin beta 4 peptide isoform Tbeta13.
XX
KW Thymosin beta 4; Tbeta4; tissue repair; angiogenesis; wound repair;
KW cell migration; vulnery; antiatherosclerotic; cytostatic; diagnosis;
KW healing disorder; fibrotic disease; ischaemia; atherosclerosis;
XX cell proliferative disorder.
OS Unidentified.
XX
PN WO200006190-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-US17282.
XX
PR 30-JUL-1998; 98US-0094690.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kleinman HK, Goldstein A, Malinda KM, Sosne G;
XX WPI; 2000-195195/17.
XX
PT A novel method to promote wound healing comprises administering
PT thymosin beta 4, useful for promoting tissue repair, angiogenesis and
PT cell migration
PS Claim 10; Fig 11; 61pp; English.
XX
CC A method has been developed for promoting wound healing in a subject
CC comprising administering a composition containing a wound healing
CC polypeptide comprising the amino acid sequence Leu-Lys-Lys-Thr-Glu-Thr
CC and conservative variants, which have wound healing activity. The wound
CC healing polypeptide is preferably thymosin beta 4 (Tbeta4) or an isoform
CC of Tbeta4. The polypeptide has vulnery, antiatherosclerotic and
CC cytostatic activities. It is useful for promoting wound healing, in vivo
CC in a subject, especially humans, or ex vivo in tissues (e.g. uro-genital,
CC gastro-intestinal, cardiovascular, muscle, connective and neural,
CC especially skin or eye tissue). Antibodies against Tbeta4 can be used
CC to inhibit/ameliorate wound healing. The level of Tbeta4 in a subject
CC can be used to diagnose a pathological state characterised by a wound
CC healing disorder, such as fibrotic disease, ischaemia, atherosclerosis
CC and cell proliferative disorders. Tbeta4 or its isoforms can also be
CC used to promote epithelial cell (e.g. skin cells, especially
CC keratinocytes, corneal cells) migration and angiogenesis. The polypeptide
CC is able to promote wound repair without any side effects, unlike prior
CC sequence growth and angiogenic factors used for such treatment. The present
CC invention represents a thymosin beta 4 peptide isoform from the present
XX

SQ Sequence 41 AA;

Query Match
Best Local Similarity 54.7%; Score 116.5; DB 21; Length 41;
Matches 28; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

YY

Thymosin beta 4 may be used in a composition alongside DNaseI to reduce the viscoelasticity of sputum causing obstructive airway

A method has been developed for promoting wound healing in a subject comprising administering a composition containing a wound healing polypeptide comprising the amino acid sequence Leu-Lys-Lys-Thr-Glu-Thr and conservative variants, which have wound healing activity. The wound healing polypeptide is preferably thymosin beta 4 (β tet4) or an isoform of β tet4. The polypeptide has vulnerary, antiatherosclerotic and cytostatic activities. It is useful for promoting wound healing, *in vivo* in a subject, especially humans, or *ex vivo* in tissues (e.g. uro-genital, gastro-intestinal, cardiovascular, muscle, connective and neural, especially skin or eye tissue). Antibodies against β tet4 can be used to inhibit/ameliorate wound healing. The level of β tet4 in a subject can be used to diagnose a pathological state characterised by a wound healing disorder, such as fibrotic disease, ischaemia, atherosclerosis and cell proliferative disorders. β tet4 or its isoforms can also be used to promote epithelial cell (e.g. skin cells, especially keratinocytes, corneal cells) migration and angiogenesis. The polypeptide is able to promote wound repair without any side effects, unlike prior art growth and angiogenic factors used for such treatment. The present sequence represents a thymosin beta 4 peptide isoform from the present invention.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 15:01:53 ; Search time 1074 Seconds
(without alignments)
3576.881 Million cell updates/sec

Title: US-09-915-178-1
Perfect score: 132
Sequence: 1 atggcacacaactagacct.....adggagtgaaatttctga 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10 *or more*

Total number of hits satisfying chosen parameters: 595492

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_bt.*
- 3: gb_in.*
- 4: gb_in.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pi.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	132	100.0	147	6	AX399230	Sequence	AX399230 Sequence
2	132	100.0	147	6	AX399232	Sequence	AX399232 Sequence
3	132	100.0	147	6	AX399234	Sequence	AX399234 Sequence
4	132	100.0	170536	9	HS518K17	Homo sapi	AL513423 Homo sapi
5	25	18.9	86594	2	AL645728	Homo sapi	AL645728 Homo sapi
6	25	18.9	133135	2	AL713970	Homo sapi	AL713970 Homo sapi
7	25	18.9	151840	2	AL691446	Mus muscu	AL691446 Mus muscu
8	25	18.9	177632	2	AC093615	Homo sapi	AC093615 Homo sapi
9	22	16.7	60372	2	AC097209	Rattus no	AC097209 Rattus no
10	22	16.7	192314	2	AC098254	Rattus no	AC098254 Rattus no
11	21	15.9	198015	2	AC130181	Rattus no	AC130181 Rattus no
12	20	15.2	38399	9	AP001477	Homo sapi	AP001477 Homo sapi
13	20	15.2	53707	9	AC116359	Homo sapi	AC116359 Homo sapi
14	20	15.2	170595	2	AC025937	Homo sapi	AC025937 Homo sapi
15	20	15.2	187097	2	AC113727	Rattus no	AC113727 Rattus no
16	20	15.2	192202	2	AC094105	Homo sapi	AC094105 Homo sapi
17	20	15.2	204080	2	AC093570	Mus muscu	AC093570 Mus muscu
18	20	15.2	207528	2	AL844896	Mus muscu	AL844896 Mus muscu
19	20	15.2	241585	2	AL844536	Mus muscu	AL844536 Mus muscu
20	20	15.2	263050	1	AP000981	Sulfolobu	AP000981 Sulfolobu
21	20	15.2	340000	9	AP001760	Homo sapi	AP001760 Homo sapi
22	19	14.4	11258	1	AE013648	Yersinia	AE013648 Yersinia
23	19	14.4	12292	1	AE011990	Xanthomon	AE011990 Xanthomon
24	19	14.4	67972	2	AC100719	Mus muscu	AC100719 Mus muscu
25	19	14.4	113654	9	AL606526	Human DNA	AL606526 Human DNA
26	19	14.4	121063	2	AC079482	Mus muscu	AC079482 Mus muscu
27	19	14.4	121063	2	AC079482	Mus muscu	AC079482 Mus muscu
28	19	14.4	127392	9	AC008570	Homo sapi	AC008570 Homo sapi
29	19	14.4	137782	10	AL645686	Mouse DNA	AL645686 Mouse DNA
30	19	14.4	155726	2	AC125887	Rattus no	AC125887 Rattus no
31	19	14.4	157361	10	AL645923	Mouse DNA	AL645923 Mouse DNA
32	19	14.4	158286	2	AC111338	Rattus no	AC111338 Rattus no
33	19	14.4	159642	2	AC120092	Rattus no	AC120092 Rattus no
34	19	14.4	160334	2	AC079549	Mus muscu	AC079549 Mus muscu
35	19	14.4	163942	9	AC034207	Homo sapi	AC034207 Homo sapi
36	19	14.4	166606	2	AC020685	Homo sapi	AC020685 Homo sapi
37	19	14.4	168766	2	AC126443	Mus muscu	AC126443 Mus muscu
38	19	14.4	172191	2	AL845505	Mus muscu	AL845505 Mus muscu
39	19	14.4	172797	2	AC122629	Rattus no	AC122629 Rattus no
40	19	14.4	174138	9	AC008871	Homo sapi	AC008871 Homo sapi
41	19	14.4	174670	2	AC112933	Mus muscu	AC112933 Mus muscu
42	19	14.4	175037	2	AC118879	Rattus no	AC118879 Rattus no
43	19	14.4	176409	2	AC097955	Rattus no	AC097955 Rattus no
44	19	14.4	176967	2	AC022742	Homo sapi	AC022742 Homo sapi
45	19	14.4	177033	2	AC102783	Mus muscu	AC102783 Mus muscu
46	19	14.4	180019	2	AC018623	Homo sapi	AC018623 Homo sapi
47	19	14.4	184157	9	AC110005	Homo sapi	AC110005 Homo sapi
48	19	14.4	185027	2	AC116851	Mus muscu	AC116851 Mus muscu
49	19	14.4	185828	2	AC116058	Rattus no	AC116058 Rattus no
50	19	14.4	186253	9	AC020892	Homo sapi	AC020892 Homo sapi
51	19	14.4	190543	2	AC097794	Rattus no	AC097794 Rattus no
52	19	14.4	194568	2	AC129614	Rattus no	AC129614 Rattus no
53	19	14.4	203578	2	AC113034	Mus muscu	AC113034 Mus muscu
54	19	14.4	209207	2	AC130718	Mus muscu	AC130718 Mus muscu
55	19	14.4	209299	2	AC111022	Mus muscu	AC111022 Mus muscu
56	19	14.4	223133	2	AL683829	Mus muscu	AL683829 Mus muscu
57	19	14.4	224040	2	AC023174	Mus muscu	AC023174 Mus muscu
58	19	14.4	229978	2	AC130218	Mus muscu	AC130218 Mus muscu
59	19	14.4	235050	1	AJ414158	Yersinia	AJ414158 Yersinia
60	19	14.4	250362	2	AC122256	Mus muscu	AC122256 Mus muscu
61	19	14.4	336512	2	AC126029	Mus muscu	AC126029 Mus muscu
62	18	13.6	174	11	G06175	human STS W	G06175 human STS W
63	18	13.6	220	11	G36127	STS h14a185	G36127 STS h14a185
64	18	13.6	243	6	AX381579	Sequence	AX381579 Sequence
65	18	13.6	353	6	AX381286	Sequence	AX381286 Sequence

66	18	13.6	395	6	AX381269	AX381269 Sequence	139	18	13.6	127361	9	AC007283	AC007283 Homo sapi
67	18	13.6	400	9	H0MTHMBX	M92381 Human thymo	c 140	18	13.6	129510	8	AL353685	AL353685 Oryza sat
68	18	13.6	428	6	AX381565	AX381565 Sequence	141	18	13.6	129608	9	OL3500047	OL3500047 Homo sapi
69	18	13.6	429	6	AX381695	AX381695 Sequence	142	18	13.6	130421	2	AC121428	AC121428 Rattus no
70	18	13.6	434	6	AX381689	AX381689 Sequence	c 143	18	13.6	133387	2	AP004061	AP004061 Oryza sat
71	18	13.6	438	6	AX381520	AX381520 Sequence	144	18	13.6	134940	2	AC018939	AC018939 Homo sapi
72	18	13.6	438	6	AX381645	AX381645 Sequence	145	18	13.6	137924	2	AC128092	AC128092 Rattus no
73	18	13.6	439	6	AX381972	AX381972 Sequence	c 146	18	13.6	137924	2	AC013762	AC013762 Homo sapi
74	18	13.6	439	9	H0MTHYB10	M20259 Human thymo	147	18	13.6	144048	9	AC007725	AC007725 Drosophill
75	18	13.6	443	6	AX381721	AX381721 Sequence	c 148	18	13.6	144152	3	AP005474	AP005474 Oryza sat
76	18	13.6	444	10	RATTHYB10	M17698 Rat thymosi	c 149	18	13.6	145953	9	AC107992	AC107992 Homo sapi
77	18	13.6	445	6	AX381789	AX381789 Sequence	c 150	18	13.6	149015	9	AF275948	AF275948 Homo sapi
78	18	13.6	446	6	AX381953	AX381953 Sequence	151	18	13.6	149034	9	AL772386	AL772386 Mouse DNA
c 79	18	13.6	446	6	AX410512	AX410512 Sequence	c 152	18	13.6	149807	10	AC063919	AC063919 Homo sapi
80	18	13.6	446	10	RATTHYBB	M58405 R.norvegicu	c 153	18	13.6	151196	9	AC131391	AC131391 Homo sapi
c 81	18	13.6	446	11	G22975	G22975 human STS W	c 154	18	13.6	152622	2	AC131391	AC131391 Homo sapi
82	18	13.6	449	6	AX381184	AX381184 Sequence	c 155	18	13.6	153087	2	AC123448	AC123448 Rattus no
83	18	13.6	451	6	AX381252	AX381252 Sequence	c 156	18	13.6	154265	2	AC127915	AC127915 Rattus no
84	18	13.6	451	6	AX381615	AX381615 Sequence	c 157	18	13.6	154318	9	AC026791	AC026791 Homo sapi
85	18	13.6	452	4	AF294616	AF294616 Bos tauru	c 158	18	13.6	155518	9	AC015528	AC015528 Homo sapi
86	18	13.6	452	6	AX381410	AX381410 Sequence	c 159	18	13.6	155930	2	AC109106	AC109106 Rattus no
87	18	13.6	453	6	AX381336	AX381336 Sequence	c 160	18	13.6	157126	2	AC121182	AC121182 Rattus no
88	18	13.6	453	6	AX410373	AX410373 Sequence	c 161	18	13.6	159360	2	AC122607	AC122607 Rattus no
89	18	13.6	453	9	S54005	S54005 thymosin be	c 162	18	13.6	160149	2	AC016380	AC016380 Homo sapi
90	18	13.6	455	6	AX381335	AX381335 Sequence	c 163	18	13.6	161095	2	AP005647	AP005647 Oryza sat
91	18	13.6	456	6	AX381281	AX381281 Sequence	c 164	18	13.6	162482	9	AC022740	AC022740 Homo sapi
92	18	13.6	465	4	AF506973	AF506973 Equus cab	c 165	18	13.6	162643	2	AP0011327	AP0011327 Mus muscu
93	18	13.6	465	6	AX381118	AX381118 Sequence	c 166	18	13.6	166266	2	AP001146	AP001146 Homo sapi
94	18	13.6	491	6	AX107107	AX107107 Sequence	c 167	18	13.6	166543	2	AC128985	AC128985 Rattus no
95	18	13.6	500	9	BC016731	BC016731 Homo sapi	c 168	18	13.6	167480	9	H58A18114	H58A18114 Human DNA
96	18	13.6	511	9	BC016025	BC016025 Homo sapi	c 169	18	13.6	168448	9	AC009469	AC009469 Homo sapi
97	18	13.6	517	6	AX381936	AX381936 Sequence	c 170	18	13.6	169341	2	AC114700	AC114700 Rattus no
98	18	13.6	539	10	RATTHYBA	M58406 R.norvegicu	c 171	18	13.6	169609	2	AC118128	AC118128 Rattus no
99	18	13.6	553	10	MNTB10075	Z48496 M.musculus	c 172	18	13.6	170696	2	AC108564	AC108564 Rattus no
100	18	13.6	559	6	AX381221	AX381221 Sequence	c 173	18	13.6	171030	9	CNS01D56F	CNS01D56F Human chr
101	18	13.6	611	5	XLXTBP4P	XL0692 Xenopus lae	c 174	18	13.6	171391	2	AC125699	AC125699 Rattus no
102	18	13.6	693	6	AX381860	AX381860 Sequence	c 175	18	13.6	173817	9	AC103834	AC103834 Homo sapi
c 103	18	13.6	693	6	AX381860	AX381860 Sequence	c 176	18	13.6	175127	2	AC016048	AC016048 Homo sapi
104	18	13.6	1262	9	H0MTHYB10	U28980 Gallus gall	c 177	18	13.6	176983	9	AC019172	AC019172 Homo sapi
105	18	13.6	1402	9	AF090913	M92383 Homo sapien	c 178	18	13.6	177826	2	AC016852	AC016852 Homo sapi
106	18	13.6	1517	6	AX428883	AX428883 Sequence	c 179	18	13.6	177988	2	AC022760	AC022760 Homo sapi
c 107	18	13.6	2230	9	AK097283	AK097283 Homo sapi	c 180	18	13.6	179216	2	AC074016	AC074016 Homo sapi
108	18	13.6	2460	10	AB040468	AB040468 Rattus no	c 181	18	13.6	179992	2	AC095165	AC095165 Rattus no
109	18	13.6	2489	3	DMCYCLB	X55542 D.melanogas	c 182	18	13.6	180699	9	AC079403	AC079403 Homo sapi
110	18	13.6	2612	3	DMCYCLB	M33192 D.melanogas	c 183	18	13.6	180993	2	AC102164	AC102164 Mus muscu
111	18	13.6	2630	3	AX102682	AX102682 Drosophill	c 184	18	13.6	181389	2	AC099496	AC099496 Homo sapi
112	18	13.6	4000	3	DMC006773	AX006773 Drosophill	c 185	18	13.6	182165	9	AC093429	AC093429 Homo sapi
113	18	13.6	4307	9	HSTYL	JX9688 H.sapiens m	c 186	18	13.6	182183	3	AC007889	AC007889 Drosophill
114	18	13.6	4407	5	AX072908	AX072908 Gallus ga	c 187	18	13.6	183023	2	AC095955	AC095955 Rattus no
115	18	13.6	23775	2	AC018178	AC018178 Drosophill	c 188	18	13.6	183438	9	AC007738	AC007738 Homo sapi
c 116	18	13.6	32303	9	AC007059	AC007059 Homo sapi	c 189	18	13.6	183999	6	AX092589	AX092589 Sequence
c 117	18	13.6	33419	10	AL662910	AL662910 Mouse DNA	c 190	18	13.6	184689	2	AC009172	AC009172 Homo sapi
c 118	18	13.6	39852	9	AC006128	AC006128 Homo sapi	c 191	18	13.6	185125	2	AC101663	AC101663 Mus muscu
c 119	18	13.6	43632	1	SC6A5	AL049485 Streptomy	c 192	18	13.6	186120	9	AL390755	AL390755 Human DNA
c 120	18	13.6	49574	2	AC098338	AC098338 Rattus no	c 193	18	13.6	186124	9	AC007598	AC007598 Homo sapi
c 121	18	13.6	54513	2	AC103847	AC103847 Homo sapi	c 194	18	13.6	186885	2	AC016297	AC016297 Homo sapi
c 122	18	13.6	54873	2	AC103803	AC103803 Homo sapi	c 195	18	13.6	187006	10	AL591436	AL591436 Mouse DNA
c 123	18	13.6	54958	2	AC103850	AC103850 Homo sapi	c 196	18	13.6	187364	10	AC021295	AC021295 Mus muscu
c 124	18	13.6	57327	10	AC003018	AC003018 Homo sapi	c 197	18	13.6	188921	2	AC025122	AC025122 Homo sapi
c 125	18	13.6	59469	2	AC110024	AC110024 Homo sapi	c 198	18	13.6	191438	3	AC008351	AC008351 Drosophill
c 126	18	13.6	60528	2	AC020123	AC020123 Drosophill	c 199	18	13.6	194295	2	AC129454	AC129454 Rattus no
c 127	18	13.6	61709	2	AC113001	AC113001 Mus muscu	c 200	18	13.6	195840	9	CNS00009	CNS00009 Human chr
c 128	18	13.6	68925	9	AC073196	AC073196 Homo sapi	c 201	18	13.6	196564	2	AL772179	AL772179 Mus muscu
c 129	18	13.6	90767	2	H0510A06	AL442104 Oryza sat	c 202	18	13.6	196674	2	AC091802	AC091802 Mus muscu
c 130	18	13.6	96128	10	AL663077	AL663077 Mouse DNA	c 203	18	13.6	198148	2	AC096943	AC096943 Rattus no
c 131	18	13.6	100751	2	AC114144	AC114144 Rattus no	c 204	18	13.6	199308	2	AC073679	AC073679 Mus muscu
c 132	18	13.6	102591	9	AC002978	AC002978 Homo sapi	c 205	18	13.6	199328	2	AC097362	AC097362 Rattus no
c 133	18	13.6	108408	2	AC022210	AC022210 Homo sapi	c 206	18	13.6	199827	2	AC026373	AC026373 Homo sapi
c 134	18	13.6	108952	2	AC096600	AC096600 Rattus no	c 207	18	13.6	200167	9	AC128881	AC128881 Rattus no
c 135	18	13.6	111020	2	AC105721	AC105721 Rattus no	c 208	18	13.6	201144	9	AF287262	AF287262 Homo sapi
c 136	18	13.6	112911	9	AC005865	AC005865 Homo sapi	c 209	18	13.6	202500	2	AL844142	AL844142 Mus muscu
c 137	18	13.6	121584	2	AC008232	AC008232 Drosophill	c 210	18	13.6	210891	2	AL116025	AL116025 Homo sapi
c 138	18	13.6	126335	2	AC127982	AC127982 Rattus no	c 211	18	13.6	212835	2	AC007612	AC007612 Homo sapi

c 212	18	13.6	218158	2	AC096363	AC096363 Rattus no	c 285	17	12.9	67683	9	AC092438	AC092438 Homo sapi
c 213	18	13.6	219017	9	AP000936	AP000936 Homo sapi	c 286	17	12.9	69954	2	AC090603	AC090603 Homo sapi
c 214	18	13.6	220462	2	AC073439	AC073439 Homo sapi	c 287	17	12.9	70394	2	AC023011	AC023011 Homo sapi
c 215	18	13.6	226483	3	AE003693	AE003693 Drosophill	c 288	17	12.9	70820	2	AC017451	AC017451 Drosophill
c 216	18	13.6	228919	2	AC090123	AC090123 Mus muscu	c 289	17	12.9	72756	2	AC018401	AC018401 Homo sapi
c 217	18	13.6	235218	2	AC074208	AC074208 Mus muscu	c 290	17	12.9	73916	9	AP000765	AP000765 Homo sapi
c 218	18	13.6	237619	2	AC073765	AC073765 Mus muscu	c 291	17	12.9	74229	2	AC111107	AC111107 Mus muscu
c 219	18	13.6	251256	2	AC099387	AC099387 Rattus no	c 292	17	12.9	79048	2	AC024976	AC024976 Homo sapi
c 220	18	13.6	263190	2	AC015657	AC015657 Mus muscu	c 293	17	12.9	79313	2	AC106500	AC106500 Rattus no
c 221	18	13.6	302225	3	AE003458	AE003458 Drosophill	c 294	17	12.9	80428	2	AC012631	AC012631 Homo sapi
c 222	18	13.6	347750	1	AP002998	AP002998 Mesorhizo	c 295	17	12.9	80655	8	AP004577	AP004577 Lotus jap
c 223	17	12.9	171	10	S40716	S40716 CD45 (signa	c 296	17	12.9	81365	8	AB025633	AB025633 Arabidops
c 224	17	12.9	430	6	AX119979	AX119979 Sequence	c 297	17	12.9	83857	2	AP004012	AP004012 Oryza sat
c 225	17	12.9	500	4	CFA278004	CFA278004 Canis fam	c 298	17	12.9	83989	8	H0505A02	AL512543 Oryza sat
c 226	17	12.9	570	6	AX250477	AX250477 Homo sapi	c 299	17	12.9	85475	9	AC013585	AC013585 Homo sapi
c 227	17	12.9	691	9	HSR326437	AJ326437 Homo sapi	c 300	17	12.9	86519	9	AC112242	AC112242 Homo sapi
c 228	17	12.9	711	9	HSR333683	AJ333683 Homo sapi	c 301	17	12.9	87340	9	AL357373	AL357373 Human DNA
c 229	17	12.9	735	9	AF151893	AF151893 Homo sapi	c 302	17	12.9	88176	2	AL390202	AL390202 Oryza sat
c 230	17	12.9	763	9	BC003540	BC003540 Homo sapi	c 303	17	12.9	89337	2	AC096092	AC096092 Rattus no
c 231	17	12.9	763	9	BC009428	BC009428 Homo sapi	c 304	17	12.9	96411	10	AL663114	AL663114 Mouse DNA
c 232	17	12.9	850	9	HMTGFBRII	D28131 Human mRNA	c 305	17	12.9	96540	8	ATAC012328	AC012328 Arabidops
c 233	17	12.9	911	9	HMTGFBRII	U69149 Human trans	c 306	17	12.9	98985	2	AL139427	AL139427 Homo sapi
c 234	17	12.9	928	9	HMTGFBRII	U52243 Human trans	c 307	17	12.9	99325	2	AL114146	AL114146 Rattus no
c 235	17	12.9	1077	6	AX121123	AX121123 Sequence	c 308	17	12.9	99591	2	AC013392	AC013392 Homo sapi
c 236	17	12.9	1089	5	AF296377	AF296377 Salmo tru	c 309	17	12.9	101814	2	AC122087	AC122087 Rattus no
c 237	17	12.9	1089	5	AF296381	AF296381 Salmo tru	c 310	17	12.9	104129	2	AC128003	AC128003 Rattus no
c 238	17	12.9	1099	5	AF296370	AF296370 Oncorhync	c 311	17	12.9	104782	9	CNS05FEZ	AL359681 Human chr
c 239	17	12.9	1185	8	AY086277	AY086277 Arabidops	c 312	17	12.9	106610	9	AC099679	AC099679 Homo sapi
c 240	17	12.9	1200	6	AX066883	AX066883 Sequence	c 313	17	12.9	106645	2	AC112845	AC112845 Rattus no
c 241	17	12.9	1227	8	AY070073	AY070073 Arabidops	c 314	17	12.9	106821	2	AC020000	AC020000 Drosophill
c 242	17	12.9	1284	10	AF251010	AF251010 Rattus no	c 315	17	12.9	107307	2	AC103269	AC103269 Rattus no
c 243	17	12.9	1704	6	AX481435	AX481435 Sequence	c 316	17	12.9	107458	9	AC023492	AC023492 Homo sapi
c 244	17	12.9	1918	6	E10743	E10743 cDNA encodi	c 317	17	12.9	107467	9	HS958B3	Z93023 Homo sapien
c 245	17	12.9	2090	6	AR031257	AR031257 Sequence	c 318	17	12.9	108752	10	AF084363	AF084363 Mus muscu
c 246	17	12.9	2090	6	AR094643	AR094643 Sequence	c 319	17	12.9	109183	2	AC104339	AC104339 Homo sapi
c 247	17	12.9	2090	6	AR096458	AR096458 Sequence	c 320	17	12.9	111350	9	ALI57814	ALI57814 Human DNA
c 248	17	12.9	2090	6	AR102454	AR102454 Sequence	c 321	17	12.9	112670	9	AL589165	AL589165 Human DNA
c 249	17	12.9	2090	6	AR170218	AR170218 Sequence	c 322	17	12.9	113853	9	ALI37853	ALI37853 Human DNA
c 250	17	12.9	2090	6	E31044	E31044 Method for	c 323	17	12.9	114007	9	HSJ1185K9	AL109807 Human DNA
c 251	17	12.9	2090	9	HMTGFBRII	M85079 Human TGF-b	c 324	17	12.9	115046	2	AC109955	AC109955 Rattus no
c 252	17	12.9	2094	6	AX451991	AX451991 Sequence	c 325	17	12.9	115279	9	AC112506	AC112506 Homo sapi
c 253	17	12.9	2095	6	I78448	I78448 Sequence 1	c 326	17	12.9	117955	9	AC019052	AC019052 Homo sapi
c 254	17	12.9	2153	5	AF287486	AF287486 Oncorhync	c 327	17	12.9	118030	2	AP000667	AP000667 Homo sapi
c 255	17	12.9	2738	4	CPRC8MPBP	Z23014 C.familiaria	c 328	17	12.9	118103	2	AC009817	AC009817 Homo sapi
c 256	17	12.9	2741	4	DGDPBBS	L13262 Canis famil	c 329	17	12.9	119308	2	AC094126	AC094126 Rattus no
c 257	17	12.9	2874	3	AY051856	AY051856 Drosophill	c 330	17	12.9	120133	2	AC108334	AC108334 Rattus no
c 258	17	12.9	3000	8	TIN251864	AJ251864 Polyocia	c 331	17	12.9	120846	9	AC018356	AC018356 Homo sapi
c 259	17	12.9	3653	5	AF387816	AF387816 Xenopus l	c 332	17	12.9	123246	8	AP004266	AP004266 Oryza sat
c 260	17	12.9	4592	10	RNU67309	U67309 Rattus norv	c 333	17	12.9	124699	9	AL590617	AL590617 Human DNA
c 261	17	12.9	5057	6	AR054007	AR054007 Sequence	c 334	17	12.9	125291	9	AP000646	AP000646 Homo sapi
c 262	17	12.9	5057	6	AR146183	AR146183 Sequence	c 335	17	12.9	126000	2	AC109739	AC109739 Rattus no
c 263	17	12.9	5057	10	RRBNOS	X59949 R.rattus MR	c 336	17	12.9	129175	9	AC022103	AC022103 Homo sapi
c 264	17	12.9	5666	9	AB061824	AB061824 Homo sapi	c 337	17	12.9	129980	2	AC126831	AC126831 Rattus no
c 265	17	12.9	5759	6	AX334519	AX334519 Sequence	c 338	17	12.9	130267	2	AC010597	AC010597 Homo sapi
c 266	17	12.9	5759	6	D50683	D50683 Homo sapien	c 339	17	12.9	130912	2	AC119050	AC119050 Gallus ga
c 267	17	12.9	10272	1	AE005682	AE005682 Caulobact	c 340	17	12.9	132870	2	AC119629	AC119629 Rattus no
c 268	17	12.9	12315	3	AF304204	AF304204 Strongylo	c 341	17	12.9	133747	2	AC123129	AC123129 Rattus no
c 269	17	12.9	37182	9	HSU9D4	Z68330 Human DNA s	c 342	17	12.9	133863	2	AC111322	AC111322 Rattus no
c 270	17	12.9	38786	5	AF170972	AF170972 Agelaius	c 343	17	12.9	134506	9	AC005738	AC005738 Homo sapi
c 271	17	12.9	43041	9	U73636	U73636 Human Chrom	c 344	17	12.9	136915	2	AC091028	AC091028 Homo sapi
c 272	17	12.9	45375	5	AF328738	AF328738 Agelaius	c 345	17	12.9	139487	2	AC123355	AC123355 Rattus no
c 273	17	12.9	48385	9	AC118990	AC118990 Homo sapi	c 346	17	12.9	139814	2	AP003964	AP003964 Oryza sat
c 274	17	12.9	50603	2	AC027167	AC027167 Homo sapi	c 347	17	12.9	140000	9	AP001791	AP001791 Homo sapi
c 275	17	12.9	50768	3	AC024853	AC024853 Caenorhab	c 348	17	12.9	141799	2	AC023581	AC023581 Homo sapi
c 276	17	12.9	55777	2	AC115729	AC115729 Mus muscu	c 349	17	12.9	142481	2	AC112432	AC112432 Rattus no
c 277	17	12.9	55946	9	AC104654	AC104654 Homo sapi	c 350	17	12.9	142718	2	AC109663	AC109663 Rattus no
c 278	17	12.9	58133	9	AL357057	AL357057 Human DNA	c 351	17	12.9	143039	2	AC125869	AC125869 Rattus no
c 279	17	12.9	59580	9	AC106875	AC106875 Homo sapi	c 352	17	12.9	145089	9	AC022418	AC022418 Homo sapi
c 280	17	12.9	62156	2	AC117678	AC117678 Mus muscu	c 353	17	12.9	145253	9	AC006329	AC006329 Homo sapi
c 281	17	12.9	63173	2	AC103995	AC103995 Homo sapi	c 354	17	12.9	145737	2	AC105649	AC105649 Rattus no
c 282	17	12.9	63436	2	AC023336	AC023336 Homo sapi	c 355	17	12.9	145910	8	OSGN00027	AL606600 Oryza sat
c 283	17	12.9	63479	2	AC124270	AC124270 Homo sapi	c 356	17	12.9	146040	2	AC129734	AC129734 Rattus no
c 284	17	12.9	65782	2	AC096277	AC096277 Rattus no	c 357	17	12.9	146743	2	AP003518	AP003518 Oryza sat

358	17	12.9	147274	2	AP005588	AP005588	Oryza sat	431	17	12.9	174031	4	AC091507	AC091507	Sus scrof
359	17	12.9	148151	9	AL513533	AL513533	Human DNA	C 432	17	12.9	174124	2	AC100778	AC100778	Homo sapi
360	17	12.9	149913	2	AC010330	AC010330	Homo sapi	C 433	17	12.9	175053	2	AC023226	AC023226	Homo sapi
361	17	12.9	149963	2	AC125673	AC125673	Rattus no	C 434	17	12.9	175456	2	AC115183	AC115183	Rattus no
362	17	12.9	150670	2	AC094577	AC094577	Rattus no	C 435	17	12.9	176209	9	AC009518	AC009518	Homo sapi
363	17	12.9	150885	2	AC023363	AC023363	Homo sapi	C 436	17	12.9	176350	2	AC094034	AC094034	Rattus no
364	17	12.9	151340	2	AC020961	AC020961	Mus muscu	C 437	17	12.9	176418	9	AC090811	AC090811	Homo sapi
365	17	12.9	151544	2	AC021650	AC021650	Homo sapi	C 438	17	12.9	176554	2	AC112308	AC112308	Rattus no
366	17	12.9	153500	2	AC128380	AC128380	Rattus no	C 439	17	12.9	176846	2	AC097730	AC097730	Mus muscu
367	17	12.9	153763	2	AC114420	AC114420	Mus muscu	C 440	17	12.9	176879	2	AC097730	AC097730	Rattus no
368	17	12.9	154109	2	AC108965	AC108965	Rattus no	C 441	17	12.9	177108	2	AC110561	AC110561	Mus muscu
369	17	12.9	154236	2	AC123394	AC123394	Rattus no	C 442	17	12.9	177158	2	AC121433	AC121433	Rattus no
370	17	12.9	154361	2	AC084189	AC084189	Homo sapi	C 443	17	12.9	177351	2	AC091170	AC091170	Homo sapi
371	17	12.9	154723	2	CNS01D02	AL133124	Homo sapi	C 444	17	12.9	178438	9	AC096774	AC096774	Homo sapi
372	17	12.9	154728	2	AC098631	AC098631	Rattus no	C 445	17	12.9	178508	2	AC023040	AC023040	Homo sapi
373	17	12.9	154728	2	AC016232	AC016232	Homo sapi	C 446	17	12.9	180008	2	AC022962	AC022962	Homo sapi
374	17	12.9	155450	2	AC073631	AC073631	Homo sapi	C 447	17	12.9	180421	2	AL805970	AL805970	Mus muscu
375	17	12.9	155877	2	AC073631	AC073631	Homo sapi	C 448	17	12.9	180423	9	AC012152	AC012152	Homo sapi
376	17	12.9	156325	2	AC117926	AC117926	Rattus no	C 449	17	12.9	180446	2	AP001997	AP001997	Homo sapi
377	17	12.9	156491	9	AL591720	AL591720	Human DNA	C 450	17	12.9	180568	2	AC125060	AC125060	Mus muscu
378	17	12.9	157536	2	AC015639	AC015639	Rattus no	C 451	17	12.9	180835	2	AC120484	AC120484	Rattus no
379	17	12.9	157603	9	AL360011	AL360011	Human DNA	C 452	17	12.9	181141	3	AC008346	AC008346	Drosophil
380	17	12.9	157636	9	AL360011	AL592112	Mouse DNA	C 453	17	12.9	181366	2	AC099442	AC099442	Rattus no
381	17	12.9	158307	10	AC096631	AC096631	Homo sapi	C 454	17	12.9	181418	2	AC102578	AC102578	Mus muscu
382	17	12.9	159322	9	AP001318	AP001318	Homo sapi	C 455	17	12.9	181501	2	AC016005	AC016005	Homo sapi
383	17	12.9	159569	9	AC010451	AC010451	Homo sapi	C 456	17	12.9	181581	2	AC113917	AC113917	Rattus no
384	17	12.9	159862	9	AL138815	AL138815	Human DNA	C 457	17	12.9	181614	2	AC119820	AC119820	Mus muscu
385	17	12.9	160210	9	AC064874	AC064874	Homo sapi	C 458	17	12.9	181651	2	AC129351	AC129351	Homo sapi
386	17	12.9	160655	2	AL157816	AL157816	Homo sapi	C 459	17	12.9	181732	2	AC127292	AC127292	Rattus no
387	17	12.9	160737	2	AC093788	AC093788	Homo sapi	C 460	17	12.9	182326	2	AC125693	AC125693	Rattus no
388	17	12.9	160853	9	AP000676	AP000676	Homo sapi	C 461	17	12.9	182565	2	AC101990	AC101990	Mus muscu
389	17	12.9	161289	9	AP001929	AP001929	Homo sapi	C 462	17	12.9	182898	2	AC112691	AC112691	Mus muscu
390	17	12.9	161548	9	AC092610	AC092610	Homo sapi	C 463	17	12.9	182988	3	AC010113	AC010113	Drosophil
391	17	12.9	162018	9	AC027384	AC027384	Homo sapi	C 464	17	12.9	183244	2	AC027188	AC027188	Homo sapi
392	17	12.9	162172	2	AC011023	AC011023	Homo sapi	C 465	17	12.9	183333	10	AL671987	AL671987	Mus muscu
393	17	12.9	162397	2	AC0112536	AC0112536	Homo sapi	C 466	17	12.9	184466	2	AC113275	AC113275	Mus muscu
394	17	12.9	162885	2	AC011321	AC011321	Homo sapi	C 467	17	12.9	184799	2	AC037448	AC037448	Homo sapi
395	17	12.9	162885	2	AC010822	AC010822	Homo sapi	C 468	17	12.9	185022	10	AL627123	AL627123	Mouse DNA
396	17	12.9	162891	10	AC003061	AC003061	Mouse Chr	C 469	17	12.9	185108	2	AC118835	AC118835	Rattus no
397	17	12.9	162891	2	AC094180	AC094180	Rattus no	C 470	17	12.9	185108	2	AC026265	AC026265	Homo sapi
398	17	12.9	162971	2	AC115395	AC115395	Rattus no	C 471	17	12.9	185324	2	AC128731	AC128731	Rattus no
399	17	12.9	163732	2	AC095112	AC095112	Rattus no	C 472	17	12.9	185505	2	AC008097	AC008097	Drosophil
400	17	12.9	163995	2	AC093212	AC093212	Homo sapi	C 473	17	12.9	185668	3	CNS01D0U	CNS01D0U	Human chr
401	17	12.9	164598	2	AC011040	AC011040	Homo sapi	C 474	17	12.9	185713	9	AC073554	AC073554	Homo sapi
402	17	12.9	165240	2	AC011040	AC011040	Homo sapi	C 475	17	12.9	185822	2	AC010784	AC010784	Homo sapi
403	17	12.9	165434	9	AC022448	AC022448	Homo sapi	C 476	17	12.9	186105	2	AC006229	AC006229	Homo sapi
404	17	12.9	165889	10	AL606841	AL606841	Mouse DNA	C 477	17	12.9	186373	9	AC096083	AC096083	Mouse DNA
405	17	12.9	166634	2	AC092602	AC092602	Homo sapi	C 478	17	12.9	186526	10	AL596083	AL596083	Mouse DNA
406	17	12.9	167692	2	AC121651	AC121651	Rattus no	C 479	17	12.9	186562	2	AL451079	AL451079	Homo sapi
407	17	12.9	167888	2	AC121651	AC121651	Rattus no	C 480	17	12.9	186744	2	AC131361	AC131361	Rattus no
408	17	12.9	167937	2	AC095024	AC095024	Sus scrof	C 481	17	12.9	187067	9	AC105389	AC105389	Homo sapi
409	17	12.9	168396	2	AL590010	AL590010	Homo sapi	C 482	17	12.9	187143	8	OSJN00107	OSJN00107	Oryza sat
410	17	12.9	168526	2	AC097677	AC097677	Rattus no	C 483	17	12.9	187278	2	AC110895	AC110895	Mus muscu
411	17	12.9	168607	2	AC121994	AC121994	Mus muscu	C 484	17	12.9	187428	2	AC009613	AC009613	Homo sapi
412	17	12.9	168933	2	AC127903	AC127903	Rattus no	C 485	17	12.9	187492	9	AC129260	AC129260	Rattus no
413	17	12.9	169758	2	AL713861	AL713861	Mus muscu	C 486	17	12.9	187710	9	CNS01DVI	CNS01DVI	Human chr
414	17	12.9	169781	10	AF336378	AF336378	Mus muscu	C 487	17	12.9	188561	2	AC103201	AC103201	Rattus no
415	17	12.9	170632	9	AL136321	AL136321	Human DNA	C 488	17	12.9	188816	2	AC132011	AC132011	Rattus no
416	17	12.9	170639	9	AL391065	AL391065	Human DNA	C 489	17	12.9	190119	2	AP001984	AP001984	Homo sapi
417	17	12.9	170928	9	AL356740	AL356740	Homo sapi	C 490	17	12.9	190136	2	AC094982	AC094982	Rattus no
418	17	12.9	171027	9	AP000756	AP000756	Homo sapi	C 491	17	12.9	190627	10	AL671982	AL671982	Mouse DNA
419	17	12.9	171279	2	AC036185	AC036185	Rattus no	C 492	17	12.9	190842	2	AC109939	AC109939	Rattus no
420	17	12.9	171707	2	AC108255	AC108255	Homo sapi	C 493	17	12.9	190842	2	AC105836	AC105836	Mouse DNA
421	17	12.9	171721	2	AC015744	AC015744	Homo sapi	C 494	17	12.9	191403	2	AL591598	AL591598	Mouse DNA
422	17	12.9	172203	9	AC005863	AC005863	Homo sapi	C 495	17	12.9	191520	10	AC010984	AC010984	Homo sapi
423	17	12.9	172468	2	AP005589	AP005589	Oryza sat	C 496	17	12.9	191540	30	AC091104	AC091104	Homo sapi
424	17	12.9	173077	2	AC024511	AC024511	Homo sapi	C 497	17	12.9	191832	9	AC097469	AC097469	Homo sapi
425	17	12.9	173083	2	AC034272	AC034272	Homo sapi	C 498	17	12.9	191883	2	AC063969	AC063969	Mus muscu
426	17	12.9	173106	9	AC008169	AC008169	Homo sapi	C 499	17	12.9	192042	2	AC102655	AC102655	Mus muscu
427	17	12.9	173201	9	AC008169	AC008169	Homo sapi	C 500	17	12.9	192428	2	AC129457	AC129457	Rattus no
428	17	12.9	173438	2	AC108527	AC108527	Rattus no	C 501	17	12.9	192453	2	AC130134	AC130134	Rattus no
429	17	12.9	173713	2	AC095840	AC095840	Rattus no	C 502	17	12.9	192954	2	AC126183	AC126183	Homo sapi
430	17	12.9	173935	10	AL670285	AL670285	Mouse DNA	C 503	17	12.9	192961	2	AC018886	AC018886	Homo sapi
	17	12.9	173935	10	AL670285	AL670285	Mouse DNA	C 503	17	12.9	194181	2	AC099694	AC099694	Mus muscu
	17	12.9	173935	10	AL670285	AL670285	Mouse DNA	C 503	17	12.9	194212	2	AC099694	AC099694	Mus muscu

504	17	12.9	194377	2	AC021726	AC021726 Homo sapi	577	16	12.1	307	6	AX187986	AX187986 Sequence
505	17	12.9	195386	2	AL805961	AL805961 Homo sapi	578	16	12.1	311	6	AX186432	AX186432 Sequence
506	17	12.9	196097	10	AL714006	AL714006 Mouse DNA	579	16	12.1	331	6	AX185097	AX185097 Sequence
507	17	12.9	196175	10	AC069019	AC069019 Mus muscu	c 580	16	12.1	400	11	GI3730	SHGC-13010
508	17	12.9	196520	2	AC083830	AC083830 Homo sapi	581	16	12.1	406	1	AF455091	AF455091 Unculture
c 509	17	12.9	197088	2	AC107502	AC107502 Rattus no	c 582	16	12.1	429	6	AX329988	AX329988 Sequence
510	17	12.9	197143	2	AC069173	AC069173 Homo sapi	c 583	16	12.1	444	6	AX331994	AX331994 Sequence
511	17	12.9	197946	10	AC098722	AC098722 Mus muscu	c 584	16	12.1	444	6	AX407484	AX407484 Sequence
512	17	12.9	199071	10	AL669938	AL669938 Mouse DNA	c 585	16	12.1	486	11	AU027620	Rattus no
c 513	17	12.9	199101	10	MAE000665	AE000665 Mus muscu	c 586	16	12.1	528	6	AX385616	AX385616 Sequence
514	17	12.9	200124	2	AC129675	AC129675 Homo sapi	c 587	16	12.1	576	5	AF212851	Aulonocar
c 515	17	12.9	200380	9	AC022898	AC022898 Homo sapi	c 588	16	12.1	799	4	AF325552	AF325552 Bos tauru
c 516	17	12.9	200488	2	AC111048	AC111048 Mus muscu	c 589	16	12.1	834	11	CNS06EQC	AL395434 T7 end of
c 517	17	12.9	200704	9	AC099781	AC099781 Homo sapi	c 590	16	12.1	865	9	HS338652	HS338652 Homo sapi
c 518	17	12.9	200767	2	AC110635	AC110635 Rattus no	c 591	16	12.1	960	10	RATUGF1B4H	D38068 Rattus norv
519	17	12.9	200885	2	AC119856	AC119856 Mus muscu	c 592	16	12.1	969	8	AB001020	AB001020 Schizosac
520	17	12.9	201399	9	AL357149	AL357149 Human DNA	593	16	12.1	1001	3	AY0711393	AY0711393 Drosophil
521	17	12.9	201412	9	AC096921	AC096921 Homo sapi	594	16	12.1	1018	1	AF526993	AF526993 Unculture
522	17	12.9	201699	9	AC079844	AC079844 Homo sapi	c 595	16	12.1	1028	10	BC002172	BC002172 Mus muscu
523	17	12.9	203111	2	AC096313	AC096313 Rattus no	596	16	12.1	1043	5	AF212849	AF212849 Aulonocar
524	17	12.9	203324	10	AL662780	AL662780 Mouse DNA	c 597	16	12.1	1053	3	TBR315078	TBR315078 Trypanoso
525	17	12.9	203558	2	AC118395	AC118395 Rattus no	598	16	12.1	1094	5	AF212850	AF212850 Aulonocar
c 526	17	12.9	203699	2	AC040973	AC040973 Homo sapi	599	16	12.1	1095	5	XELXPACB2	XELXPACB2
527	17	12.9	203936	2	AC094828	AC094828 Rattus no	600	16	12.1	1212	6	AX086207	AX086207 Sequence
528	17	12.9	204477	2	AC122374	AC122374 Mus muscu	601	16	12.1	1212	9	HSM801628	HSM801628 Homo sapi
529	17	12.9	204888	2	AL731800	AL731800 Mus muscu	602	16	12.1	1213	3	AY060898	AY060898 Drosophil
c 530	17	12.9	205759	10	AL669853	AL669853 Mouse DNA	603	16	12.1	1238	3	AF136971	AF136971 Homo sapi
c 531	17	12.9	207086	2	AC034290	AC034290 Homo sapi	c 604	16	12.1	1259	8	AY040533	AY040533 Gossypium
c 532	17	12.9	207122	2	AC117235	AC117235 Mus muscu	605	16	12.1	1265	9	BC002444	BC002444 Homo sapi
c 533	17	12.9	207877	2	AC129206	AC129206 Mus muscu	606	16	12.1	1277	5	XELXPACB	XELXPACB
c 534	17	12.9	207922	2	AC073790	AC073790 Mus muscu	c 607	16	12.1	1344	5	XL090895	XL090895 Xenopus lae
c 535	17	12.9	208187	2	AL583884	AL583884 Mus muscu	608	16	12.1	1385	9	AK022861	AK022861 Homo sapi
c 536	17	12.9	208709	9	CNS01RH3	AL592162 Mus muscu	609	16	12.1	1406	14	HSMA41A	HSMA41A Gallid herp
c 537	17	12.9	208953	2	AC095986	AC095986 Rattus no	610	16	12.1	1453	6	AX073680	AX073680 Sequence
c 538	17	12.9	209507	2	AC126279	AC126279 Homo sapi	611	16	12.1	1464	9	HSM801555	HSM801555 Homo sapi
c 539	17	12.9	210105	2	AC125948	AC125948 Rattus no	c 612	16	12.1	1641	8	YSPRGS4	YSPRGS4
540	17	12.9	211759	2	AC106937	AC106937 Rattus no	613	16	12.1	1710	9	AF33981A	AF33981A Homo sapi
541	17	12.9	213916	2	AC073473	AC073473 Homo sapi	614	16	12.1	1815	14	GHU17702	GHU17702 Gallid herp
542	17	12.9	214709	2	AC116514	AC116514 Mus muscu	615	16	12.1	1926	9	BC033843	BC033843 Homo sapi
c 543	17	12.9	214800	2	AC112851	AC112851 Rattus no	616	16	12.1	1980	8	SCABC1G	SCABC1G
544	17	12.9	215516	2	AC024694	AC024694 Mus muscu	c 617	16	12.1	2199	6	EL17395	EL17395 cDNA encodi
545	17	12.9	217073	2	AC094162	AC094162 Rattus no	c 618	16	12.1	2199	8	AB010105	AB010105 Grifola f
c 546	17	12.9	217186	2	AC118472	AC118472 Mus muscu	619	16	12.1	2274	9	AF134159	AF134159 Homo sapi
c 547	17	12.9	218747	2	AL611985	AL611985 Mus muscu	620	16	12.1	2335	10	H010058S08	H010058S08
548	17	12.9	220035	2	AC122047	AC122047 Mus muscu	621	16	12.1	2410	3	AF077868	AF077868 Caenorhab
549	17	12.9	221883	2	AC104752	AC104752 Mus muscu	622	16	12.1	2527	9	AK027639	AK027639 Homo sapi
c 550	17	12.9	221898	10	AL669891	AL669891 Mouse DNA	623	16	12.1	2545	9	AK023008	AK023008 Homo sapi
c 551	17	12.9	223496	2	AL732573	AL732573 Mus muscu	624	16	12.1	2638	9	AK056497	AK056497 Homo sapi
c 552	17	12.9	225957	9	AC069175	AC069175 Homo sapi	625	16	12.1	2639	9	AB081807	AB081807 Streptomy
c 553	17	12.9	226467	2	AC121855	AC121855 Mus muscu	626	16	12.1	2696	9	BC018759	BC018759 Homo sapi
c 554	17	12.9	226576	3	CNS07EGE	AL590447 chromosom	627	16	12.1	2741	14	HSMAN1I	HSMAN1I
c 555	17	12.9	227801	2	AL713993	AL713993 Homo sapi	c 628	16	12.1	2817	6	EL17394	EL17394 gDNA encodi
556	17	12.9	229957	10	AL670231	AL670231 Mouse DNA	629	16	12.1	2847	8	AY091029	AY091029 Arabidops
c 557	17	12.9	234019	2	AC117951	AC117951 Rattus no	630	16	12.1	2999	9	HSM803265	HSM803265 Homo sapi
c 558	17	12.9	238521	2	AC078932	AC078932 Mus muscu	631	16	12.1	3149	6	AX451700	AX451700 Sequence
c 559	17	12.9	244804	2	AC109236	AC109236 Mus muscu	c 632	16	12.1	3240	8	AB010104	AB010104 Grifola f
c 560	17	12.9	256804	2	AC113622	AC113622 Rattus no	633	16	12.1	3270	8	AB3858	AB3858 Sequence 3
561	17	12.9	260699	2	AC006893	AC006893 Caenorhab	634	16	12.1	3308	14	HEU86698	HEU86698 Human endog
562	17	12.9	267077	2	AL773532	AL773532 Mus muscu	c 635	16	12.1	3392	8	PECXYLAN	PECXYLAN
563	17	12.9	273744	3	AE003558	AE003558 Drosophil	c 636	16	12.1	3424	9	AK055899	AK055899 Homo sapi
564	17	12.9	281797	3	AE003794	AE003794 Drosophil	637	16	12.1	3437	6	AK46720	AK46720 Sequence 3
c 565	17	12.9	286552	2	AC079559	AC079559 Mus muscu	638	16	12.1	3437	6	AR110167	AR110167 Sequence
c 566	17	12.9	332050	1	AP005276	AP005276 Corynebac	639	16	12.1	3437	6	AR211698	AR211698 Sequence
567	17	12.9	349980	6	AX127146	AX127146 Sequence	640	16	12.1	3437	6	AX333688	AX333688 Sequence
568	16	12.1	215	5	OPU02706	U02706 Oreochromis	641	16	12.1	3437	9	HSMPM1	HSMPM1
569	16	12.1	215	5	OPU02706	U02706 Oreochromis	642	16	12.1	3456	6	A46718	A46718 Sequence 1
c 570	16	12.1	220	6	OPSATA05	W5735 O. placidus	643	16	12.1	3456	6	AR211697	AR211697 Sequence
571	16	12.1	234	5	SGU02720	AR069084 Sequence	644	16	12.1	3456	6	AR211697	AR211697 Sequence
572	16	12.1	234	5	SGSATA04	X75727 S.gallilaeus	645	16	12.1	3513	1	AK095489	AK095489 Homo sapi
573	16	12.1	235	5	SGU02718	X75727 S.gallilaeus	646	16	12.1	3574	1	KPNBUDOPRN	KPNBUDOPRN
574	16	12.1	235	5	SGSATA02	X75719 S.gallilaeus	c 647	16	12.1	3604	9	AK055469	AK055469 Homo sapi
575	16	12.1	235	5	SGSATA02	G65736 stcb20F6_47	648	16	12.1	3762	8	AY078948	AY078948 Arabidops
c 576	16	12.1	268	11	G65736		649	16	12.1	3837	9	AF116574	AF116574 Homo sapi

c 650	16	12.1	3858	1	AF240778	AF240778 Pasteurel	c 723	16	12.1	30213	3	U41032	U41032 Caenorhabdi
c 651	16	12.1	4013	10	MMAR001794	AF0011794 Mus muscu	c 724	16	12.1	32682	2	AC014984	AC014984 Drosophill
c 652	16	12.1	4023	9	AF350251	AF500251 Homo sapi	c 725	16	12.1	32828	3	CEK08E5	Z303974 Caenorhabdi
c 653	16	12.1	4076	8	SCYGL119W	Z72641 S.cerevisia	c 726	16	12.1	33274	8	SPCP20C8	AL512862 S.pombe c
c 654	16	12.1	4308	1	PWTOXA	X52478 Pasteurella	c 727	16	12.1	34195	3	US2003	U52003 Caenorhabdi
c 655	16	12.1	4316	1	PMTTXX	Z28388 P.multocida	c 728	16	12.1	34589	3	AC112240	AC112240 Homo sapi
c 656	16	12.1	4316	1	PMPMT	X57775 P.multocida	c 729	16	12.1	35251	2	AC113511	AC113511 Mus muscu
c 657	16	12.1	4380	6	PMTOX	X51512 Pasteurella	c 730	16	12.1	35782	3	AF039711	AF039711 Caenorhab
c 658	16	12.1	4380	6	A08187	A08187 Synthetic n	c 731	16	12.1	36052	3	L14429	L14429 Caenorhabdi
c 659	16	12.1	4380	6	A27814	A27814 P.multicoda	c 732	16	12.1	36133	3	HSA007973	HSA007973
c 660	16	12.1	4380	6	AR107541	AR107541 Sequence	c 733	16	12.1	36450	2	AC035800	AC035800 Human DNA
c 661	16	12.1	4413	9	HSA012755	AJ012755 Homo sapi	c 734	16	12.1	36598	2	AC095907	AC095907 Rattus no
c 662	16	12.1	4428	10	MMU81030	U81030 Mus musculu	c 735	16	12.1	36727	9	AL512289	AL512289 Human DNA
c 663	16	12.1	4591	9	AB014534	AB014534 Homo sapi	c 736	16	12.1	38155	6	AR204183	AR204183 Sequence
c 664	16	12.1	4664	10	AF079520	AF079520 Mus muscu	c 737	16	12.1	38491	8	SPCC338	SPCC338 Homo sapi
c 665	16	12.1	4732	9	AB051522	AB051522 Homo sapi	c 738	16	12.1	38734	3	AF099919	AF099919 Caenorhab
c 666	16	12.1	4815	6	AX360058	AX360058 Sequence	c 739	16	12.1	39099	3	AC000084	AC000084 Homo sapi
c 667	16	12.1	4946	9	HUMPRPH1	M13057 Human acidi	c 740	16	12.1	39569	9	AC000084	AL049755 S.pombe c
c 668	16	12.1	4946	11	G28580	G28580 human STS S	c 741	16	12.1	40489	8	SPCC589	AL35082 Human DNA
c 669	16	12.1	5153	10	AF083372	AF083372 Mus muscu	c 742	16	12.1	40886	9	AC016762	AC016762 Homo sapi
c 670	16	12.1	5184	9	AF041835	AF041835 Homo sapi	c 743	16	12.1	43000	9	HS3D19	AL049753 Homo sapi
c 671	16	12.1	5454	1	AF315586	AF315586 Pseudomon	c 744	16	12.1	43307	9	CE2005	Z79752 Caenorhabdi
c 672	16	12.1	5500	1	PP030471	U30471 Plasmid pSA	c 745	16	12.1	43440	3	AF022141	AF022141 Homo sapi
c 673	16	12.1	5792	9	AL713876	AL713876 Human DNA	c 746	16	12.1	43473	9	AF020801	AF020801 Homo sapi
c 674	16	12.1	6018	9	S44029	S44029 red visual	c 747	16	12.1	44548	9	AC005862	AC005862 Homo sapi
c 675	16	12.1	6299	9	AB007864	AB007864 Homo sapi	c 748	16	12.1	45000	5	FRU90880	U90880 Fugu rubrip
c 676	16	12.1	6390	6	AX097470	AX097470 Sequence	c 749	16	12.1	46288	5	AL354764	AL354764 Human DNA
c 677	16	12.1	6431	1	ECU12441	U12441 Escherichia	c 750	16	12.1	47352	2	AC129582	AC129582 Mus muscu
c 678	16	12.1	6492	8	SJRI8RNA	Z32848 S.japonicus	c 751	16	12.1	47400	2	AC129582	AC130262 Rattus no
c 679	16	12.1	6706	10	AF017806	AF017806 Mus muscu	c 752	16	12.1	48197	2	AC130262	AC130262 Rattus no
c 680	16	12.1	6940	6	AX409077	AX409077 Sequence	c 753	16	12.1	48433	2	AC120152	AC120152 Mus muscu
c 681	16	12.1	6940	9	D79992	D79992 Human mRNA	c 754	16	12.1	48908	6	AR204241	AR204241 Sequence
c 682	16	12.1	6972	9	HAAXTRSYV	X90840 H.sapiens m	c 755	16	12.1	50170	9	AL355872	AL355872 Human DNA
c 683	16	12.1	7138	9	HSX80554V	AL834444 Homo sapi	c 756	16	12.1	50314	2	AC107912	AC107912 Homo sapi
c 684	16	12.1	7286	1	AE005332	AE005332 Escherich	c 757	16	12.1	50514	2	AC100970	AC100970 Homo sapi
c 685	16	12.1	7865	8	SP18RRNAA	Z19578 S.pombe gen	c 758	16	12.1	51173	2	AC103764	AC103764 Mus muscu
c 686	16	12.1	7878	6	AX332512	AX332512 Sequence	c 759	16	12.1	52083	2	AC100992	Continuation (5 of
c 687	16	12.1	7878	9	HSTRE210	X63546 H.sapiens m	c 760	16	12.1	53372	2	AC098413	AC098413 Rattus no
c 688	16	12.1	8201	6	I76205	I76205 Sequence 9	c 761	16	12.1	53721	2	AC098413	AC017732 Drosophill
c 689	16	12.1	8201	9	HSTRE213	X63547 H.sapiens m	c 762	16	12.1	54784	2	AC017732	AC115729 Mus muscu
c 690	16	12.1	8495	3	AF017096	AF017096 Drosophill	c 763	16	12.1	55777	2	AC125102_4	Continuation (5 of
c 691	16	12.1	9152	9	HSNFX1112	Z47735 H.sapiens N	c 764	16	12.1	55892	9	HSJ85A12	AL049858 Human DNA
c 692	16	12.1	9649	5	AF256651	AF256651 Calman cr	c 765	16	12.1	57049	9	AL589825	AL589825 Human DNA
c 693	16	12.1	9677	9	AF111198	AF111198 Homo sapi	c 766	16	12.1	57578	9	AL589825	AL589825 Homo sapi
c 694	16	12.1	10029	1	AE005325	AE005325 Escherich	c 767	16	12.1	58342	2	AC104022	AC104022 Homo sapi
c 695	16	12.1	10029	1	AE013918	AE013918 Versinia	c 768	16	12.1	58511	2	AC131414	AC131414 Rattus no
c 696	16	12.1	10062	1	AE010425	AE010425 Methanopy	c 769	16	12.1	59509	2	AC123720	AC123720 Mus muscu
c 697	16	12.1	10129	1	AE002081	AE002081 Deinococc	c 770	16	12.1	61344	9	AL607076	AL607076 Human DNA
c 698	16	12.1	10260	2	AC129145	AC129145 Rattus no	c 771	16	12.1	62072	2	AC101766	AC101766 Mus muscu
c 699	16	12.1	10758	1	AE001231	AE001231 Treponema	c 772	16	12.1	62294	2	AC115977	AC115977 Rattus no
c 700	16	12.1	11129	1	AE001069	AE001069 Archaeogl	c 773	16	12.1	62954	2	AC130137	AC130137 Rattus no
c 701	16	12.1	11301	3	AF139060	AF139060 Caenorhab	c 774	16	12.1	62974	2	AC116492	AC116492 Homo sapi
c 702	16	12.1	11325	1	AE004406	AE004406 Vibrio ch	c 775	16	12.1	64196	2	AC110804	AC110804 Homo sapi
c 703	16	12.1	11809	1	AE005290	AE005290 Escherich	c 776	16	12.1	64351	2	AC111051	AC111051 Mus muscu
c 704	16	12.1	12848	6	AR204356	AR204356 Sequence	c 777	16	12.1	65028	2	AC127651	AC127651 Rattus no
c 705	16	12.1	13045	14	GH017705	U17705 Gallid herp	c 778	16	12.1	65700	2	AC121141	AC121141 Homo sapi
c 706	16	12.1	13104	9	AE004656	AE004656 Pseudomon	c 779	16	12.1	67066	2	AC084712	AL138798 Human DNA
c 707	16	12.1	13236	9	AB012113	AB012113 Homo sapi	c 780	16	12.1	68166	2	AC121112	AC121112 Mus muscu
c 708	16	12.1	13505	1	AE005441	AE005441 Escherich	c 781	16	12.1	68314	9	AL138798	AC11027 Mus muscu
c 709	16	12.1	13624	1	AE006459	AE006459 Escherich	c 782	16	12.1	68678	2	AC111027	AL591485 Mus muscu
c 710	16	12.1	13847	3	HS175B9B	Z69652 Human DNA s	c 783	16	12.1	68785	5	AL591664	AL591664 Zebrafish
c 711	16	12.1	14302	3	AF068718	AF068718 Caenorhab	c 784	16	12.1	69335	2	AC102217	AC102217 Mus muscu
c 712	16	12.1	17056	6	AR164808	AR164808 Sequence	c 785	16	12.1	70873	2	AC119927	AC119927 Mus muscu
c 713	16	12.1	18120	9	HSB20F6	Z82174 Human DNA s	c 786	16	12.1				
c 714	16	12.1	18765	1	AE004731	AE004731 Pseudomon	c 787	16	12.1				
c 715	16	12.1	20385	1	AE008892	AE008892 Salmonell	c 788	16	12.1				
c 716	16	12.1	21480	9	HSOC8B6	Z68193 Human DNA s	c 789	16	12.1				
c 717	16	12.1	23106	9	HS271718	AJ271718 Homo sapi	c 790	16	12.1				
c 718	16	12.1	23506	1	AE008863	AE008863 Salmonell	c 791	16	12.1				
c 719	16	12.1	24453	9	HS404P13	AL035069 Human DNA	c 792	16	12.1				
c 720	16	12.1	26100	3	DMC190E7	AL022017 Drosophill	c 793	16	12.1				
c 721	16	12.1	26881	9	HSV434E11	Z70758 Human DNA s	c 794	16	12.1				
c 722	16	12.1	28650	8	SPAC22G7	Z54328 S.pombe chr	c 795	16	12.1				

796	16	12.1	71763	2	AC100350	AC100350 Mus muscu	869	16	12.1	97600	8	AP004570	AP004570 Oryza sat
c 797	16	12.1	71820	2	AC100627	AC100627 Mus muscu	c 870	16	12.1	97710	9	AL445210	AL445210 Human DNA
c 798	16	12.1	72281	2	HSF200148	AL109765 Homo sapi	c 871	16	12.1	99778	2	AC112883	AC112883 Rattus no
799	16	12.1	72308	2	AC104994	AC104994 Homo sapi	c 872	16	12.1	99901	9	AC112715	AC112715 Homo sapi
800	16	12.1	72511	2	AC025954	AC025954 Homo sapi	c 873	16	12.1	100259	9	AC005800	AC005800 Homo sapi
801	16	12.1	73359	2	AC025012	AC025012 Homo sapi	c 874	16	12.1	100292	10	AL627346	AL627346 Mouse DNA
c 802	16	12.1	73746	2	AC101286	AC101286 Mus muscu	c 875	16	12.1	100300	8	AC114970	AC114970 Homo sapi
c 803	16	12.1	73920	10	AC091397	AC091397 Rattus no	c 876	16	12.1	100746	8	AC005489	AC005489 Genomic s
c 804	16	12.1	74229	2	AC111107	AC111107 Mus muscu	c 877	16	12.1	101055	2	AC107941	AC107941 Homo sapi
c 805	16	12.1	74315	2	AC023029	AC023029 Homo sapi	c 878	16	12.1	101759	2	AP005365	AP005365 Homo sapi
806	16	12.1	74712	2	AC121278	AC121278 Mus muscu	c 879	16	12.1	102477	9	AC008935	AC008935 Homo sapi
807	16	12.1	75367	2	AC107515	AC107515 Rattus no	c 880	16	12.1	102540	8	AC079281	AC079281 Arabidops
c 808	16	12.1	75525	9	AL391561	AL391561 Human DNA	c 881	16	12.1	102840	9	AL161719	AL161719 Human DNA
809	16	12.1	76746	2	AC121670	AC121670 Rattus no	c 882	16	12.1	103122	9	AC005663	AC005663 Homo sapi
c 810	16	12.1	76746	2	AC121670	AC121670 Rattus no	c 883	16	12.1	103243	2	AC106472	AC106472 Rattus no
c 811	16	12.1	76966	2	AC032037	AC032037 Homo sapi	c 884	16	12.1	103458	2	AC127085	AC127085 Rattus no
c 812	16	12.1	77290	8	AC074284	AC074284 Arabidops	c 885	16	12.1	104171	2	AC019499	AC019499 Drosophil
c 813	16	12.1	77728	9	AP000146	AP000146 Homo sapi	c 886	16	12.1	104492	9	AC003985	AC003985 Homo sapi
c 814	16	12.1	77728	9	AP000231	AP000231 Homo sapi	c 887	16	12.1	104733	2	AC122598	AC122598 Rattus no
c 815	16	12.1	79054	8	F21F23	AC027656 Sequence	c 888	16	12.1	104753	2	AC114062	AC114062 Rattus no
c 816	16	12.1	79304	2	AC103063	AC103063 Rattus no	c 889	16	12.1	105250	2	AP004099	AP004099 Oryza sat
c 817	16	12.1	79899	8	AB011474	AB011474 Arabidops	c 890	16	12.1	105250	2	AC094644	AC094644 Rattus no
c 818	16	12.1	80460	10	AL513014	AL513014 Mouse DNA	c 891	16	12.1	105866	2	AC021602	AC021602 Homo sapi
c 819	16	12.1	80828	9	AC093247	AC093247 Homo sapi	c 892	16	12.1	106806	2	AC095551	AC095551 Rattus no
c 820	16	12.1	81044	2	AC103124	AC103124 Rattus no	c 893	16	12.1	107733	9	AC008472	AC008472 Homo sapi
c 821	16	12.1	81054	9	AL356052	AL356052 Human DNA	c 894	16	12.1	107745	9	AL139042	AL139042 Human DNA
c 822	16	12.1	81283	2	AC097851	AC097851 Rattus no	c 895	16	12.1	108055	2	AC127721	AC127721 Rattus no
c 823	16	12.1	81410	9	AP004715	AP004715 Homo sapi	c 896	16	12.1	108317	2	AC123104	AC123104 Rattus no
c 824	16	12.1	81414	8	AB024037	AB024037 Arabidops	c 897	16	12.1	108523	9	AC000159	AC000159 Homo sapi
c 825	16	12.1	81580	8	AP000736	AP000736 Arabidops	c 898	16	12.1	108742	2	AC023817	AC023817 Homo sapi
826	16	12.1	82404	9	AL333399	AL333399 Human DNA	c 899	16	12.1	109219	9	AF159227	AF159227 Homo sapi
827	16	12.1	82435	9	AC092424	AC092424 Homo sapi	c 900	16	12.1	109225	2	AC091417	AC091417 Rattus no
828	16	12.1	82660	2	AC107433	AC107433 Rattus no	c 901	16	12.1	109299	3	AC117838	AC117838 Caenorhab
c 829	16	12.1	83097	8	AB025624	AB025624 Arabidops	c 902	16	12.1	110000	2	AC009579	AC009579 Homo sapi
c 830	16	12.1	84001	9	AL162739	AL162739 Human DNA	c 903	16	12.1	110000	2	AC087331	AC087331
c 831	16	12.1	84557	2	AC129132	AC129132 Rattus no	c 904	16	12.1	110000	2	AC087331	AC087331
c 832	16	12.1	84586	9	AL338685	AL338685 Human DNA	c 905	16	12.1	110000	2	AC117400	AC117400
c 833	16	12.1	84780	9	AC005885	AC005885 Homo sapi	c 906	16	12.1	110000	2	AC122682	AC122682
834	16	12.1	84866	2	AC103533	AC103533 Rattus no	c 907	16	12.1	110000	2	AC123950	AC123950
835	16	12.1	84866	2	AC103533	AC103533 Rattus no	c 908	16	12.1	110000	2	AC123950	AC123950
836	16	12.1	85472	2	AC095888	AC095888 Rattus no	c 909	16	12.1	110000	2	AC125140	AC125140
c 837	16	12.1	85579	2	AC004744	AC004744 Homo sapi	c 910	16	12.1	110000	2	HSY313FA	HSY313FA
c 838	16	12.1	85750	2	AC103346	AC103346 Rattus no	c 911	16	12.1	110630	2	OSJN00140	OSJN00140
839	16	12.1	86371	9	AL355672	AL355672 Human DNA	c 912	16	12.1	110970	9	AF165144	AF165144 Homo sapi
840	16	12.1	86696	9	AC097769	AC097769 Rattus no	c 913	16	12.1	111081	2	AC010249	AC010249 Homo sapi
841	16	12.1	86774	9	AL359766	AL359766 Human DNA	c 914	16	12.1	111688	2	AC105020	AC105020 Homo sapi
842	16	12.1	87286	2	AC014436	AC014436 Drosophil	c 915	16	12.1	111864	9	AL591499	AL591499 Human DNA
843	16	12.1	87402	9	HSJ437M21	AL043758 Human DNA	c 916	16	12.1	112059	9	AL162727	AL162727 Human DNA
844	16	12.1	87524	2	AC097876	AC097876 Rattus no	c 917	16	12.1	112365	9	AC027317	AC027317 Homo sapi
c 845	16	12.1	87822	2	AC013928	AC013928 Drosophil	c 918	16	12.1	113172	8	AC009519	AC009519 Genomic s
846	16	12.1	88204	2	AC127210	AC127210 Rattus no	c 919	16	12.1	113254	9	AL137009	AL137009 Human DNA
847	16	12.1	88278	2	AC015486	AC015486 Homo sapi	c 920	16	12.1	113601	2	AP003887	AP003887 Oryza sat
c 848	16	12.1	88535	2	AC099423	AC099423 Rattus no	c 921	16	12.1	113601	2	HS316D5	HS316D5
c 849	16	12.1	89147	2	AC107911	AC107911 Homo sapi	c 922	16	12.1	114000	9	AL583806	AL583806 Human DNA
c 850	16	12.1	89728	5	AL672079	AL672079 Zebrafish	c 923	16	12.1	114111	9	AC112909	AC112909 Homo sapi
851	16	12.1	91433	3	AC087074	AC087074 Caenorhab	c 924	16	12.1	114597	2	AC129877	AC129877 Rattus no
c 852	16	12.1	92001	9	AC117476	AC117476 Homo sapi	c 925	16	12.1	115499	2	AC115363	AC115363 Rattus no
c 853	16	12.1	92369	2	AC128342	AC128342 Rattus no	c 926	16	12.1	115614	9	AL139158	AL139158 Human DNA
c 854	16	12.1	92444	2	AC111809	AC111809 Rattus no	c 927	16	12.1	116184	2	AC121241	AC121241 Medicago
c 855	16	12.1	92444	2	AC111809	AC111809 Rattus no	c 928	16	12.1	116380	9	HS688G8	HS688G8
c 856	16	12.1	93260	2	AC127067	AC127067 Rattus no	c 929	16	12.1	117029	2	AC101119	AC101119 Rattus no
c 857	16	12.1	94023	9	AC008720	AC008720 Homo sapi	c 930	16	12.1	118129	9	AC093601	AC093601 Homo sapi
c 858	16	12.1	94652	2	AC108876	AC108876 Oryza sat	c 931	16	12.1	118334	9	AC005075	AC005075 Homo sapi
c 859	16	12.1	95105	9	AC016561	AC016561 Homo sapi	c 932	16	12.1	118841	9	AC107973	AC107973 Homo sapi
c 860	16	12.1	95560	2	AC127620	AC127620 Rattus no	c 933	16	12.1	118988	2	AC109040	AC109040 Rattus no
c 861	16	12.1	95908	9	AC008628	AC008628 Homo sapi	c 934	16	12.1	119395	9	AC091862	AC091862 Homo sapi
c 862	16	12.1	96157	9	AL138789	AL138789 Human DNA	c 935	16	12.1	120228	8	AC112514	AC112514 Oryza sat
c 863	16	12.1	96232	2	AP001921	AP001921 Homo sapi	c 936	16	12.1	120391	2	AC017146	AC017146 Drosophil
864	16	12.1	96717	9	AL359182	AL359182 Human DNA	c 937	16	12.1	120391	2	AC017146	AC017146 Drosophil
c 865	16	12.1	96779	9	AL592463	AL592463 Human DNA	c 938	16	12.1	120391	2	AC017146	AC017146 Drosophil
c 866	16	12.1	97059	2	AC129683	AC129683 Rattus no	c 939	16	12.1	120391	2	AC017146	AC017146 Drosophil
c 867	16	12.1	97137	2	AL355172	AL355172 Homo sapi	c 940	16	12.1	120391	2	AC017146	AC017146 Drosophil
c 868	16	12.1	97598	2	AC108238	AC108238 Rattus no	941	16	12.1	120391	2	AC017146	AC017146 Drosophil

```
942 16 12.1 120586 9 AL590322 Human DNA
c 943 16 12.1 120733 9 AC022124 Homo sapi
944 16 12.1 121360 9 HSP19646
945 16 12.1 121591 2 AC103260
c 946 16 12.1 121931 9 AC008390
c 947 16 12.1 122228 9 AC000003
c 948 16 12.1 122335 2 AC120636
c 949 16 12.1 122823 9 AC005996
c 950 16 12.1 122884 9 HSL158B12
c 951 16 12.1 123022 9 AC090717
c 952 16 12.1 123554 9 AB023049
c 953 16 12.1 123668 9 AC090728
c 954 16 12.1 123925 9 AC003976
c 955 16 12.1 124067 9 AP000435
c 956 16 12.1 125267 4 AC090033
c 957 16 12.1 125528 2 AC027389
c 958 16 12.1 125853 2 AP000613
c 959 16 12.1 126130 9 HSL1178H5
c 960 16 12.1 126837 9 AL353652
c 961 16 12.1 126921 2 AC130576
c 962 16 12.1 126936 2 AC090472
c 963 16 12.1 126990 9 HS73M23
c 964 16 12.1 127016 2 AC090730
c 965 16 12.1 127119 2 AC123277
c 966 16 12.1 127144 9 AC008883
c 967 16 12.1 127905 9 AL513550
c 968 16 12.1 128036 2 AC025071
c 969 16 12.1 128227 2 AC118189
c 970 16 12.1 128364 2 AC122094
c 971 16 12.1 128437 9 AC084346
c 972 16 12.1 128879 8 AP003866
c 973 16 12.1 129096 2 AC026412
c 974 16 12.1 129655 2 AC109027
c 975 16 12.1 130278 9 AC005664
c 976 16 12.1 130336 9 AC006346
c 977 16 12.1 130434 2 AC118459
c 978 16 12.1 130561 9 AC107983
c 979 16 12.1 130609 2 AC091798
c 980 16 12.1 130871 2 AC116517
c 981 16 12.1 130898 2 AC130057
c 982 16 12.1 130988 2 AC130057
c 983 16 12.1 130935 2 AP004192
c 984 16 12.1 131033 5 AL591370
c 985 16 12.1 131547 2 AP003982
c 986 16 12.1 131805 9 AC008850
c 987 16 12.1 132075 2 AC112539
c 988 16 12.1 132336 2 AF215842
c 989 16 12.1 132367 10 AL808022
c 990 16 12.1 132933 9 AL137002
c 991 16 12.1 133927 9 AL512664
c 992 16 12.1 134933 8 AC092750
c 993 16 12.1 134976 8 AP004968
c 994 16 12.1 135237 2 AP000814
c 995 16 12.1 135250 2 AC097048
c 996 16 12.1 135331 9 AC008798
c 997 16 12.1 135360 2 AC126311
c 998 16 12.1 135815 9 HS43408
c 999 16 12.1 135888 2 AL845353
c1000 16 12.1 135889 2 AP005469

ALIGNMENTS

RESULT 1
LOCUS AX399230 147 bp
DEFINITION Sequence 3 from Patent WO0190155.
ACCESSION AX399230
VERSION AX399230.1 GI:21261549
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

AX399230 linear PAT 28-MAY-2002
Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 60
Db 6 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 65

Qy 61 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 120
Db 66 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 125

Qy 121 GAAATTTCTCTGA 132
Db 126 GAAATTTCTCTGA 137

RESULT 2
LOCUS AX399232 147 bp
DEFINITION Sequence 5 from Patent WO0190155.
ACCESSION AX399232
VERSION AX399232.1 GI:21261550
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

AX399232 linear PAT 28-MAY-2002
Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 60
Db 6 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 65

Qy 61 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 120
Db 66 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 125

Qy 121 GAAATTTCTCTGA 132
Db 126 GAAATTTCTCTGA 137

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Spytek, K.A., Majumder, K., Tchernev, V.T., Mishra, V., Padigaru, M.,
Spaderna, S.K., Shenoy, S., Rastelli, L., Li, L., Taupier, R.J. and
Gangolli, E.
Novel proteins and nucleic acids encoding same
Patent: WO 0190155-A 3 29-NOV-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
1. .147
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 56 a 30 c 41 g 20 t
ORIGIN
Query Match 100.0%; Score 132; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 60
Db 6 ATGCGACACAACTAGACCTGGAGAAATTCGACGCTTGGATAAGGCCCAAGCTGAAGGCC 65

Qy 61 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 120
Db 66 ACAGAGATGCAGAGAACACTCTGTATGACCAAAGAGACACAGACGAGAGAGTGGAGT 125

Qy 121 GAAATTTCTCTGA 132
Db 126 GAAATTTCTCTGA 137
```


Sequencing vector: M13; M7815; 9% of reads
 Sequencing vector: plasmid; L08752; 90% of reads
 Chemistry: Dye-terminator; 12% of reads
 Chemistry: Dye-terminator ABI; 0% of reads
 Chemistry: Dye-terminator ET-amersham; 0% of reads
 Dye-terminator Big Dye; 86% of reads
 Consensus quality: 86046 bases at least Q40
 Consensus quality: 86121 bases at least Q30
 Consensus quality: 86246 bases at least Q20
 Insert size: 86494; sum-of-contigs
 Insert size: 100607; 2.1% error; agarose-fp
 Quality coverage: 10.68x in Q20 bases; sum-of-contigs Quality
 coverage: 9.68x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 46382: contig of 46382 bp in length
 * 46383 46482: gap of 100 bp
 * 46483 86594: contig of 40112 bp in length.

FEATURES

source

1. .86594
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP5-832C2"
 /clone_lib="RPCI-5"

misc_feature

1. .46382
 /note="assembly fragment:01669
 fragment_chain:1"

misc_feature

46483..86594
 /note="assembly fragment:00659
 fragment_chain:1
 clone_end:SP6
 vector_side:right"

BASE COUNT 19164 a 24662 c 24281 g 18387 t 100 others
 ORIGIN

Query Match 18.9%; Score 25; DB 2; Length 86594;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CAGGAGAGTGGAGTGAATTCCT 130

Db 76479 CAGGAGAGTGGAGTGAATTCCT 76503

RESULT 6

AL713970 133135 bp DNA linear HTG 19-JUN-2002

LOCUS Homo sapiens chromosome 1 clone RP11-197P23, *** SEQUENCING IN

PROGRESS ***, 15 unordered pieces.

ACCESSION AL713970

VERSION AL713970.8 GI:21531382

KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 133135)

Ellington, A.

Direct Submission

Submitted (17-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 21, 2002 this sequence version replaced gi:20451552.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA197P23

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 127939 bases at least Q40

Consensus quality: 128929 bases at least Q30

Consensus quality: 129574 bases at least Q20

Insert size: 131735; sum-of-contigs

Insert size: 169742; 13.7% error; agarose-fp

Quality coverage: 7.78x in Q20 bases; sum-of-contigs Quality
 coverage: 6.17x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 4994: contig of 4994 bp in length
 * 4995 5094: gap of 100 bp
 * 5095 25519: contig of 20425 bp in length
 * 25520 25619: gap of 100 bp
 * 25620 35375: contig of 9756 bp in length
 * 35376 35475: gap of 100 bp
 * 35476 37722: contig of 2247 bp in length
 * 37723 37822: gap of 100 bp
 * 37823 49560: contig of 11738 bp in length
 * 49561 49660: gap of 100 bp
 * 49661 53726: contig of 4066 bp in length
 * 53727 53826: gap of 100 bp
 * 53827 84978: contig of 31152 bp in length
 * 84979 85078: gap of 100 bp
 * 85079 87297: contig of 2219 bp in length
 * 87298 87397: gap of 100 bp
 * 87398 100683: contig of 13286 bp in length
 * 100684 100783: gap of 100 bp
 * 100784 104917: contig of 4134 bp in length
 * 104918 105017: gap of 100 bp
 * 105018 114222: contig of 9205 bp in length
 * 114223 114322: gap of 100 bp
 * 114323 119300: contig of 4978 bp in length
 * 119301 119400: gap of 100 bp
 * 119401 122573: contig of 3173 bp in length
 * 122574 122673: gap of 100 bp
 * 122674 130806: contig of 8133 bp in length
 * 130807 130906: gap of 100 bp
 * 130907 133135: contig of 2229 bp in length.

FEATURES

source

1. .133135
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP11-197P23"
 /clone_lib="RPCI-11.1"
 1. .4994

misc_feature

/note="assembly fragment:02932
 fragment_chain:1"

misc_feature

5095..25519

misc_feature

/note="assembly fragment:01032
 fragment_chain:1"

misc_feature

25620..35375

misc_feature

/note="assembly fragment:01141
 fragment_chain:1"

misc_feature

35476..37722

misc_feature

/note="assembly fragment:01459
 fragment_chain:1"

misc_feature

37823..49560

```

/note="assembly_fragment:00833
fragment_chain:1"
misc_feature
49661..53726
/note="assembly_fragment:00092
fragment_chain:2"
misc_feature
53827..84978
/note="assembly_fragment:02950
fragment_chain:2"
misc_feature
85079..87297
/note="assembly_fragment:00125
fragment_chain:2"
misc_feature
87398..100683
/note="assembly_fragment:01435
fragment_chain:2"
misc_feature
100784..104917
/note="assembly_fragment:01582
fragment_chain:3"
misc_feature
105018..114222
/note="assembly_fragment:01477
fragment_chain:3"
misc_feature
114323..119300
/note="assembly_fragment:01864
fragment_chain:3"
misc_feature
119401..122573
/note="assembly_fragment:00334
fragment_chain:4"
misc_feature
122674..130806
/note="assembly_fragment:00597
fragment_chain:4"
misc_feature
130907..133135
/note="assembly_fragment:01905"
BASE COUNT 29794 a 36915 c 36289 g 28728 t 1409 others
ORIGIN

```

Query Match 18.9%; Score 25; DB 2; Length 133135;

Best Local Similarity 100.0%; Pred. No. 0.0022; Length 133135;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 106 CAGGAGAAGTGGAGTGAATTTCT 130
|||||
Db 82938 CAGGAGAAGTGGAGTGAATTTCT 82962

```

```

RESULT 7
AL691446 151840 bp DNA linear HTG 24-JUL-2002
LOCUS
DEFINITION Mus musculus chromosome 2 clone RP23-136J11, *** SEQUENCING IN
PROGRESS ***, 10 unordered pieces.
ACCESSION AL691446
VERSION AL691446.2 GI:21531337
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bates, K.
Direct Submission
Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquies@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:19572633.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquies@sanger.ac.uk
----- Project Information
Center project name: BM136J11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 0% of reads
Chemistry: Dye-terminator B1g Dye; 99% of reads

```

Consensus quality: 148339 bases at least Q40
 Consensus quality: 149486 bases at least Q30
 Consensus quality: 150246 bases at least Q20
 Insert size: 150940; sum-of-contigs
 Insert size: 237597; 5.1% error; agarose-fp
 Quality coverage: 11.92x in Q20 bases; sum-of-contigs Quality
 coverage: 7.78x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

 * 1 2778: contig of 2778 bp in length
 * 2779 2878: gap of 100 bp
 * 2879 8919: contig of 6041 bp in length
 * 8920 9019: gap of 100 bp
 * 9020 18791: contig of 9772 bp in length
 * 18792 18891: gap of 100 bp
 * 18892 30426: contig of 11535 bp in length
 * 30427 30526: gap of 100 bp
 * 30527 64454: contig of 33928 bp in length
 * 64455 64554: gap of 100 bp
 * 64555 85715: contig of 21161 bp in length
 * 85716 85815: gap of 100 bp
 * 85816 89857: contig of 4042 bp in length
 * 89858 89957: gap of 100 bp
 * 89958 106785: contig of 16828 bp in length
 * 106786 106885: gap of 100 bp
 * 106886 113841: contig of 6956 bp in length
 * 113842 113941: gap of 100 bp
 * 113942 151840: contig of 37899 bp in length.

FEATURES
 Location/Qualifiers
 1..151840

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-136J11"
/clone_lib="RPCI-23"
1..2778
/note="assembly_fragment:02749
fragment_chain:1"
2879..8919
/note="assembly_fragment:01224
fragment_chain:1"
9020..18791
/note="assembly_fragment:03159
fragment_chain:1"
18892..30426
/note="assembly_fragment:03065
fragment_chain:1"
30527..64454
/note="assembly_fragment:01666
fragment_chain:2"
64555..85715
/note="assembly_fragment:04137
fragment_chain:2"
85816..89857
/note="assembly_fragment:02847
fragment_chain:3"
89958..106785
/note="assembly_fragment:03601
fragment_chain:3"
106886..113841
/note="assembly_fragment:05543
fragment_chain:4"
113942..151840
/note="assembly_fragment:04887
fragment_chain:4"

```

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

BASE COUNT 34703 a 42897 c 43283 g 30057 t 900 others

/note="assembly_name:Contig61"

```

BASE COUNT      37019 a 48918 c 48934 g 40853 t      2008 others
ORIGIN

Query Match      18.9%; Score 25; DB 2; Length 177632;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CAGGAGAGTGGAGTGAATTCCT 130
|||||
Db 150599 CAGGAGAGTGGAGTGAATTCCT 150575

RESULT 9
AC097209
LOCUS          Rattus norvegicus clone CH230-209D24, *** SEQUENCING IN PROGRESS
DEFINITION    *** 36 unordered pieces.
ACCESSION     AC097209
VERSION       AC097209.4 GI:21735659
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE        Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 60372)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Albrooks,S.L., Amaraturge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbala,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T.; Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 60372)
Worley,K.C.
Direct Submission
Submitted (12-OCT-2001) Human Genome Sequencing Center, Department

```

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:17973805.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIMK
Center clone name: CH230-209D24
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 18096 bases at least Q40
Consensus quality: 20317 bases at least Q30
Consensus quality: 22036 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1116: contig of 1116 bp in length
1117 1216: gap of unknown length
1217 2301: contig of 1085 bp in length
2302 2401: gap of unknown length
2402 3901: contig of 1500 bp in length
3902 4001: gap of unknown length
4002 5011: contig of 1010 bp in length
5012 5112: gap of unknown length
5112 6140: contig of 1029 bp in length
6141 7365: contig of 1125 bp in length
7366 7465: gap of unknown length
7466 8533: contig of 1068 bp in length
8534 8634: gap of unknown length
8634 9937: contig of 1303 bp in length
9937 10036: gap of unknown length
10037 11520: contig of 1484 bp in length
11521 11620: gap of unknown length
11621 12663: contig of 1043 bp in length
12664 12763: gap of unknown length
12764 13845: contig of 1081 bp in length
13845 13945: gap of unknown length
13945 15744: contig of 1800 bp in length
15745 15844: gap of unknown length
15845 17260: contig of 1416 bp in length
17261 17360: gap of unknown length
17361 18646: contig of 1286 bp in length
18647 20062: contig of 1316 bp in length
20063 20162: gap of unknown length
20163 21879: contig of 1717 bp in length
21880 21979: gap of unknown length
21980 23604: contig of 1625 bp in length
23605 23704: gap of unknown length
23705 25340: contig of 1636 bp in length
25341 25441: gap of unknown length
25442 27218: contig of 1778 bp in length
27219 27318: gap of unknown length

```

* 27319 28832: contig of 1514 bp in length
* 28833 gap of unknown length
* 30530 contig of 1598 bp in length
* 30531 gap of unknown length
* 30531 32775: contig of 2145 bp in length
* 32776 32875: gap of unknown length
* 32876 34689: contig of 1814 bp in length
* 34690 36643: contig of 1854 bp in length
* 36644 36743: gap of unknown length
* 36744 39177: contig of 2434 bp in length
* 39178 39277: gap of unknown length
* 39278 40634: contig of 1357 bp in length
* 40635 42613: gap of unknown length
* 42614 42713: gap of 1879 bp in length
* 42714 45224: contig of 2511 bp in length
* 45225 45324: gap of unknown length
* 45325 47660: contig of 2336 bp in length
* 47661 47760: gap of unknown length
* 47761 49795: contig of 2035 bp in length
* 49796 49895: gap of unknown length
* 49896 52117: contig of 2222 bp in length
* 52118 52217: gap of unknown length
* 52218 53830: contig of 1613 bp in length
* 53831 53930: gap of unknown length
* 53931 55507: contig of 1576 bp in length
* 55507 55607: gap of unknown length
* 55607 57693: contig of 2087 bp in length
* 57694 57793: gap of unknown length
* 57794 58812: contig of 1019 bp in length
* 58813 60372: gap of unknown length
* 58913 Location/Qualifiers
      1. 60372
        /organism="Rattus norvegicus"
        /db_xref="taxon:10116"
        /clone="CH230-209D24"
BASE COUNT 16444 a 12089 c 11630 g 16679 t 3530 others
ORIGIN

```

FEATURES

Source

Query Match 16.7%; Score 22; DB 2; Length 60372;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 AGAGACACAGAGAGAGAGAG 114

|||||

Db 23269 AGAGACACAGAGAGAGAG 23290

RESULT 10

AC098254/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-1c4, *** SEQUENCING IN PROGRESS ***,

64 unordered pieces.

AC098254

AC098254.3 GI:21953975

VERSION HTG; HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 192314)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,

Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyie, M.D., Dathorne, S.R., David, R.,

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlssoon, E., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozador, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUDS
Center clone name: CH230-1G4
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124741 bases at least Q40
Consensus quality: 130791 bases at least Q30
Consensus quality: 137646 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 64 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1202: contig of 1202 bp in length

1203 1302: gap of unknown length
 1303 2470: contig of 1168 bp in length
 2471 2570: gap of unknown length
 2571 3814: contig of 1244 bp in length
 3815 3914: gap of unknown length
 3915 5367: contig of 1453 bp in length
 5368 5467: gap of unknown length
 5468 6821: contig of 1354 bp in length
 6822 6921: gap of unknown length
 6922 8132: contig of 1211 bp in length
 8133 8232: gap of unknown length
 8233 9889: contig of 1657 bp in length
 9890 11626: gap of unknown length
 9990 11626: contig of 1637 bp in length
 11627 11726: gap of unknown length
 11727 13008: contig of 1282 bp in length
 13009 13108: gap of unknown length
 13109 14592: contig of 1484 bp in length
 14593 14692: gap of unknown length
 14693 15718: contig of 1026 bp in length
 15719 15818: gap of unknown length
 15819 17454: contig of 1636 bp in length
 17455 17554: gap of unknown length
 17555 19138: contig of 1584 bp in length
 19139 19239: gap of unknown length
 19239 20377: contig of 1138 bp in length
 20377 20477: gap of unknown length
 20477 21841: contig of 1365 bp in length
 21842 21941: gap of unknown length
 21942 23808: contig of 1867 bp in length
 23809 23908: gap of unknown length
 23909 25201: contig of 1292 bp in length
 25201 25301: gap of unknown length
 25301 26438: contig of 1138 bp in length
 26439 26538: gap of unknown length
 26539 27588: contig of 1050 bp in length
 27589 27688: gap of unknown length
 27689 29362: contig of 1673 bp in length
 29362 30997: contig of 1536 bp in length
 30998 31097: gap of unknown length
 31098 32929: contig of 1832 bp in length
 32930 33029: gap of unknown length
 33030 34610: contig of 1581 bp in length
 34611 34710: gap of unknown length
 34711 36964: contig of 2254 bp in length
 36965 37064: gap of unknown length
 37065 38944: contig of 1880 bp in length
 38945 39045: gap of unknown length
 39045 40758: contig of 1714 bp in length
 40759 40858: gap of unknown length
 40859 42629: contig of 1771 bp in length
 42630 42729: gap of unknown length
 42730 44658: contig of 1929 bp in length
 44659 44758: gap of unknown length
 44759 46330: contig of 1572 bp in length
 46331 48430: gap of unknown length
 48431 48745: contig of 2315 bp in length
 48746 48845: gap of unknown length
 48846 50969: contig of 2124 bp in length
 50970 51069: gap of unknown length
 51070 52350: contig of 1281 bp in length
 52351 52450: gap of unknown length
 52451 54791: contig of 2341 bp in length
 54792 54892: gap of unknown length
 54892 56266: contig of 1375 bp in length
 56267 56366: gap of unknown length
 56367 58908: contig of 2542 bp in length
 58909 59008: gap of unknown length
 59009 61210: contig of 2202 bp in length
 61211 61310: gap of unknown length
 61311 64169: contig of 2859 bp in length
 64170 64269: gap of unknown length

* 64270 65546: contig of 1277 bp in length
 * 65547 65646: gap of unknown length
 * 65647 67455: contig of 1809 bp in length
 * 67456 67555: gap of unknown length
 * 67556 71809: contig of 4254 bp in length
 * 71810 71909: gap of unknown length
 * 71910 74306: contig of 2397 bp in length
 * 74307 74406: gap of unknown length
 * 74407 76355: contig of 1949 bp in length
 * 76356 76456: gap of unknown length
 * 76456 79431: contig of 2975 bp in length
 * 79431 79531: gap of unknown length
 * 79531 83084: contig of 3553 bp in length
 * 83084 83184: gap of unknown length
 * 83184 87278: contig of 4095 bp in length
 * 87279 87378: gap of unknown length
 * 87379 89371: contig of 1993 bp in length
 * 89372 89472: gap of unknown length
 * 89472 93782: contig of 4310 bp in length
 * 93782 93882: gap of unknown length
 * 93882 96981: contig of 3099 bp in length
 * 96981 97080: gap of unknown length
 * 97081 100549: contig of 3469 bp in length
 * 100550 100649: gap of unknown length
 * 100650 102942: contig of 2292 bp in length
 * 102942 103042: gap of unknown length
 * 103042 107119: contig of 4077 bp in length
 * 107119 107219: gap of unknown length
 * 107219 110789: contig of 3570 bp in length
 * 110789 110888: gap of unknown length
 * 110889 115458: contig of 4570 bp in length
 * 115459 115558: gap of unknown length
 * 115559 119571: contig of 4013 bp in length

Query Match 16.7%; Score 22; DB 2; Length 192314;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 AGAGACCACAGCAGCAGGAGAAG 114
 |||||
 Db 36812 AGAGACCACAGCAGCAGGAGAAG 36791

RESULT 11

AC130181
 LOCUS Rattus norvegicus clone CH230-5J1, linear HTG 08-AUG-2002
 DEFINITION Rattus norvegicus clone CH230-5J1, *** SEQUENCING IN PROGRESS ***
 56 unordered pieces.
 AC130181
 VERSION AC130181.1 GI:22138425
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

AUTHORS 1 (bases 1 to 198015)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chaves,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
Honsi, P., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlssoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Lucier, R., Luna, R., Ma, J.,
Lozano, R.J., Lu, X., Lucier, R., Martin, R., Martindale, A., Martinez, E.,
Maheshwari, M., Mapua, P., Massey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Orgunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojals, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 198015)
Worley, K.C.

Direct Submission
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GBLD
Center clone name: CH230-5J1

Summary Statistics
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 151044 bases at least Q40
Consensus quality: 160277 bases at least Q30
Consensus quality: 166259 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1536: contig of 1536 bp in length
1537: 1636: gap of unknown length
1637: 3117: contig of 1481 bp in length
3118: 3217: gap of unknown length
3218: 4484: contig of 1267 bp in length
4485: 4584: gap of unknown length
4585: 6182: contig of 1598 bp in length
6183: 6282: gap of unknown length
6283: 7357: contig of 1075 bp in length
7358: 7457: gap of unknown length
7458: 9367: contig of 1910 bp in length
9368: 9467: gap of unknown length
9468: 10942: contig of 1475 bp in length
10943: 11042: gap of unknown length
11043: 13268: contig of 2226 bp in length
13269: 13368: gap of unknown length

13369: 15041: contig of 1673 bp in length
15041: 15141: gap of unknown length
15142: 16627: contig of 1486 bp in length
16628: 16727: gap of unknown length
16728: 17943: contig of 1216 bp in length
17944: 18043: gap of unknown length
18044: 19081: contig of 1038 bp in length
19082: 19181: gap of unknown length
19182: 20726: contig of 1545 bp in length
20727: 20826: gap of unknown length
20827: 22566: contig of 1740 bp in length
22567: 22666: gap of unknown length
22668: 24418: contig of 1752 bp in length
24419: 24518: gap of unknown length
24519: 26895: contig of 2377 bp in length
26896: 26995: gap of unknown length
26996: 29066: contig of 2071 bp in length
29067: 29166: gap of unknown length
29167: 30375: contig of 1209 bp in length
30376: 30475: gap of unknown length
30476: 32675: contig of 2200 bp in length
32676: 32775: gap of unknown length
32776: 35034: contig of 2259 bp in length
35035: 35134: gap of unknown length
35135: 37314: contig of 2180 bp in length
37315: 37414: gap of unknown length
37415: 39405: contig of 1991 bp in length
39406: 39505: gap of unknown length
39506: 42743: contig of 3238 bp in length
42744: 42843: gap of unknown length
42845: 45730: contig of 2887 bp in length
45731: 45830: gap of unknown length
45831: 47280: contig of 1450 bp in length
47281: 47380: gap of unknown length
47381: 50304: contig of 3124 bp in length
50305: 50604: gap of unknown length
50605: 53646: contig of 3042 bp in length
53647: 53746: gap of unknown length
53747: 56155: contig of 2409 bp in length
56156: 56255: gap of unknown length
56256: 57617: contig of 1362 bp in length
57618: 57717: gap of unknown length
57718: 59390: contig of 1673 bp in length
59391: 59490: gap of unknown length
59491: 61910: contig of 2420 bp in length
61911: 62010: gap of unknown length
62011: 64435: contig of 2425 bp in length
64436: 64535: gap of unknown length
64536: 66876: contig of 2341 bp in length
66877: 66976: gap of unknown length
66977: 70641: contig of 3665 bp in length
70642: 70741: gap of unknown length
70742: 74174: contig of 3433 bp in length
74175: 74274: gap of unknown length
74275: 77442: contig of 3168 bp in length
77443: 77542: gap of unknown length
77543: 79515: gap of unknown length
79516: 82758: contig of 3243 bp in length
82759: 82858: gap of unknown length
82859: 86464: contig of 3606 bp in length
86465: 86564: gap of unknown length
86565: 91223: contig of 4659 bp in length
91224: 91323: gap of unknown length
91324: 96124: contig of 4801 bp in length
96125: 96224: gap of unknown length
96225: 99485: contig of 3261 bp in length
99486: 99585: gap of unknown length
99586: 104436: contig of 4851 bp in length
104437: 104536: gap of unknown length
104537: 108432: contig of 3896 bp in length
108433: 108532: gap of unknown length
108533: 111718: contig of 3186 bp in length

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

* 111719 111818: gap of unknown length
* 111819 116364: contig of 4546 bp in length
* 116365 116464: gap of unknown length
* 116465 120991: contig of 4527 bp in length
* 120992 121091: gap of unknown length
* 121092 121778: contig of 6087 bp in length
* 121779 127278: gap of unknown length
* 127279 130963: contig of 3685 bp in length
* 130964 131063: gap of unknown length
* 131064 136356: contig of 5293 bp in length
* 136357 136456: gap of unknown length
* 136457 143165: contig of 6709 bp in length
* 143166 143265: gap of unknown length
* 143266 150881: contig of 7616 bp in length
* 150882 163191: contig of 12210 bp in length
* 163192 163291: gap of unknown length
* 163292 172896: contig of 9604 bp in length
* 172896 172995: gap of unknown length
* 172996 185774: contig of 12779 bp in length
* 185775 185874: gap of unknown length
* 185875 198015: contig of 12141 bp in length.
FEATURES
  source
    1. 198015
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"

Query Match      15.9%; Score 21; DB 2; Length 198015;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 AGAGACCACAGCAGGAGAA 113
  Db 42390 AGAGACCACAGCAGGAGAA 42410

RESULT 12
AP001477 38399 bp DNA linear PRI 09-MAY-2000
LOCUS
DEFINITION Homo sapiens genomic DNA, chromosome 21q22.3, clone:f50C10,
telomere region, complete sequence.
ACCESSION AP001477
VERSION AP001477.1 GI:7768605
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:f50C10.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 38399)
  Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Published Only in Database (2000)
  2 (bases 1 to 38399)
  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
  Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Direct Submission
  Submitted (16-MAR-2000) Masahira Hattori, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
  Japan (E-mail:hattori@gs.c.riken.go.jp,
  URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
  Fax:81-42-778-9924)
  Location/Qualifiers
    1. 38399
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="21"
    /map="21q22.3"
    /clone="f50C10"
  BASE COUNT 7773 a 9530 c 10510 g 10586 t
  ORIGIN

* 111818: gap of unknown length
* 116364: contig of 4546 bp in length
* 116365 120991: contig of 4527 bp in length
* 120992 121091: gap of unknown length
* 121092 121778: contig of 6087 bp in length
* 121779 127278: gap of unknown length
* 127279 130963: contig of 3685 bp in length
* 130964 131063: gap of unknown length
* 131064 136356: contig of 5293 bp in length
* 136357 136456: gap of unknown length
* 136457 143165: contig of 6709 bp in length
* 143166 143265: gap of unknown length
* 143266 150881: contig of 7616 bp in length
* 150882 163191: contig of 12210 bp in length
* 163192 163291: gap of unknown length
* 163292 172896: contig of 9604 bp in length
* 172896 172995: gap of unknown length
* 172996 185774: contig of 12779 bp in length
* 185775 185874: gap of unknown length
* 185875 198015: contig of 12141 bp in length.
FEATURES
  source
    1. 198015
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"

Query Match      15.9%; Score 21; DB 2; Length 198015;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 AGAGACCACAGCAGGAGAA 113
  Db 42390 AGAGACCACAGCAGGAGAA 42410

RESULT 12
AP001477 38399 bp DNA linear PRI 09-MAY-2000
LOCUS
DEFINITION Homo sapiens genomic DNA, chromosome 21q22.3, clone:f50C10,
telomere region, complete sequence.
ACCESSION AP001477
VERSION AP001477.1 GI:7768605
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:f50C10.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 38399)
  Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Published Only in Database (2000)
  2 (bases 1 to 38399)
  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
  Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  Direct Submission
  Submitted (16-MAR-2000) Masahira Hattori, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
  Japan (E-mail:hattori@gs.c.riken.go.jp,
  URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
  Fax:81-42-778-9924)
  Location/Qualifiers
    1. 38399
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="21"
    /map="21q22.3"
    /clone="f50C10"
  BASE COUNT 7773 a 9530 c 10510 g 10586 t
  ORIGIN

```

```

Query Match      15.2%; Score 20; DB 9; Length 38399;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AATTGCCAGCTTGGATAGG 46
  Db 26428 AATTGCCAGCTTGGATAGG 26447

RESULT 13
AC116359/c 53707 bp DNA linear PRI 29-MAY-2002
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RP11-692C23, complete sequence.
ACCESSION AC116359
VERSION AC116359.2 GI:21240691
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 53707)
  DOE Joint Genome Institute and Stanford Human Genome Center.
  Direct Submission
  Unpublished
  2 (bases 1 to 53707)
  DOE Joint Genome Institute.
  Direct Submission
  Submitted (27-MAR-2002) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  3 (bases 1 to 53707)
  DOE Joint Genome Institute and Stanford Human Genome Center.
  Direct Submission
  Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell
  Drive, Walnut Creek, CA 94598, USA
  On May 29, 2002 this sequence version replaced gi:19745041.
  Draft Sequence Produced by DOE Joint Genome Institute
  www.jgi.doe.gov
  Finishing Completed at Stanford Human Genome Center
  www.shgc.stanford.edu
  Quality: Phrap Quality >=40 100% of Sequence;
  Estimated Total Number of Errors is 0.
  NOTE: This insert is not the entire sequence of the clone (entire
  sequence is 171.7kb). It is clipped at the overlaps with AC094105
  and AC091891. the number of bases overlapped with AC094105 is 8849
  and with AC091891 is 44862.
  Location/Qualifiers
    1. 53707
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="5"
    /clone="RP11-692C23"
  BASE COUNT 14758 a 10959 c 11116 g 16874 t
  ORIGIN

Query Match      15.2%; Score 20; DB 9; Length 53707;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGATGCAGAGAAGCACTCT 83
  Db 49318 GAGATGCAGAGAAGCACTCT 49299

RESULT 14
AC025937/c 170595 bp DNA linear HTG 26-MAY-2000
LOCUS
DEFINITION Homo sapiens clone RP11-692C23, WORKING DRAFT SEQUENCE, 18
  unordered pieces.
ACCESSION AC025937
VERSION AC025937.3 GI:8077762
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 170595)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Unpublished

2 (bases 1 to 170595)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F., Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,N., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2000 this sequence version replaced gi:7408053.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8334

Center clone name: 692_C_23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 160465 bases at least Q40

Consensus quality: 165270 bases at least Q30

Consensus quality: 167427 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 168895; sum-of-contigs

Quality coverage: 4.7 in Q20 bases; agarose-fp

Quality coverage: 4.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1144: contig of 1144 bp in length

* 1145 1244: gap of 100 bp

* 1245 2825: contig of 1581 bp in length

* 2826 2925: gap of 100 bp

* 2926 4246: contig of 1321 bp in length

* 4247 4346: gap of 100 bp

* 4347 6039: contig of 1693 bp in length

* 6040 6139: gap of 100 bp

* 6140 8144: contig of 2005 bp in length

* 8145 8244: gap of 100 bp

* 8245 13130: contig of 4886 bp in length

* 13131 13230: gap of 100 bp

* 13231 16109: contig of 2879 bp in length

* 16110 16209: gap of 100 bp

* 16210 19026: contig of 2817 bp in length

* 19027 19126: gap of 100 bp

* 19127 24489: contig of 5363 bp in length

* 24490 24589: gap of 100 bp

* 24590 28306: contig of 3717 bp in length

* 28307 28406: gap of 100 bp

* 28407 38498: contig of 10092 bp in length

* 38499 38598: gap of 100 bp

* 38599 48302: contig of 9704 bp in length

* 48303 48402: gap of 100 bp

* 48403 57446: contig of 9044 bp in length

* 57447 57546: gap of 100 bp

* 57547 68273: contig of 10727 bp in length

* 68274 68373: gap of 100 bp

* 68374 79825: contig of 11452 bp in length

* 79826 79925: gap of 100 bp

* 79926 101549: contig of 21624 bp in length

* 101550 101649: gap of 100 bp

* 101650 130009: contig of 28360 bp in length

* 130010 130109: gap of 100 bp

* 130110 170595: contig of 40486 bp in length.

Location/Qualifiers

1. .170595

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="RPC1-11 Human Male BAC"

1. .11144

/note="assembly_fragment"

1245. .2825

/note="assembly_fragment"

2926. .4246

/note="assembly_fragment"

4347. .6039

/note="assembly_fragment"

6140. .8144

/note="assembly_fragment"

8245. .13130

/note="assembly_fragment"

13231. .16109

/note="assembly_fragment"

16210. .19026

/note="assembly_fragment"

19127. .24489

/note="assembly_fragment"

24590. .28306

/note="assembly_fragment"

clone_end:SP6

vector_side:left

28407. .38498

/note="assembly_fragment"

38599. .48302

/note="assembly_fragment"

48403. .57446

/note="assembly_fragment"

clone_end:17

vector_side:right

57547. .68273

/note="assembly_fragment"

68374. .79825

/note="assembly_fragment"

79926. .101549

/note="assembly_fragment"

101650. .130009

/note="assembly_fragment"

130110. .170595

/note="assembly_fragment"

45763 a 37848 c 38643 g 46640 t 1701 others

BASE COUNT

ORIGIN

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Query Match 15.2%; Score 20; DB 2; Length 170595;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGATGCAGAGAACACTCT 83
 |||||
 Db 125491 GAGATGCAGAGAACACTCT 125472

RESULT 15
 AC113727/c
 LOCUS AC113727
 DEFINITION Rattus norvegicus clone CH230-4709, *** SEQUENCING IN PROGRESS ***,
 71 unordered pieces.
 AC113727
 VERSION AC113727.3 GI:21744507
 KEYWORDS HTG; HTGS-PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 1 (bases 1 to 187097)
 Muzny D.M., Adams C., Adio-Oduola B., Ali-oshan, F.R., Allen, C.,
 Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Ayelle, M., Banks, T.,
 Barbakia, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowles, M., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
 Homs, F., Howard, J., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Lucier, R., Luna, R., Ma, J.,
 Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E.,
 Maheshwari, M., Mapua, P., Martin, R., Meador, M., Mei, G., Metzker, M.,
 Massey, E., Mawhiney, E., McLeod, M.P., Mohabbat, K., Morgan, M., Morris, S.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
 Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Neilson, D.,
 Weinstock, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 187097)
 Worley, K.C.

REFERENCE
 Direct Submission
 Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 187097)

AUTHORS

TITLE

JOURNAL

COMMENT

Worley, K.C.
 Direct Submission
 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 13, 2002 this sequence version replaced gi:19525893.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GSDG
 Center clone name: CH230-4709
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 120207 bases at least Q40
 Consensus quality: 124896 bases at least Q30
 Consensus quality: 129455 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 71 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1
 1170: contig of 1170 bp in length
 1171: gap of unknown length
 1270: contig of 1005 bp in length
 1271: gap of unknown length
 2275: gap of unknown length
 2375: contig of 1376 bp in length
 2376: gap of unknown length
 3751: contig of 1376 bp in length
 3752: gap of unknown length
 3851: gap of unknown length
 3852: contig of 1009 bp in length
 4860: gap of unknown length
 4861: contig of 1368 bp in length
 4960: gap of unknown length
 4961: contig of 1594 bp in length
 6328: contig of 1122 bp in length
 6329: gap of unknown length
 6428: gap of unknown length
 8022: contig of 1284 bp in length
 8122: gap of unknown length
 8123: contig of 1001 bp in length
 9244: contig of 1351 bp in length
 9245: gap of unknown length
 10628: contig of 1498 bp in length
 10629: gap of unknown length
 10728: gap of unknown length
 10729: contig of 1429 bp in length
 11729: gap of unknown length
 11730: contig of 1115 bp in length
 11829: gap of unknown length
 13180: contig of 1498 bp in length
 13181: gap of unknown length
 13280: contig of 1041 bp in length
 13281: gap of unknown length
 14321: contig of 1429 bp in length
 14322: gap of unknown length
 15850: contig of 1429 bp in length
 15851: gap of unknown length
 15950: contig of 1115 bp in length
 17063: gap of unknown length
 17065: contig of 1498 bp in length
 17165: gap of unknown length
 17166: contig of 1498 bp in length
 18663: gap of unknown length
 18664: contig of 1708 bp in length
 20471: gap of unknown length
 20571: contig of 1544 bp in length
 20572: gap of unknown length
 22116: contig of 1368 bp in length
 22117: gap of unknown length
 22118: contig of 1417 bp in length
 23583: gap of unknown length
 23584: contig of 1628 bp in length
 25100: gap of unknown length
 25101: contig of 1628 bp in length
 26828: gap of unknown length
 26829: contig of 1124 bp in length
 28052: gap of unknown length
 28053: contig of 1285 bp in length
 29437: gap of unknown length

29438 29537: gap of unknown length
29538 30900: contig of 1363 bp in length
30901 31000: gap of unknown length
31001 32025: contig of 1025 bp in length
32026 32125: gap of unknown length
32126 33494: contig of 1369 bp in length
33495 33594: gap of unknown length
33595 34746: contig of 1152 bp in length
34747 34846: gap of unknown length
34847 36376: contig of 1530 bp in length
36377 36476: gap of unknown length
36477 38351: contig of 1875 bp in length
38352 38451: gap of unknown length
38452 40679: contig of 2228 bp in length
40680 40779: gap of unknown length
40780 42712: contig of 1933 bp in length
42713 42812: gap of unknown length
42813 44002: contig of 1190 bp in length
44003 44102: gap of unknown length
44103 46067: contig of 1965 bp in length
46068 46167: gap of unknown length
46168 47905: contig of 1738 bp in length
47906 48005: gap of unknown length
48006 49836: contig of 1831 bp in length
49837 49936: gap of unknown length
49937 51790: contig of 1854 bp in length
51791 51890: gap of unknown length
51891 54730: contig of 2840 bp in length
54731 54830: gap of unknown length
54831 56607: contig of 1777 bp in length
56608 56707: gap of unknown length
56709 57790: contig of 1083 bp in length
57791 57890: gap of unknown length
57891 59527: contig of 1637 bp in length
59528 59627: gap of unknown length
59629 62056: contig of 2429 bp in length
62057 62156: gap of unknown length
62157 63464: contig of 1308 bp in length
63465 63564: gap of unknown length
63565 65003: contig of 1439 bp in length
65004 65103: gap of unknown length
65104 67035: contig of 1932 bp in length
67036 67135: gap of unknown length
67136 69383: contig of 2248 bp in length
69384 69483: gap of unknown length
69484 71920: contig of 2437 bp in length
71921 72020: gap of unknown length
72021 74582: contig of 2562 bp in length
74583 74682: gap of unknown length
74683 77272: contig of 2590 bp in length
77273 77372: gap of unknown length
77373 79400: contig of 2028 bp in length
79401 79500: gap of unknown length
79501 81759: contig of 2259 bp in length
81760 83356: contig of 1497 bp in length
83357 83456: gap of unknown length
83457 87053: contig of 3597 bp in length
87054 87153: gap of unknown length
87154 90859: contig of 3706 bp in length
90860 90959: gap of unknown length
90960 94572: contig of 3613 bp in length
94573 94672: gap of unknown length
94673 98285: contig of 3613 bp in length
98286 98385: gap of unknown length
98386 101083: contig of 2698 bp in length

Query Match 15.2% Score 20; DB 2; Length 187097;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
93 AGAGACCACAGAGCAGGAGA 112
|||||

Db 112893 AGAGACCACAGAGCAGGAGA 112874

RESULT 16

AC094105

LOCUS

DEFINITION

AC094105 192202 bp DNA linear HTG 15-NOV-2001;
Homo sapiens chromosome 5 clone RP11-468D11, WORKING DRAFT
SEQUENCE, 18 unordered pieces.

ACCESSION

AC094105

VERSION

AC094105.2 GI:16930895

KEYWORDS

HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 192202)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 192202)
DOE Joint Genome Institute.
Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (14-SEP-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Nov 15, 2001 this sequence version replaced gi:15617666.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 586160
Center clone name: RPCI-11_468D11

Summary Statistics
Consensus quality: 174989 bases at least Q40
Consensus quality: 184243 bases at least Q30
Consensus quality: 186010 bases at least Q20
Estimated insert size: 186280; agarose-fp estimation
Estimated insert size: 190502; sum-of-contigs estimation
Quality coverage: 6.08 in Q20 bases; agarose-fp estimation
Quality coverage: 5.95 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1
* 1154: contig of 1154 bp in length
* 1155 1254: gap of unknown length
* 1255 2278: contig of 1024 bp in length
* 2279 2378: gap of unknown length
* 2379 3567: contig of 1189 bp in length
* 3568 3667: gap of unknown length
* 3669 5532: contig of 1865 bp in length
* 5533 5632: gap of unknown length
* 5633 7425: contig of 1793 bp in length
* 7426 7525: gap of unknown length
* 7526 9566: contig of 2041 bp in length
* 9567 9666: gap of unknown length
* 9667 12444: contig of 2778 bp in length
* 12445 12544: gap of unknown length
* 12545 15344: contig of 2800 bp in length
* 15345 15444: gap of unknown length
* 15445 19247: contig of 3803 bp in length
* 19248 19248: gap of unknown length
* 19249 22855: contig of 3508 bp in length
* 22856 22956: gap of unknown length
* 22957 29417: contig of 6461 bp in length
* 29418 37476: contig of 7960 bp in length
* 37477 29517

* 37477 37576: gap of unknown length
* 37577 49250: contig of 11674 bp in length
* 49251 49350: gap of unknown length
* 49351 65052: contig of 15702 bp in length
* 65053 65152: gap of unknown length
* 65153 81489: contig of 16337 bp in length
* 81490 81589: gap of unknown length
* 81590 109688: contig of 19379 bp in length
* 109689 101068: gap of unknown length
* 101069 144968: contig of 43900 bp in length
* 144969 145068: gap of unknown length
* 145069 192202: contig of 47134 bp in length.

FEATURES
source
1..192202
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-468D11"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 55136 a 41193 c 40457 g 53685 t 1731 others
ORIGIN

Query Match 15.2%; Score 20; DB 2; Length 192202;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGATGCAGAGAACTCT 83
|||||
Db 107984 GAGATGCAGAGAACTCT 108003
|||||

RESULT 17
AC093570/c 204080 bp DNA linear HTG 14-AUG-2002
LOCUS
DEFINITION Mus musculus chromosome 5 clone rp23-115a12 strain C57BL/6J,
WORKING DRAFT SEQUENCE, 3 ordered pieces.
AC093570
AC093570.21 GI:22218505
VERSION
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hu.X., Ornitz,D. and Roe,B.A.
1 (bases 1 to 204080)
TITLE Mus musculus BAC Clone rp23-115a12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204080)
AUTHORS Hu,X., Ornitz,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2001) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 204080)
AUTHORS Hu,X., Ornitz,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2002) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Aug 14, 2002 this sequence version replaced gi:21955040.
Center: Department of Chemistry And Biochemistry
Center code:UOKNOR

NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

* the accession number will be preserved.
* 1 12448: contig of 12448 bp in length
* 12449 12548: gap of unknown length
* 12549 65898: contig of 53350 bp in length
* 65899 204080: contig of 138082 bp in length.

FEATURES
Location/Qualifiers
1..204080
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="5"
/clone="rp23-115a12"
/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
BASE COUNT 57304 a 45888 c 44284 g 56404 t 200 others
ORIGIN

Query Match 15.2%; Score 20; DB 2; Length 204080;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAGCCACAGATGCAGAA 74
|||||
Db 133715 AAGCCACAGATGCAGAA 133696
|||||

RESULT 18
AL844896/c 207528 bp DNA linear HTG 29-JUL-2002
LOCUS
DEFINITION Mus musculus chromosome 2 clone RP23-356L21, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
AL844896
AL844896.2 GI:22022653
VERSION
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Plumb,B.
1 (bases 1 to 207528)
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 30, 2002 this sequence version replaced gi:22003377.
Center: Genome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

Project Information
Center project name: BM356L21

Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 203878 bases at least Q40
Consensus quality: 204610 bases at least Q30
Consensus quality: 205218 bases at least Q20
Insert size: 205828; sum-of-contigs
Insert size: 215378; 4.9% error; agarose-fp
Quality coverage: 7.98x in Q20 bases; sum-of-contigs Quality
coverage: 7.77x in Q20 bases; agarose-fp

NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 8473: contig of 8473 bp in length
* 8474 8573: gap of 100 bp

```
* 8574 28095: contig of 19522 bp in length
* 28096 28195: gap of 100 bp
* 51973: contig of 23778 bp in length
* 51974 52073: gap of 100 bp
* 52074 59439: contig of 7366 bp in length
* 59440 59539: gap of 100 bp
* 59540 63503: contig of 3964 bp in length
* 63504 63603: gap of 100 bp
* 63604 68011: contig of 4408 bp in length
* 68012 68111: gap of 100 bp
* 68112 80828: contig of 12717 bp in length
* 80829 80928: gap of 100 bp
* 80929 87731: contig of 6803 bp in length
* 87732 87831: gap of 100 bp
* 87832 94248: contig of 6417 bp in length
* 94249 94348: gap of 100 bp
* 94349 105931: contig of 11583 bp in length
* 105932 106031: gap of 100 bp
* 106032 122416: contig of 16385 bp in length
* 122417 122516: gap of 100 bp
* 122517 140300: contig of 17784 bp in length
* 140301 140400: gap of 100 bp
* 140401 148485: contig of 8085 bp in length
* 148486 148585: gap of 100 bp
* 148586 161944: contig of 13359 bp in length
* 161945 162044: gap of 100 bp
* 162045 171791: contig of 9747 bp in length
* 171792 171891: gap of 100 bp
* 171892 180695: contig of 8804 bp in length
* 180696 180795: gap of 100 bp
* 180796 202956: contig of 22161 bp in length
* 202957 203056: gap of 100 bp
* 203057 207528: contig of 4472 bp in length.
Location/Qualifiers
1. .207528
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosomes="2"
/clone="RP23-356L21"
/clone_lib="RPCI-23"
1. .8473
/note="assembly_fragment:00006
fragment_chain:1
clone_end:SP6
vector_side:left"
8574. .28095
/note="assembly_fragment:01817
fragment_chain:1"
28196. .51973
/note="assembly_fragment:02608
fragment_chain:1"
52074. .59439
/note="assembly_fragment:01398
fragment_chain:1"
59540. .63503
/note="assembly_fragment:01886
fragment_chain:1"
63604. .68011
/note="assembly_fragment:00680
fragment_chain:2"
68112. .80828
/note="assembly_fragment:02870
fragment_chain:2"
80929. .87731
/note="assembly_fragment:01917
fragment_chain:2"
87832. .94248
/note="assembly_fragment:02086
fragment_chain:2"
94349. .105931
/note="assembly_fragment:02823
fragment_chain:2"
106032. .122416
```

FEATURES

```
Source
Query Match 15.2%; Score 20; DB 2; Length 207528;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 GCAGGAGAGTGGAGTGAAA 124
|||||
Db 143847 GCAGGAGAGTGGAGTGAAA 143828

RESULT 19
AL844536/c
LOCUS
DEFINITION
Mus musculus chromosome 2 clone RP23-22A15, *** SEQUENCING IN
PROGRESS ***, 11 unordered pieces.
ACCESSION
AL844536
VERSION
AL844536.3 GI:22204804
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 241585)
Plumb,B.
Direct Submission
Submitted (02-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21955751.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM22A15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 236896 bases at least Q40
Consensus quality: 238326 bases at least Q30
Consensus quality: 239491 bases at least Q20
Insert size: 240585; sum-of-contigs
Insert size: 207539; 1.7% error; agarose-fp
Quality coverage: 4.96x in Q20 bases; sum-of-contigs Quality
coverage: 5.80x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
```

* consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 26384: contig of 26384 bp in length
 * 26385 26484: gap of 100 bp
 * 26485 38315: contig of 11831 bp in length
 * 38316 38415: gap of 100 bp
 * 38416 41944: contig of 3529 bp in length
 * 41945 42044: gap of 100 bp
 * 42045 56520: contig of 14476 bp in length
 * 56521 56620: gap of 100 bp
 * 56621 77754: contig of 21134 bp in length
 * 77755 77854: gap of 100 bp
 * 77855 96164: contig of 18310 bp in length
 * 96165 96264: gap of 100 bp
 * 96265 101917: contig of 5653 bp in length
 * 101918 102017: gap of 100 bp
 * 102018 146947: contig of 44930 bp in length
 * 146948 147047: gap of 100 bp
 * 147048 187542: contig of 40495 bp in length
 * 187543 187642: gap of 100 bp
 * 187643 192747: contig of 5105 bp in length
 * 192748 192847: gap of 100 bp
 * 192848 241585: contig of 48738 bp in length.

FEATURES

source

1. 241585
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="2"
 /clone_lib="RPCI-23"

misc_feature

1. 26384
 /note="assembly_fragment:01220
 fragment_chain:1"

misc_feature

26485..38315
 /note="assembly_fragment:01223
 fragment_chain:1"

misc_feature

38416..41944
 /note="assembly_fragment:01396
 fragment_chain:1"

misc_feature

42045..56520
 /note="assembly_fragment:01233
 fragment_chain:1"

misc_feature

56621..77754
 /note="assembly_fragment:00572
 fragment_chain:2"

misc_feature

77855..96164
 /note="assembly_fragment:01046
 fragment_chain:2"

misc_feature

96265..101917
 /note="assembly_fragment:01569
 fragment_chain:2"

misc_feature

102018..146947
 /note="assembly_fragment:00752
 fragment_chain:2"

misc_feature

147048..187542
 /note="assembly_fragment:00109
 fragment_chain:2"

misc_feature

187643..192747
 /note="assembly_fragment:00452
 fragment_chain:2"

misc_feature

192848..241585
 /note="assembly_fragment:00041
 fragment_chain:2"

misc_feature

68487 a 53697 c 52331 g 66069 t 1001 others

BASE COUNT
ORIGIN

Query Match 15.2%; Score 20; DB 2; Length 241585;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 GCAGGAGAAAGTGAGTGAAG 124
 Db 59880 GCAGGAGAAAGTGAGTGAAG 59861

RESULT 20
 AP000981/c 263050 bp DNA linear BCT 11-OCT-2001
 LOCUS Sulfolobus tokodaii genomic DNA, complete sequence, section:1/10.
 DEFINITION AP000981 BA000023
 ACCESSION AP000981.1 GI:15620945
 VERSION
 KEYWORDS
 SOURCE Sulfolobus tokodaii (strain:7) DNA.
 ORGANISM Sulfolobus tokodaii
 Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 Sulfolobus.

REFERENCE
 1 Kavarabayasi, Y., Hino, Y., Horikawa, H., Jin-no, K., Takahashi, M.,
 Sekine, M., Baba, S., Ankai, A., Kosugi, H., Hosoyama, A., Fukui, S.,
 Nagai, Y., Nishijima, K., Otsuka, R., Nakazawa, H., Takamiya, M.,
 Kato, Y., Yoshizawa, T., Tanaka, T., Kudoh, Y., Yamazaki, J.,
 Kushida, N., Oguchi, A., Aoki, K., Masuda, S., Yanagii, H.,
 Nishimura, M., Yamagishi, A., Oshima, T. and Kikuchi, H.
 Complete genome sequence of an aerobic thermophilic
 crenarchaeon, Sulfolobus tokodaii strain7
 DNA Res. 8 (4), 123-140 (2001)
 21456156
 2 (bases 1 to 263050)
 Kavarabayasi, Y., Tanaka, T., Hino, Y. and Kikuchi, H.
 Submitted (22-DEC-1999) Yutaka Kavarabayasi, National Institute of
 Technology and Evaluation, Biotechnology Center, Nishihara 2-49-10,
 Shibuya-ku, Tokyo 151-0066, Japan (E-mail: kyutaka@nite.go.jp,
 URL: http://www.bio.nite.go.jp/, Tel: 81-3-3481-8951,
 Fax: 81-3-3481-8424)

TITLE
 Kavarabayasi, Y. is officially affiliated with the National
 Institute of Advanced Industrial Science and Technology, Tsukuba,
 Ibaraki 305-0046, Japan
 Yamagishi, A. and Oshima, T. are at Tokyo University of Pharmacy
 and Life Science, Hachioji, Tokyo 192-0392, Japan
 The other authors are at the National Institute of Technology and
 Evaluation, Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan
 Homology analysis is performed by Smith-Waterman algorithm against
 Genbank release 109; EMBL release 56.0; SwissProt release 38.0;
 PIR-Protein release 62.0; and OWL release 31.4.
 E-mail address for comments and questions: kyutaka@nite.go.jp
 ORF organization, sequence alignment and more information are
 available at W.W.W. site of Biotechnology Center,
 URL: http://www.bio.nite.go.jp/dogan/genome_list-e.html/.

FEATURES
 source
 1. 263050
 /organism="Sulfolobus tokodaii"
 /strain="7"
 /db_xref="taxon:111955"
 complement(526..1632)
 /gene="ST0001"
 complement(526..1632)
 /gene="ST0001"
 /codon_start=1
 /transl_table=11
 /product="368aa long hypothetical protein"
 /protein_id="BAB64942.1"
 /db_xref="GI:15620946"
 /translation="MSVIVYTVIDGELNVKQKFFSNLATAVNLISQSFDEPLKLS
 LHEIKKQDTEGLDEVKADKSPFYSLSHKVFDDIFNNRLKALLSEVEKIDIEKKIK
 ELIKKKEADKDEVNPLVMSFKTPDILSVFKLSDSKFEFEYELGKIVLTKPKYS
 EELGYAPFLFTKPKRIGKFGDISVDYETIRVLQNLNEERENFVLGKILGKLT
 LKSKTRLEIRNVSEFLNTEYLLIALRYLHWILTSKLTIGEAENCLPILIASVDKPTQ
 FVKEIKDLYHRIENGEVDLESIRKEIENLGNITLPSRNIQSVREVNKNELFKIG

gene	MKLGNPITMIYVLCMSIYVYKVGDFDKVPRV" complement(1883. .2173) /gene="STS001" complement(1883. .2173) /gene="STS001" /note="PIR:C71147 percent identity: 36.264 in 91aa." /codon_start=1 /transl_table=11 /product="96aa long conserved hypothetical protein" /protein_id="BAB64943.1" /db_xref="GI:15620947" /translation="MEVSNVWKVVLTRBELTEQDAIKAVTIKEIYLPOLLTLNKSVN LIERAMEISVKEKIFIDYSLYIALAERKSKLVTDKKQHEIAKKIVISELI" 2263. .2496 /gene="STS002" 2263. .2496 /gene="STS002" /note="OWL:A00972 percent identity: 28.070 in 57aa." /codon_start=1 /transl_table=11 /product="77aa long conserved hypothetical protein" /protein_id="BAB64944.1" /db_xref="GI:15620948" /translation="MRQLLSLSLTNSALLEVSGIWRISLIFFKLISSFNSISILL IKFSSPHLLIYFSSISRNLSILKLYTFIL" complement(2268. .2537) /gene="STS003" complement(2268. .2537) /gene="STS003" /note="PIR:H69325 percent identity: 40.580 in 69aa." /codon_start=1 /transl_table=11 /product="89aa long conserved hypothetical protein" /protein_id="BAB64945.1" /db_xref="GI:15620949" /translation="MSKIETFFSVYVYMKTVYSLRIDKLEEMEKYNIKWNEI ENFIRREELKEELIKKINEILQTMPTNSSSABLVEDRDNN" complement(2722. .2937) /gene="STS004" complement(2722. .2937) /gene="STS004" /note="PIR:S74019 percent identity: 84.058 in 69aa." /codon_start=1 /transl_table=11 /product="71aa long conserved hypothetical protein" /protein_id="BAB64946.1" /db_xref="GI:15620950" /translation="MGKITGSDIDVILVIKRNRKALIDFFYEVERELGEKVSYL FDVKVYDEKELPFKSFRLDAVRK" 3144. .3401 /gene="STS005" 3144. .3401 /gene="STS005" /note="Swiss Prot:P37413 percent identity: 52.000 in 25aa. motif=prenyl group binding site (CAAX box)" /codon_start=1 /transl_table=11 /product="85aa long hypothetical protein" /protein_id="BAB64947.1" /db_xref="GI:15620951" /translation="MSFSLVILRKVAYPISKYVKNESNLIPWVLGGSPSLKSLGK VVLKHLTLMPHKGLAEIIVLKLLSSPLPSSKILQCCMT" complement(3247. .3399) /gene="STS006" complement(3247. .3399) /gene="STS006" /note="PIR:S74018 percent identity: 58.696 in 46aa." /codon_start=1 /transl_table=11 /product="50aa long conserved hypothetical protein" /protein_id="BAB64948.1" /db_xref="GI:15620952" /translation="WSYNIAEEFLRAKDYLKASELLFOOGLYEASALDSEVSARLYL	gene	NFLNLG" 3744. .5483 /gene="ST0002" 3744. .5483 /gene="ST0002" /note="Swiss_Prot:P55577 percent identity: 37.004 in 227aa." /codon_start=1 /transl_table=11 /product="579aa long hypothetical prolyl endopeptidase" /protein_id="BAB64949.1" /db_xref="GI:15620953" /translation="MDEYEILENLSDPRTISFTEKENKETESKLGKKAMELYPLLLE MDEYVLFMFAYDEENPAILLYGEKSQLLGKNTIYIPPEGYVASEIWKVYNSKEIGV STIERKSGDKIITLLISPEGIKRELGEWSEPFYFKGELCYIKSYRSPDPDGGDYPAD RVCFKDEIVYGDMPKPEFVTKVFDQDFTLVKQKGRYGEVYVYGFDSLRKRVDEGE VTDVIDFOQGEVYOKNNAYVLGNTKVEVDYVPLGVSHIGDKTAVBVIKEYRTPPLIF YDIKKKIGEEVHDNTTFMDGKGHTLFLVETSFNYKFRVYVKKSDGEGEVLMOQGNVD VTVKOLYVKGDVLLHGFLVSKANNPKGVIVYGGFRIPLLPSTSVNRVLLNNGYSI LITLRGGYENGEEHKGAGMLNKNKVFDAEFLRLVKLMGGKAVAMSGSNGLLVG ATINEYPELIDCAVIGHPVLDMLRYDKLYVGYKVEEYGDNPDKYTEYLISYSPYHN LKKGLPKTFVYTGINDDRVHPAHALKYVAKSKSLGNDVMLFVNDSGHSIADPESKARE ESYVVSFTIECLR" complement(5970. .8819) /gene="ST0003" complement(5970. .8819) /gene="ST0003" /note="Swiss_Prot:Q04069 percent identity: 32.836 in 67aa. motif=ATP/GTP-binding site motif A (P-loop)" /codon_start=1 /transl_table=11 /product="949aa long hypothetical protein" /protein_id="BAB64950.1" /db_xref="GI:15620954" /translation="MIDCSSILSLDLVFKFSDSGVPVYTTNNVKPRDVLPTLCNRN VRLDLNMYQHOLEAINKLMOGKALVYNAETGGKTEIWVSIALEMQLKGEFNVLA PKLAGDQIERIYKIIEAGFSVSKQKTKIYEIVGDIYKIDGVDVSNYIQSVAR AKTLTNPVVKNALQFNHKISDLFKKRLIVVDFDFYFGSSKSTVLLHIIGIKDF GIKQIVIMSATISDPVVKPFDFEIGGKSPANDTYIVLGKRDELNAISKALNV SPDDLKGFYKVASDPKKEIYQLQFDNAQLLPEYLDLKGCCDELATIFRSRISSEAN NLVGLKGVNVDGTAPVAHVHSGIDKYVROQVENDMRSGKLKVVVTVTKLQGIIDVG NTRVYVHGIPDSVREFIOREGKPGMASIKRTESVLFPLSLSDAVLLEDYSTIKEW LSLSESILLDPNDFELKIDVIRGILNDRFLAKSVGITGTLPOISYEQLHKTVPKL LFDGRNCNVYDKRDVVEKHQCGIDPMLNAIVRNSVINGRHHVETSDFSSSIM CNNINISHVNNATAIYEDICFSWKQHPDLNDIERGKYSKVSLSLDVLFEGDGGFKY VHEIARKFWYIETRRIQGEYKVEKIELEYTTPSNLKYDFLTYYVASELEPDDVNVK DKGMFTLALLRLNYGIDGLINFGVNSGILKWESEPTALLRRLMRKMKVKVGRTE LDCKLLDDVRNAQPPRRLELVLYDLPYTFNFDNFENKAIARFVHYLCNTIPQL QVISTGMPKPSLIRSLIIDSFGGKYAVSSPTGEISLFDNEEAEVKAALKINIEFDA IVPYGVSIGKKIKFQNEVYIDKEINRLGGLPTPFSKRELVLNDLSLLKEENADN SITRGEVELTKIFRKRAETIRLMINLWKAYLTDK" 9382. .9549 /gene="STS007" 9382. .9549 /gene="STS007" /note="OWL:AF072619 percent identity: 27.500 in 40aa." /codon_start=1 /transl_table=11 /product="55aa long hypothetical cytochrome b" /protein_id="BAB64951.1" /db_xref="GI:15620955" /translation="MKACTPSLLRENFIELIVMLTPISLRSSRRDLTLSPSRQREQSL CILNIYELFYI" complement(9819. .10127) /gene="ST0004"	gene	Query Match 15.2%; Score 20; DB 1; Length 263050; Best Local Similarity 100.0%; Pred. No. 2; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 108 GGAGAGTGGAGTGAATTT 127 DB 68451 GGAGAGTGGAGTGAATTT 68432
------	--	------	---	------	--

RESULT 21

AP001760

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AP001760 340000 bp DNA linear PRI 10-MAY-2000
 Homo sapiens genomic DNA, chromosome 21q, section 104/105.
 AP001760 AL163305 BA000005
 AP001760.1 GI:7768687

Homo sapiens DNA.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
 Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
 Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
 Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
 Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
 Zimmermann,W., Rosenthal,A., Kudo,H., J., Shibuya,K., Kawasaki,K.,
 Asakawa,S., Shintani,A., Sasaki,K., Nagamine,K., Mitsuyama,S.,
 Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstiek,G.,
 Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
 Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S.,
 Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
 Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
 Yaspo,M.L.

The DNA sequence of human chromosome 21

Nature 405 (6784), 311-319 (2000)

20289799

2 (bases 1 to 340000)

Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
 Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
 Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
 Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
 Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
 Zimmermann,W., Rosenthal,A., Kudo,H., J., Shibuya,K., Kawasaki,K.,
 Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
 Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstiek,G.,
 Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
 Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S.,
 Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
 Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
 Yaspo,M.L.

Direct Submission

Submitted (10-APR-2000)

The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Kelo University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)

On May 30, 2000 this sequence version replaced gi:7717454.

The chromosome 21 mapping and sequencing consortium consisting of
 * RIKEN Genomic Sciences Center, Human Genome Research Group, *
 Sagami-hara 228-8555, Japan,

* e-mail: hattori@sc.riken.go.jp

* URL: http://hgp.gsc.riken.go.jp/

and

* Institute of Molecular Biotechnology, Genome Analysis, *

Beutenbergstrasse 11, D-07745 Jena, Germany,

* e-mail: gscj-submit@genome.imb-jena.de

* URL: http://genome.imb-jena.de/

and

* Kelo University School of Medicine, Molecular Biology, * Tokyo

160-8582, Japan,

* e-mail: nshimizu@med-keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/

and

* GBF, Dept. of Genome Analysis,

* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e-mail:

info.genome@gbf.de

* URL: http://genome.gbf.de/

and

* Max-Planck Institute for Molecular Genetics,
 * Ihnestrasse 73, D-14195 Berlin, Germany,
 * e-mail: info-chr21@molgen.mpg.de
 * URL: http://chr21.rz-berlin.mpg.de/
 AL163305: Submitted (10-APR-2000).

FEATURES

source

1. 340000

location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

<1. 21604

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="CTD2308H15, 5' partial"

/clone_lib="CTD BAC library"

/note="Accession No. AP000471"

21162. 59560

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="f50C10"

/clone_lib="CMF21 Fosmid library"

/note="Accession No. AP001477"

59460. 86378

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="f27E1"

/clone_lib="CMF21 Fosmid library"

/note="Accession No. AP000335"

85477. 121753

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="p3588"

/clone_lib="CMP21 P1 library"

/note="Accession No. AP000336"

121730. 175282

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="p1957"

/clone_lib="CMP21 P1 library"

/note="Accession No. AP000337"

174577. 256692

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="pP1D4"

/clone_lib="RP1 PAC library"

/note="Accession No. AP000338"

256594. 334367

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone_lib="RP1 PAC library"

/note="Accession No. AP000339"

333446. >340000

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="p1136, 3' partial"

/clone_lib="CMP21 P1 library"

```
repeat_region /note="Accession No. AP000340"
735..1036
/feature="AluJb"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
1437..1518
/feature="AluSg/x"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
complement(2134..2242)
/feature="MER4B"
/rpt_family="LRR/MER4-group"
/rpt_type=DISPERSED
2409..2992
/feature="Cpg island"
2905..124461
/feature="PCNT"
join(2905..3010,5105..5317,13125..13496,24856..24936,
25471..25726,26185..26240,27740..27914,28412..28548,
30157..30268,31832..32054,32715..32796,34181..34355,
35703..35920,42209..42663,45313..45370,45404..45868,
60423..60569,64561..64712,67471..67613,67928..68160,
69399..69561,69893..70105,75993..76222,76742..76858,
76963..76983,78318..78524,80279..80449,81059..81211,
89917..90795,91565..91720,94797..95567,96932..97034,
100698..100852,104559..104699,106350..106523,
107123..107318,108738..108960,109235..109385,
110257..110943,114631..114875,115706..115808,
116891..117064,118810..118929,119582..119811,
121224..121300,122537..122675,123421..123548,
124011..124461)
/feature="PCNT"
/note="pericentrin, kendrin (KIAA0402), Accession No.
U52962"
2905..3010
/feature="PCNT"
/number=1
3261..3402
/note="(CGGGG)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
3391..3994
/feature="PCNT"
/note="Cpg island"
5105..5317
/feature="PCNT"
/number=2
5460..5753
/note="AluSx"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
complement(5779..6086)
/note="Alu"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
complement(6127..6292)
/note="FRAM"
/rpt_family="SINE/Alu"
Query Match 15.2%; Score 20; DB 9; Length 340000;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AATTGCCAGCTTGGATAAGG 46
|||||
Db 47589 AATTGCCAGCTTGGATAAGG 47608

RESULT 22
AE013648/c
LOCUS
DEFINITION Yersinia pestis KIM section 48 of 415 of the complete genome.
ACCESSION AE013648 AE009952

AE013648.1 GI:21957165
Yersinia pestis KIM
Yersinia pestis KIM
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
1 (bases 1 to 11258)
Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G. F.,
Liss, P., Perna, N. T., Rose, D. J., Mau, B., Zhou, S., Schwartz, D. C.,
Fetherston, J. D., Lindler, L. E., Brubaker, R. R., Plana, G. V.,
Straley, S. C., McDonough, K. A., Nilles, M. L., Matson, J. S.,
Blattner, F. R. and Perry, R. D.
Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
12142430
2 (bases 1 to 11258)
Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G. F.,
Liss, P., Perna, N. T., Rose, D. J., Mau, B., Zhou, S., Schwartz, D. C.,
Fetherston, J. D., Lindler, L. E., Brubaker, R. R., Plana, G. V.,
Straley, S. C., McDonough, K. A., Nilles, M. L., Matson, J. S.,
Blattner, F. R. and Perry, R. D.
Direct Submission
Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445
Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
1..11258
/organism="Yersinia pestis KIM"
/strain="KIM"
/db_xref="taxon:187410"
85..204
/product="5S ribosomal RNA"
/function="rRNA; macromolecule synthesis; modification:
Ribosomal and stable RNAs"
666..1703
/feature="murB"
/note="y0471"
666..1703
/feature="murB"
/function="enzyme; murein sacculus, peptidoglycan"
/note="residues 7 to 345 of 345 are 61.94 pct identical to
residues 4 to 342 of 342 from E. coli K12 : B3972;
residues 7 to 345 of 345 are 62.53 pct identical to
residues 4 to 342 of 342 from GenPept : >gb|AA122970.1|
(AE008893) UDP-N-acetylenolpyruvylglucosamine reductase
[Salmonella typhimurium LT2]"
/codon_start=1
/transl_table=11
/product="UDP-N-acetylenolpyruvylglucosamine reductase"
/protein_id="AA084059.1"
/db_xref="GI:21957166"
/translation="MSNQRSLSKHLNFTALPAYASNVISAGSVETLIAWHESKAKRQ
NMPGLENLALIPCGVSGAPIONIGAYVELKQVCEYVDLLDMDKGTQIRISAEECOFG
YRDSIFKHYGNGFAIVSGIKLMSKWTPLGYGDLHMDPLTVATDIFNSVCTMR
SKLPDPMVTGNAGSPFPNVPVSAIAEEIVHCYNAPHYLOPDGSVKLAAGLIDQCS
LKGYQIGGAHVHQOQALVLINQSEATGQDVHLIARYIRQVQARFSIWLEPEVRIAD
NGEVNAVEHLS"
814..996
/feature="y0470"
814..996
/feature="y0470"
/function="unknown"
/note="residues 9 to 58 of 60 are 34.00 pct identical to
residues 247 to 295 of 436 from GenPept :
>gb|AAD22321.1|AC006955.7 (AC006955) hypothetical protein
[arabidopsis thaliana]"
/codon_start=1
/transl_table=11
/product="hypothetical"
/protein_id="AA084060.1"
/db_xref="GI:21957167"
/translation="MKVAMCYLLKISLGQYYSIGLWGLLLPKTVLLGIYMSVLKIGI
NMVTHCKIICRGWKI"
```


REFERENCE
AUTHORS

- 1 (bases 1 to 12292)
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chamberg, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S.,
Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,
Mench, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M.,
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
Rosi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezara, R.I.D., Trindade dos
Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
Kitajima, J.P.
- Comparison of the genomes of two Xanthomonas pathogens with
differing host specificities
Nature 417 (6887), 459-463 (2002)
22022145
PUBMED
12024217
- 2 (bases 1 to 12292)
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chamberg, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S.,
Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,
Mench, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M.,
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
Rosi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezara, R.I.D., Trindade dos
Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
Kitajima, J.P.

TITLE

JOURNAL
MEDLINE
PUBMEDREFERENCE
AUTHORSTITLE
JOURNALFEATURES
source

- Location/Qualifiers
1. .12292
/organism="Xanthomonas axonopodis pv. citri str. 306"
/strain="306"
/db_xref="taxon:190486"
/note="pathovar: citri"
complement(215. .778)
/gene="adk"
/note="XAC3437"
complement(215. .778)
/gene="adk"
/note="Identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="adenylate kinase"
/protein_id="AAM38280.1"
/db_xref="GI:21109795"
/translation="MRLVLLGPPGSGKGTQATRLKDTDFPHISTGLLRAEVAAGSP
LGLKAEVARDGLVDDILLGLMLEARLGADYAKGFIIDGYPRNVAQNALDELICK
IQGPLDARDVQGLVASELLVERLAGAKESREDNPNESVKRLQVYDSTAPYIGFYE
ORGLKARDVQGLVLEVERISKALGR"
939. .2195
/gene="pfkA"
/note="XAC3438"
939. .2195
/gene="pfkA"
/note="Identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1

gene

CDS

- /transl_table=11
/product="6-phosphofructokinase"
/protein_id="AAM38281.1"
/db_xref="GI:21109796"
/translation="MTGNLLYAQSGVTAIVATAGVTAARARIKVLAAANGIL
GALREELIDTSKESAAAIAAQAOTPGAGFSCRYKLKSLSEDSAKYERLLDLRAHDY
RWFLYNGNSDADTAMKWSQAKAYGYPLCHIGVPTKIDNLAATDTCPGFSGAAKT
VYSREALDVAAMDSTKVFTEYAGRHAGLWAAAGLAGLQDPDAPQIILLPERA
YDQAQFLAKVQVVEKVCVVVASEGIDQAHKGFVADAGAAVDFGHAOLGGVSFL
YDQAQFLGKVKVHTLPDYLORSARHLASTDWEQAQVGAAYKAYAKGNNAVIPVI
ERYSDAPYRKWIPADPLHKVANHHEKMPSPFLKDKGFGITERARRYAPFLIKGAALA
YSGDGLPKYVSLKNVAVKKLPWAG"
complement(2444. .2920)
/gene="XAC3439"
complement(2444. .2920)
/note="putative; ORF located using Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM38282.1"
/db_xref="GI:21109797"
/translation="MLTSQAFADPTPELKPAPCTAQAVCAVHTLRQIPACVRLEG
VFTGNAQPYTILSVRSSTPCQPRARFVDFAKAPSVASGWFINDVIRVPSAACPQQ
AVTVYWRKPADAKPQLDGGQSRILEDAKQQAAGKIPQVPMFAQMTMEGRACQ"
3219. .5246
/gene="XAC3440"
3219. .5246
/gene="XAC3440"
/note="Identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="H+ translocating pyrophosphate synthase"
/protein_id="AAM38283.1"
/db_xref="GI:21109798"
/translation="MLEHYGLWALGCAVLAIYVIGSVARVWVAQPSGNARMQEIAAA
IQEGARAYLNRYLTISVAGAVFLVGLFSWYTAIFGALGAVSLGAGYIGNVSY
RANVTAEARHGIGKAMDVAFRGGAITGMVLVGLLGVAGYAFVLLQGMGLPLEQNL
HALVGLFGSSLTIFARGLGDTADLVGKVEAGIPDDPRNPVIAIDNVG
DNVGCAGNAADLFETVATVIAITMLGSLTADTGSNAVLYPLVIGVSTIAITVGA
AFVVKDGGSSINGALYKGVISGVLAALAYWPTQSLMRDNIHGATYALYACALIGLVL
TGLVWITEYITGTYTPVOHVASASTGHGTNIAGLIGISMKSTALPVIACRAIWG
AFHFGGLYGIATAATAMLNAGMIVALDAYPTIDNAGGIAEMAEPLPEVNTIDPLD
AVGNTTKAVTKGTAIGSAALALVLFYHNTLQAANPDQVYAFDLSDHTVITIGLIG
GLPYTLFGAMAEAGCAAVVEVRPFELPGINAGTAKPOYDRAVDMLTRSAIG
EMVPSLLPVVPIYVLLGLLGRALGLLGTIVTGLFLAISMTGGGAWDNKKYIE
DGHFGKSGSEAKAITGDTGDPYKDTAGPAINPLIKINIIVALLVPLP"
complement(3527. .6006)
/gene="XAC3441"
complement(3527. .6006)
/note="putative; ORF located using Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM38284.1"
/db_xref="GI:21109799"
/translation="MSRLARLVLLLSLTAQIAAATPPPTFVDVADVPANGEGWEAF
IDLEQLRDRFDNQICDTFGGDFSDYQPLRLRCVSHRVTVGVRSVCWTTFGASEVSD
PRSGYLRSDSRVWRCTAPLKAGTRLDEMYRTLAVANFLPEPLPGGAPFYDGLIGCL"
6204. .6740
/gene="ppa"
/note="XAC3442"
6204. .6740
/gene="ppa"
/note="Identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="inorganic pyrophosphatase"
/protein_id="AAM38285.1"
/db_xref="GI:21109800"

gene

CDS

gene /translation="MGLELVTSGKNLPPEINNVVIEIPKDPSEPKVEVDKASGAIFVDR
ILSPMPYPCNYGYVNTICGDDPADVLVLPPLPGSVVRCRPGVGLRMSDEAGS
DEKILAVIEKIFGYAHIEDINQVSSHMERIGHFHYKDKLGKWKVLDGWGAA
EAKRILVESVRYNSDAP"
6856 .8004
/gene="XAC3443"
CDS /gene="XAC3443"
6856 .8004
/gene="XAC3443"
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="response regulator"
/protein_id="AAM38286.1"
/db_xref="GI:21109801"
/translation="MSVTGDFWGLRILFVGLDEASPLSDVYVADLGDQWQAQOVA
DNGSAIEAALSPPDAIVAPLPLDTAATLGLQIRLPRDPIRIALIDAQGGORFPP
ARITGAHREFLPMPLAPVLEAVTSLEELRELLSNPRRAAIGRIKPLSPHPLP
LMHLEEDGADADIAKLIAGDPAIAAKVLIQCNLSAFSGGRSTDLRTAVTRLGVA
TLRLVLASREVFSVOTLPPAERNAMORRALLSSRLAAKVLPTPSAELGTAALLADIG
LLPLGVDEREAPAEAGDERLGHTEAGAYLLGLGLPMPPIEAVAFHRRPLRSSMRSE
WYTGAVHATVALASGESVDEEYLTQVGIARLPWSREQADTLGLTEA"
complement(8422..11268)
/gene="btub"
/note="XAC3444"
complement(8422..11268)
/gene="btub"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="nonB-dependent receptor"
/protein_id="AAM38287.1"
/db_xref="GI:21109802"
/translation="WMNLTSAVRLGLLPAGTAYALTAFAPAAQESTTTLDRLEITGS
RIRADVETQPIITLDRQALEKGLTSVADVLONLTSAGSPALSRADLSGEDVGG
YYVDRLNLAQRTLVLYNGKRLGISTGLQDLQIOPMSAERIEVLKDGASSTIGSDA
IAGVNNITRRFGDAENSVQFGQGGDDTQYFTVSGQGGVTVLSAIEYSKQD
PVFAKNWFRSDGSPNSPNSPISQNGSWCNPLQVCDPDTAVQWTLNAGNGP
NNPADIYRTPAEYANQNMVQGTIGKSVFANVDVADAITFNADIAYNERTTD
QIAGYPTGSGFTGLEGSFAPNIGQVDFRRLVEVPRASENOLKTLRAPLTSG
YFDIGKTWDVCLWNRENTKSRGDMSLIASRQALGPSFINGQVACGTADP
ISLSARWNPPLPYNVAGQSLADPQLERLPTFTGLTKTTSFANLSGVSVEL
PAGDLGVAVGYEHRKEGRFSPDFAQSGESTGLGAKTQGSIDSEVLELNVLPLS

gene

CDS

gene

CDS

Query Match 14.4%; Score 19; DB 1; Length 12292;

Best Local Similarity 100.0%; Pred. No. 7.2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GAAGAAATGCCAGCTGG 40

Db 2168 GAAGAAATGCCAGCTGG 2186

RESULT 24

AC100719

LOCUS

DEFINITION

Mus musculus chromosome 1 clone RP23-170D17 map 1, LOW-PASS

SEQUENCE SAMPLING.

AC100719

AC100719.1 GI:17048085

HTG; HTGS PHASE0.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 67972)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 67972)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhvalter,B.,

Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., MCPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Olliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Zainoun,J., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zimoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L15998

Center clone name: 170_D_17

* NOTE: This record contains 83 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 733: contig of 733 bp in length
* 734 833: gap of 100 bp
* 834 1566: contig of 733 bp in length
* 1567 1666: gap of 100 bp
* 1667 2369: contig of 703 bp in length
* 2370 2469: gap of 100 bp
* 2470 3187: contig of 718 bp in length
* 3188 3287: gap of 100 bp
* 3288 3989: contig of 702 bp in length
* 3990 4089: gap of 100 bp
* 4090 4822: contig of 733 bp in length
* 4823 4922: gap of 100 bp
* 4923 5633: contig of 711 bp in length
* 5634 5733: gap of 100 bp
* 5734 6440: contig of 707 bp in length
* 6441 6540: gap of 100 bp
* 6541 7272: contig of 732 bp in length
* 7273 7372: gap of 100 bp
* 7373 8088: contig of 716 bp in length
* 8089 8188: gap of 100 bp
* 8189 8872: contig of 684 bp in length
* 8873 8972: gap of 100 bp
* 8973 9667: contig of 695 bp in length
* 9668 9767: gap of 100 bp
* 9768 10499: contig of 732 bp in length
* 10500 10599: gap of 100 bp
* 10600 11336: contig of 737 bp in length

* 11337 11436: gap of 100 bp
* 11437 12154: contig of 718 bp in length
* 12155 12254: gap of 100 bp
* 12255 13006: contig of 752 bp in length
* 13007 13106: gap of 100 bp
* 13107 13834: contig of 728 bp in length
* 13835 13934: gap of 100 bp
* 13935 14636: contig of 702 bp in length
* 14637 14736: gap of 100 bp
* 14737 15461: contig of 725 bp in length
* 15462 15561: gap of 100 bp
* 15562 16294: contig of 733 bp in length
* 16295 16394: gap of 100 bp
* 16395 17110: contig of 716 bp in length
* 17111 17210: gap of 100 bp
* 17211 17912: contig of 702 bp in length
* 17913 18012: gap of 100 bp
* 18013 18735: contig of 723 bp in length
* 18736 18835: gap of 100 bp
* 18836 19608: contig of 773 bp in length
* 19609 19708: gap of 100 bp
* 19709 20429: contig of 721 bp in length
* 20430 20529: gap of 100 bp
* 20530 21256: contig of 727 bp in length
* 21257 21356: gap of 100 bp
* 21357 22098: contig of 742 bp in length
* 22099 22198: gap of 100 bp
* 22199 22920: contig of 722 bp in length
* 22921 23020: gap of 100 bp
* 23021 23746: contig of 726 bp in length
* 23747 23846: gap of 100 bp
* 23847 24521: contig of 675 bp in length
* 24522 24621: gap of 100 bp
* 24622 25347: contig of 726 bp in length
* 25348 25447: gap of 100 bp
* 25448 26173: contig of 726 bp in length
* 26174 26273: gap of 100 bp
* 26274 27014: contig of 741 bp in length
* 27015 27114: gap of 100 bp
* 27115 27830: contig of 716 bp in length
* 27831 27930: gap of 100 bp
* 27931 28624: contig of 694 bp in length
* 28625 28724: gap of 100 bp
* 28725 29427: contig of 703 bp in length
* 29428 29527: gap of 100 bp
* 29528 30253: contig of 726 bp in length
* 30254 30353: gap of 100 bp
* 30354 31081: contig of 728 bp in length
* 31082 31181: gap of 100 bp
* 31182 31907: contig of 726 bp in length
* 31908 32007: gap of 100 bp
* 32008 32744: contig of 737 bp in length
* 32745 32844: gap of 100 bp
* 32845 33566: contig of 722 bp in length
* 33567 33666: gap of 100 bp
* 33667 34373: contig of 707 bp in length
* 34374 34473: gap of 100 bp
* 34474 35203: contig of 730 bp in length
* 35204 35303: gap of 100 bp
* 35304 36036: contig of 733 bp in length
* 36037 36136: gap of 100 bp
* 36137 36853: contig of 717 bp in length
* 36854 36953: gap of 100 bp
* 36954 37659: contig of 706 bp in length
* 37660 37759: gap of 100 bp
* 37760 38451: contig of 692 bp in length
* 38452 38551: gap of 100 bp
* 38552 39247: contig of 696 bp in length
* 39248 39347: gap of 100 bp
* 39348 40059: contig of 712 bp in length
* 40060 40159: gap of 100 bp
* 40160 40879: contig of 720 bp in length
* 40880 40979: gap of 100 bp

* 40980 41705: contig of 726 bp in length
* 41706 41805: gap of 100 bp
* 41806 42510: contig of 705 bp in length
* 42511 42610: gap of 100 bp
* 42611 43328: contig of 718 bp in length
* 43329 43428: gap of 100 bp
* 43429 44168: contig of 740 bp in length
* 44169 44268: gap of 100 bp
* 44269 44974: contig of 706 bp in length
* 44975 45074: gap of 100 bp
* 45075 45775: contig of 701 bp in length
* 45776 45875: gap of 100 bp
* 45876 46580: contig of 705 bp in length
* 46581 46680: gap of 100 bp
* 46681 47417: contig of 737 bp in length
* 47418 47517: gap of 100 bp
* 47518 48249: contig of 732 bp in length
* 48250 48349: gap of 100 bp
* 48350 49081: contig of 732 bp in length
* 49082 49181: gap of 100 bp
* 49182 49913: contig of 732 bp in length
* 49914 50013: gap of 100 bp
* 50014 50741: contig of 728 bp in length
* 50742 50841: gap of 100 bp
* 50842 51583: contig of 742 bp in length
* 51584 51683: gap of 100 bp
* 51684 52409: contig of 726 bp in length
* 52410 52509: gap of 100 bp
* 52510 53244: contig of 735 bp in length
* 53245 53344: gap of 100 bp
* 53345 54063: contig of 719 bp in length
* 54064 54163: gap of 100 bp
* 54164 54794: contig of 631 bp in length
* 54795 54894: gap of 100 bp
* 54895 55603: contig of 709 bp in length
* 55604 55703: gap of 100 bp
* 55704 56424: contig of 721 bp in length

Query Match

Best Local Similarity 14.4%; Score 19; DB 2; Length 67972;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 AAGCCCAAGCTGAAGGCCA 61
|||||
Db 35409 AAGCCCAAGCTGAAGGCCA 35427

RESULT 25

AL606526/c

LOCUS

DEFINITION

Human DNA sequence from clone RP13-534F18 on chromosome 1, complete

sequence.

ACCESSION

AL606526

VERSION

AL606526.10

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 113654)

Almeida, J.

Direct Submission

Submitted (15-NOV-2001)

Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquerry@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Nov 16, 2001 this sequence version replaced gi:15808280.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows otherwise noted: all

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/Celegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP13-534F18 is from the library RPCI-13.3 constructed by the group of Pieter de Jong. For further details see <http://www.choiri.org/bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP13-534F18 it may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP13-534F18 is at 113654 in this sequence. The true right end of clone RP5-947P14 is at 2000 in this sequence.

FEATURES

source
1. 113654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP13-534F18"
/clone_lib="RPCI-13.3"
BASE COUNT 39092 a 19726 c 20088 g 34748 t
ORIGIN

Query Match 14.4%; Score 19; DB 9; Length 113654;
Best Local Similarity 100.0%; Pred. NO. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 112 AAGTGGAGTGAATTCCT 130
|||||
DB 46920 AAGTGGAGTGAATTCCT 46902

RESULT 26
AC079482
LOCUS
DEFINITION Mus musculus clone RP23-160C18, WORKING DRAFT SEQUENCE, 31
ACCESSION AC079482.1 GI:9964847
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 121063)
DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 121063)
DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1798378
Center clone name: RPCI-23_160C18

Summary Statistics
Consensus quality: 90928 bases at least Q40
Consensus quality: 105213 bases at least Q30
Consensus quality: 108646 bases at least Q20
Estimated insert size: 178000; agarose-fp estimation
Estimated insert size: 118063; sum-of-contigs estimation
Quality coverage: 8.18 in Q20 bases; agarose-fp estimation
Quality coverage: 12.33 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1019: contig of 1019 bp in length
1020 1119: gap of unknown length
1120 2299: contig of 1180 bp in length
2300 2399: gap of unknown length
2400 3406: contig of 1007 bp in length
3407 3506: gap of unknown length
3507 4734: contig of 1228 bp in length
4735 4834: gap of unknown length
4835 6332: contig of 1498 bp in length
6333 6433: gap of unknown length
6434 7748: contig of 1316 bp in length
7749 7849: gap of unknown length
7849 9368: contig of 1520 bp in length
9369 9469: gap of unknown length
9469 11273: contig of 1805 bp in length
11274 11374: gap of unknown length
11374 12788: contig of 1415 bp in length
12789 12889: gap of unknown length
12889 14002: contig of 1114 bp in length
14003 14102: gap of unknown length
14103 15710: contig of 1608 bp in length
15711 15811: gap of unknown length
15811 17108: contig of 1298 bp in length
17109 17209: gap of unknown length
17209 18332: contig of 1124 bp in length
18333 18432: gap of unknown length
18433 20862: contig of 2430 bp in length
20863 20963: gap of unknown length
20963 23495: contig of 2533 bp in length
23496 23595: gap of unknown length
23596 25703: contig of 2108 bp in length
25704 25804: gap of unknown length
25804 27804: contig of 2001 bp in length
27805 27904: gap of unknown length
27905 32483: contig of 4579 bp in length
32484 32583: gap of unknown length
32584 33670: contig of 1086 bp in length
33670 33770: gap of unknown length
33770 36378: contig of 2609 bp in length
36379 36478: gap of unknown length
36479 43329: contig of 6851 bp in length
43330 43429: gap of unknown length
43430 49029: contig of 5600 bp in length
49030 49129: gap of unknown length
49130 55349: contig of 6220 bp in length
55350 61174: gap of unknown length
61175 61274: gap of unknown length
61275 66048: contig of 4774 bp in length
66049 66148: gap of unknown length
66149 74177: contig of 8029 bp in length
74178 74278: gap of unknown length
74278 80199: contig of 5922 bp in length
80200 80299: gap of unknown length
80300 87977: contig of 7678 bp in length
87978 88077: gap of unknown length

[illegible]

COMMENT

On Apr 7, 2002 this sequence version replaced gi:17974075. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C-elegans/wormpep> RP23-330D1 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: <http://mrcseq.har.mrc.ac.uk>
Contact: mouseq@har.mrc.ac.uk

FEATURES

source Location/Qualifiers
1..137782
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="13"
/clone="RP23-330D1"
/clone.lib="RPCI-23"

BASE COUNT 40627 a 27285 c 27611 g 42259 t
ORIGIN

Query Match 14.4%; Score 19; DB 10; Length 137782;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGCCCAAGCTGAAGGCCA 61
|||||
Db 136870 AAGCCCAAGCTGAAGGCCA 136888

RESULT 30
AC125887 155726 bp DNA linear HTG 23-JUL-2002
LOCUS Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS
DEFINITION *** 74 unordered pieces.

ACCESSION AC125887
VERSION AC125887.1 GI:21671483
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 155726)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbra,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

RESULT 28

AC008570/c 127392 bp DNA linear PRI 29-SEP-2001
LOCUS Homo sapiens chromosome 5 clone CTC-549A4, complete sequence.
ACCESSION AC008570
VERSION AC008570.6 GI:15808505
KEYWORDS HTG.
SOURCE Homo sapiens.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 127392)
TITLE Direct Submission
JOURNAL Direct Submission
Unpublished
2 (bases 1 to 127392)
REFERENCE DOE Joint Genome Institute.

REFERENCE

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 127392)
REFERENCE DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Direct Submission
Submitted (29-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 29, 2001 this sequence version replaced gi:15290295.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 176.7kb). It is clipped at the overlap with AC027314.
The number of bases overlapped is 59007.

REFERENCE

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Direct Submission
Submitted (29-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 29, 2001 this sequence version replaced gi:15290295.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 176.7kb). It is clipped at the overlap with AC027314.
The number of bases overlapped is 59007.

COMMENT

On Sep 29, 2001 this sequence version replaced gi:15290295.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 176.7kb). It is clipped at the overlap with AC027314.
The number of bases overlapped is 59007.

FEATURES

source Location/Qualifiers
1..127392
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-549A4"

BASE COUNT 31643 a 26827 c 28041 g 40881 t
ORIGIN

Query Match 14.4%; Score 19; DB 9; Length 127392;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 AGGAGAAGTGAGTGAAT 125
|||||
Db 116032 AGGAGAAGTGAGTGAAT 116014

RESULT 29

AL645686 137782 bp DNA linear ROD 29-JUN-2002
LOCUS Mouse DNA sequence from clone RP23-330D1 on chromosome 13, complete sequence.
DEFINITION AL645686
VERSION AL645686.10 GI:20068620
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 137782)
REFERENCE Lovell,J.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
 Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
 Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, E., Mawhney, E., McLeod, M.P., Meador, K., Morgan, M., Morris, S.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, M., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
 Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Vatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 155726)
 Worley, K.C.
 Direct Submission
 Submitted (02-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 155726)
 Worley, K.C.
 Direct Submission
 Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GWLD
 Center clone name: CH230-274J3
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 93488 bases at least Q40
 Consensus quality: 99060 bases at least Q30
 Consensus quality: 102929 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 74 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1065: contig of 1065 bp in length
 * 1066 1165: gap of unknown length
 * 1166 2186: contig of 1021 bp in length
 * 2187 2286: gap of unknown length

2287 3495: contig of 1209 bp in length
 3496 3595: gap of unknown length
 3596 4549: contig of 1054 bp in length
 4550 4749: gap of unknown length
 4750 5775: contig of 1026 bp in length
 5776 5875: gap of unknown length
 5876 7013: contig of 1138 bp in length
 7014 8585: contig of 1472 bp in length
 8586 8686: gap of unknown length
 8687 9693: contig of 1007 bp in length
 9694 11295: contig of 1503 bp in length
 11296 12652: contig of 1257 bp in length
 12653 12752: gap of unknown length
 12753 14036: contig of 1284 bp in length
 14037 14136: gap of unknown length
 14137 15653: contig of 1517 bp in length
 15654 15753: gap of unknown length
 15754 17043: contig of 1290 bp in length
 17044 17143: gap of unknown length
 17144 18447: contig of 1304 bp in length
 18448 18547: gap of unknown length
 18549 20190: contig of 1643 bp in length
 20191 20290: gap of unknown length
 20291 21436: contig of 1146 bp in length
 21437 21536: gap of unknown length
 21537 23361: contig of 1825 bp in length
 23362 23461: gap of unknown length
 23462 24927: contig of 1466 bp in length
 24928 25027: gap of unknown length
 25029 26574: contig of 1547 bp in length
 26575 27768: contig of 1094 bp in length
 27769 27868: gap of unknown length
 27869 29089: contig of 1221 bp in length
 29090 30291: contig of 1102 bp in length
 30292 30391: gap of unknown length
 30392 31332: contig of 1241 bp in length
 31333 31732: gap of unknown length
 31733 33206: contig of 1474 bp in length
 33207 33306: gap of unknown length
 33307 34489: contig of 1183 bp in length
 34490 36149: contig of 1560 bp in length
 36150 36249: gap of unknown length
 36250 38072: contig of 1823 bp in length
 38073 39507: contig of 1335 bp in length
 39508 39607: gap of unknown length
 39608 41207: contig of 1600 bp in length
 41208 41307: gap of unknown length
 41308 43733: contig of 2426 bp in length
 43734 43833: gap of unknown length
 43834 45306: contig of 1473 bp in length
 45307 45406: gap of unknown length
 45407 46935: contig of 1529 bp in length
 46936 47035: gap of unknown length
 47036 48280: contig of 1245 bp in length
 48281 48380: gap of unknown length
 48381 50905: contig of 2525 bp in length
 50906 51005: gap of unknown length
 51006 52013: contig of 1008 bp in length
 52014 52113: gap of unknown length
 52114 53357: contig of 1244 bp in length
 53358 53457: gap of unknown length
 53458 54671: contig of 1214 bp in length
 54672 54771: gap of unknown length
 54772 56149: contig of 1378 bp in length
 56150 56249: gap of unknown length
 56250 58450: contig of 2201 bp in length

* 58451 58550: gap of unknown length
 * 58551 59702: contig of 1152 bp in length
 * 59703 59802: gap of unknown length
 * 59803 61210: contig of 1408 bp in length
 * 61211 61310: gap of unknown length
 * 61311 62734: contig of 1424 bp in length
 * 62735 62834: gap of unknown length
 * 62835 65673: contig of 2839 bp in length
 * 65674 65774: gap of unknown length
 * 65775 67274: contig of 1501 bp in length
 * 67275 67375: gap of unknown length
 * 67375 69075: contig of 1701 bp in length
 * 69076 69175: gap of unknown length
 * 69176 70560: contig of 1385 bp in length
 * 70561 70660: gap of unknown length
 * 70661 72978: contig of 2318 bp in length
 * 72979 73079: gap of unknown length
 * 73079 75785: contig of 2707 bp in length
 * 75786 75885: gap of unknown length
 * 75886 77423: contig of 1537 bp in length
 * 77423 77523: gap of unknown length
 * 77523 79028: contig of 1505 bp in length
 * 79028 79128: gap of unknown length
 * 79128 81056: contig of 1929 bp in length
 * 81057 81157: gap of unknown length
 * 81157 83212: contig of 2055 bp in length
 * 83212 83312: gap of unknown length
 * 83312 85650: contig of 2339 bp in length
 * 85651 85750: gap of unknown length
 * 85751 87045: contig of 1294 bp in length
 * 87045 87144: gap of unknown length

Query Match 14.4%; Score 19; DB 2; Length 155726;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 GAGACCACGAGCAGGAGA 112

Db 102872 GAGACCACGAGCAGGAGA 102890

RESULT 31

AL645923

LOCUS

DEFINITION Mouse DNA sequence from clone RP23-75H1 on chromosome 13, complete

ACCESSION AL645923.14 GI:19572045

VERSION HTG.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (29 JUN 2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquey@sanger.ac.uk
 On Mar 21, 2002 this sequence version replaced gi:19335835.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-75H1 is from the RPI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6

Center: Genome Center

Center: UK Medical Research Council

Center code: UK-MRC

Web site: <http://mrcseq.har.mrc.ac.uk>

Contact: mouse@har.mrc.ac.uk

FEATURES

source

Location/Qualifiers
 1..157361
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="13"
 /clone="RP23-75H1"
 /clone_lib="RPI-23"

BASE COUNT 45215 a 31432 c 31628 g 49086 t

ORIGIN

Query Match 14.4%; Score 19; DB 10; Length 157361;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGCCCAAGCTGAAGGCCA 61

Db 82294 AAGCCCAAGCTGAAGGCCA 82312

RESULT 32

AC111338

LOCUS

DEFINITION Rattus norvegicus clone CH230-240A17, *** SEQUENCING IN PROGRESS
 ***, 68 unordered pieces.

ACCESSION AC111338.2 GI:21735860

VERSION HTG; HTGS, PHASE1.

KEYWORDS Norway rat.

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 158286)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T., Barbra, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briefa, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabelli, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,

Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwu,S., Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Plickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojokan,I., Rolfe,M., Ruiz,S., Savary,G., Scher,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taylor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 158286)
Worley,K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 158286)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18701102.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GMBI
Center clone name: CH230-240A17

Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 103746 bases at least Q40
Consensus quality: 108208 bases at least Q30
Consensus quality: 111376 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 68 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1244: contig of 1244 bp in length
1245 1344: gap of unknown length
1345 2875: contig of 1531 bp in length
2876 2976: gap of unknown length
2976 4032: contig of 1057 bp in length
4033 4132: gap of unknown length
4133 5396: contig of 1264 bp in length
5397 5496: gap of unknown length
5497 6969: contig of 1473 bp in length
6970 7069: gap of unknown length
7070 8370: contig of 1301 bp in length
8371 8470: gap of unknown length
8471 9974: contig of 1504 bp in length
9975 10074: gap of unknown length
10075 11969: contig of 1895 bp in length
11970 12069: gap of unknown length
12070 13421: contig of 1352 bp in length

13422 13521: gap of unknown length
13522 14649: contig of 1128 bp in length
14650 14749: gap of unknown length
14750 16351: contig of 1602 bp in length
16352 16451: gap of unknown length
16452 17940: contig of 1489 bp in length
17941 18040: gap of unknown length
18041 19287: contig of 1247 bp in length
19288 19387: gap of unknown length
19388 20768: contig of 1381 bp in length
20769 22395: contig of 1527 bp in length
22396 22495: gap of unknown length
22496 23636: contig of 1141 bp in length
23637 23736: gap of unknown length
23737 25287: contig of 1551 bp in length
25288 26570: contig of 1183 bp in length
26571 26670: gap of unknown length
26671 28078: contig of 1408 bp in length
28079 28178: gap of unknown length
28179 29573: contig of 1395 bp in length
29574 29673: gap of unknown length
29674 31324: contig of 1651 bp in length
31325 32599: contig of 1175 bp in length
32600 34751: contig of 2052 bp in length
34752 34851: gap of unknown length
34852 36020: contig of 1169 bp in length
36021 37941: contig of 1821 bp in length
37942 38041: gap of unknown length
38042 39144: contig of 1103 bp in length
39145 39244: gap of unknown length
39245 41215: contig of 1971 bp in length
41216 43354: contig of 2039 bp in length
43355 43454: gap of unknown length
43455 45504: contig of 2050 bp in length
45505 45604: gap of unknown length
45605 47070: contig of 1466 bp in length
47071 48306: contig of 1136 bp in length
48307 48406: gap of unknown length
48407 49467: contig of 1061 bp in length
49468 49567: gap of unknown length
49568 51036: contig of 1469 bp in length
51037 53136: gap of unknown length
53137 53712: contig of 2576 bp in length
53713 53812: gap of unknown length
53813 55162: contig of 1350 bp in length
55163 55262: gap of unknown length
55263 57096: contig of 1834 bp in length
57097 57196: gap of unknown length
57197 58767: contig of 1571 bp in length
58768 58867: gap of unknown length
58868 60411: contig of 1544 bp in length
60412 60511: gap of unknown length
60512 62118: contig of 1607 bp in length
62119 62218: gap of unknown length
62219 63943: contig of 1725 bp in length
63944 64043: gap of unknown length
64044 66201: contig of 2158 bp in length
66202 66301: gap of unknown length
66302 68867: contig of 2566 bp in length
68868 68967: gap of unknown length
68968 71412: contig of 2445 bp in length
71413 71512: gap of unknown length
71513 74169: contig of 2657 bp in length
74170 74269: gap of unknown length
74270 78013: contig of 3744 bp in length
78014 78113: gap of unknown length

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

* 78114 80476: contig of 2363 bp in length
 * 80477 80576: gap of unknown length
 * 80577 83565: contig of 2989 bp in length
 * 83566 83665: gap of unknown length
 * 83666 85949: contig of 2284 bp in length
 * 85950 86049: gap of unknown length
 * 86050 89250: contig of 3201 bp in length
 * 89251 89350: gap of unknown length
 * 89351 91850: contig of 2500 bp in length
 * 91851 91950: gap of unknown length
 * 91951 93870: contig of 1920 bp in length
 * 93871 93970: gap of unknown length
 * 93971 96867: contig of 2897 bp in length
 * 96868 96967: gap of unknown length
 * 96968 97066: contig of 2739 bp in length
 * 97067 97806: gap of unknown length
 * 97807 101862: contig of 2056 bp in length

Query Match 14.4%; Score 19; DB 2; Length 159286;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CTGATGACCAAGAGACCA 100

Db 76185 CTGATGACCAAGAGACCA 76203

RESULT 33

AC120092/c

LOCUS AC120092 159642 bp DNA linear HTG 14-JUL-2002
 Rattus norvegicus clone CH230-420B3, *** SEQUENCING IN PROGRESS
 ***, 52 unordered pieces.

ACCESSION AC120092.3 GI:21747391

VERSION HTG: HTGS, PHASE1.

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Mammalia; Euthera; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 159642)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbara,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buha,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
 Homs,J.F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Nextson,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
 Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,

Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 159642)

Worley,K.C.

Direct Submission

Submitted (03-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 159642)

Worley,K.C.

Direct Submission

Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 14, 2002 this sequence version replaced gi:21240251.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVZX

Center clone name: CH230-420B3

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 113642 bases at least Q40

Consensus quality: 118756 bases at least Q30

Consensus quality: 121702 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 52 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 1114: contig of 1114 bp in length

* 1115: gap of unknown length

* 1215: contig of 1039 bp in length

* 2254: gap of unknown length

* 2354: contig of 1424 bp in length

* 3877: gap of unknown length

* 4982: contig of 1105 bp in length

* 5082: gap of unknown length

* 6266: contig of 1184 bp in length

* 6367: gap of unknown length

* 6367: contig of 1205 bp in length

* 7671: gap of unknown length

* 7672: contig of 1051 bp in length

* 8723: gap of unknown length

* 8823: contig of 1254 bp in length

* 10077: contig of 1384 bp in length

* 10177: contig of 1384 bp in length

* 11561: gap of unknown length

* 11661: contig of 1068 bp in length

* 12729: gap of unknown length

* 12828: contig of 1088 bp in length

* 13917: gap of unknown length

* 14017: contig of 1931 bp in length

* 15948: gap of unknown length

* 16048 17736: contig of 1689 bp in length
* 17737 17836: gap of unknown length
* 17837 19231: contig of 1395 bp in length
* 19231 19331: gap of unknown length
* 19331 20481: contig of 1150 bp in length
* 20481 20581: gap of unknown length
* 20581 22887: contig of 2305 bp in length
* 22887 22986: gap of unknown length
* 22986 24533: contig of 1547 bp in length
* 24533 24634: gap of unknown length
* 24634 27351: contig of 2718 bp in length
* 27351 27451: gap of unknown length
* 27451 29085: contig of 1534 bp in length
* 29085 31338: gap of unknown length
* 31338 31438: gap of unknown length
* 31438 33141: contig of 1703 bp in length
* 33141 33241: gap of unknown length
* 33241 35675: contig of 2434 bp in length
* 35675 35775: gap of unknown length
* 35775 37592: contig of 1817 bp in length
* 37592 39329: gap of unknown length
* 39329 39429: gap of unknown length
* 39429 40554: contig of 1225 bp in length
* 40554 40754: gap of unknown length
* 40754 43168: contig of 2414 bp in length
* 43168 43268: gap of unknown length
* 43268 45414: contig of 2146 bp in length
* 45414 45514: gap of unknown length
* 45514 49320: contig of 3806 bp in length
* 49320 49420: gap of unknown length
* 49420 52472: contig of 3052 bp in length
* 52472 52572: gap of unknown length
* 52572 55255: contig of 2683 bp in length
* 55255 59303: gap of unknown length
* 59303 59403: gap of unknown length
* 59403 64041: gap of unknown length
* 64041 67011: contig of 2871 bp in length
* 67011 70301: gap of unknown length
* 70301 70401: contig of 3190 bp in length
* 70401 73883: contig of 3482 bp in length
* 73883 73983: gap of unknown length
* 73983 77036: contig of 3053 bp in length
* 77036 77136: gap of unknown length
* 77136 80975: contig of 3839 bp in length
* 80975 84129: contig of 3054 bp in length
* 84129 84229: gap of unknown length
* 84229 87620: contig of 3391 bp in length
* 87620 87721: gap of unknown length
* 87721 90509: contig of 2789 bp in length
* 90509 94032: contig of 3423 bp in length
* 94032 94132: gap of unknown length
* 94132 97299: contig of 3167 bp in length
* 97299 97399: gap of unknown length
* 97399 100648: contig of 3249 bp in length
* 100648 100748: gap of unknown length
* 100748 103849: contig of 3101 bp in length
* 103849 103950: gap of unknown length
* 103950 109523: contig of 5574 bp in length
* 109523 109624: gap of unknown length
* 109624 114061: contig of 4438 bp in length
* 114061 114161: gap of unknown length
* 114161 119832: contig of 5671 bp in length
* 119832 125547: gap of unknown length
* 125547 125647: contig of 5615 bp in length
* 125647 132259: contig of 6612 bp in length

* 132260 132359: gap of unknown length
* 132359 137599: contig of 5240 bp in length
* 137599 137600: gap of unknown length
* 137600 146877: contig of 9178 bp in length
* 146877 146977: gap of unknown length
* 146977 159642: contig of 12665 bp in length.
* 159642 Location/Qualifiers
* 159642
* 159642 /organism="Rattus norvegicus"
* 159642 /db_xref="taxon:10116"

Query Match 14.4%; Score 19; DB 2; Length 159642;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GGAAGAAATTCGAGCTTG 39
|||||
Db 44463 GGAAGAAATTCGAGCTTG 44445

RESULT 34
AC079549
LOCUS AC079549 160334 bp DNA linear HTG 02-SEP-2000
DEFINITION Mus musculus clone RP23-421E13, WORKING DRAFT SEQUENCE, 36
unordered pieces.
AC079549
AC079549.1 GI:9964914
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 160334)
Sequencing of Mouse
Unpublished
2 (bases 1 to 160334)
DOE Joint Genome Institute.
Direct Submission
Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1898645
Center clone name: RPCI-23_421E13

Summary Statistics
Consensus quality: 130033 bases at least Q40
Consensus quality: 148274 bases at least Q30
Consensus quality: 151667 bases at least Q20
Estimated insert size: 197000; agarose-fp estimation
Estimated insert size: 156834; sum-of-contigs estimation
Quality coverage: 3.52 in Q20 bases; agarose-fp estimation
Quality coverage: 4.42 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1191: contig of 1191 bp in length
* 1192 1291: gap of unknown length
* 1292 2391: contig of 1100 bp in length
* 2392 2491: gap of unknown length
* 2492 3695: contig of 1204 bp in length
* 3696 3795: gap of unknown length
* 3796 4803: contig of 1008 bp in length

```
* 4804 4903: gap of unknown length.
* 4904 6037: contig of 1134 bp in length
* 6038 6137: gap of unknown length
* 6138 7603: contig of 1466 bp in length
* 7604 7703: gap of unknown length
* 7704 8945: contig of 1242 bp in length
* 8946 9045: gap of unknown length
* 11077 11177: contig of 2032 bp in length
* 11178 13117: gap of unknown length
* 13118 13217: gap of unknown length
* 13218 14663: contig of 1246 bp in length
* 14664 14563: gap of unknown length
* 14564 16339: contig of 1676 bp in length
* 16240 16339: gap of unknown length
* 16340 18236: contig of 1897 bp in length
* 18237 18336: gap of unknown length
* 18337 20463: contig of 2127 bp in length
* 20464 20563: gap of unknown length
* 20564 23184: contig of 2621 bp in length
* 23185 23284: gap of unknown length
* 23285 25190: contig of 1906 bp in length
* 25191 25290: gap of unknown length
* 25291 27703: contig of 2413 bp in length
* 27704 27803: gap of unknown length
* 27804 28555: contig of 2052 bp in length
* 28556 29956: gap of unknown length
* 29957 33001: contig of 3046 bp in length
* 33002 33101: gap of unknown length
* 33102 34938: contig of 1837 bp in length
* 34939 35038: gap of unknown length
* 35039 35668: contig of 3530 bp in length
* 35669 38668: gap of unknown length
* 38669 40978: contig of 2309 bp in length
* 40978 41078: gap of unknown length
* 41078 44724: contig of 3647 bp in length
* 44725 46888: gap of unknown length
* 46889 46988: contig of 2064 bp in length
* 46989 52032: contig of 5044 bp in length
* 52033 52132: gap of unknown length
* 52133 57669: contig of 5537 bp in length
* 57670 57769: gap of unknown length
* 57770 63675: contig of 5906 bp in length
* 63676 63775: gap of unknown length
* 63776 67199: contig of 3424 bp in length
* 67200 72135: gap of unknown length
* 72135 73233: contig of 5835 bp in length
* 73235 81223: contig of 7989 bp in length
* 81224 81323: gap of unknown length
* 81324 87283: contig of 5960 bp in length
* 87284 87384: gap of unknown length
* 87384 89401: contig of 2018 bp in length
* 89402 89501: gap of unknown length
* 89502 100676: contig of 11175 bp in length
* 100677 100776: gap of unknown length
* 100777 116153: contig of 15377 bp in length
* 116154 116253: gap of unknown length
* 116254 127943: contig of 11690 bp in length
* 127944 128043: gap of unknown length
* 128044 143038: contig of 14995 bp in length
* 143039 143139: gap of unknown length
* 143139 160334: contig of 17196 bp in length.
FEATURES
    source
    1. .160334
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /clone_lib="RPCI mouse BAC library 23"
        /clone="RP23-421E13"
45827 a 32566 c 33459 g 44842 t 3640 others
```

```
Query Match 14.4%; Score 19; DB 2; Length 160334;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGCCCAAGCTGAAGGCCA 61
   |||||
Db 39137 AAGCCCAAGCTGAAGGCCA 39155

RESULT 35
AC034207 163942 bp DNA linear PRI 03-NOV-2001
LOCUS Homo sapiens chromosome 5 clone CTC-329H14, complete sequence.
DEFINITION AC034207
ACCESSION AC034207.6 GI:16603986
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 163942)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 163942)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 163942)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 163942)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 5 (bases 1 to 163942)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 3, 2001 this sequence version replaced gi:15887323.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99% of Sequence;
Estimated Total Number of Errors is 1.2.
FEATURES
    source
    1. .163942
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="5"
        /clone="CTC-329H14"
BASE COUNT 52833 a 32579 c 31594 g 46936 t
ORIGIN

Query Match 14.4%; Score 19; DB 9; Length 163942;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CAAGAGACACACAGACAG 108
   |||||
Db 66703 CAAGAGACACACAGACAG 66721

RESULT 36
AC020685 166606 bp DNA linear HTG 08-APR-2000
LOCUS Homo sapiens chromosome 15 clone RP11-414J1 map 15, WORKING DRAFT
DEFINITION
```

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

SEQUENCE, 14 unordered pieces.
AC020685
AC020685.3 GI:7528075
HTG: HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166606)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-414J1

Unpublished
2 (bases 1 to 166606)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Becker, R., Bada, F.,
Boguslavsky, L., Bouckhalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeAtellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, T., Lehoczy, J., Levine, R., Lie, L., Liu, G., Locke, K.,
MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.

Direct Submission

Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 8, 2000 this sequence version replaced gi:6751753.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WTBFR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L4965

Center clone name: 414_J_1

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159639 bases at least Q40
Consensus quality: 162851 bases at least Q30
Consensus quality: 163954 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 165306; sum-of-contigs
Quality coverage: 5.6 in Q20 bases; agarose-fp
Quality coverage: 5.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1059: contig of 1059 bp in length
* 1060 1159: gap of 100 bp
* 1160 6470: contig of 5311 bp in length
* 6471 6570: gap of 100 bp
* 6571 9999: contig of 3429 bp in length
* 10000 10099: gap of 100 bp
* 10100 14075: contig of 3976 bp in length
* 14076 14175: gap of 100 bp

* 14176 19098: contig of 4923 bp in length
* 19099 19198: gap of 100 bp
* 19199 26231: contig of 7033 bp in length
* 26232 26331: gap of 100 bp
* 26332 35257: contig of 8926 bp in length
* 35258 35357: gap of 100 bp
* 35358 49626: contig of 14269 bp in length
* 49627 49726: gap of 100 bp
* 49727 64090: contig of 14364 bp in length
* 64091 64190: gap of 100 bp
* 64191 81200: contig of 17010 bp in length
* 81201 81300: gap of 100 bp
* 81301 97396: contig of 16096 bp in length
* 97397 97496: gap of 100 bp
* 97497 115927: contig of 18431 bp in length
* 115928 116027: gap of 100 bp
* 116028 136724: contig of 20697 bp in length
* 136725 136824: gap of 100 bp
* 136825 166606: contig of 29782 bp in length.

FEATURES

source

1. 166606
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15"
/clone_lib="RPCI-11 Human Male BAC"

1. 1059

/note="assembly_fragment"

1160. 6470

/note="assembly_fragment"

6571. 9999

/note="assembly_fragment"

10100. 14075

/note="assembly_fragment"

14176. 19098

/note="assembly_fragment"

19199. 26231

/note="assembly_fragment"

26332. 35257

/note="assembly_fragment"

35358. 49626

/note="assembly_fragment"

clone_end:SP6

vector_side:right

49727. 64090

/note="assembly_fragment"

64191. 81200

/note="assembly_fragment"

81301. 97396

/note="assembly_fragment"

clone_end:T7

vector_side:left

97497. 115927

/note="assembly_fragment"

116028. 136724

/note="assembly_fragment"

136825. 166606

/note="assembly_fragment"

48221 a 33530 c 33827 g 49727 t 1301 others

BASE COUNT

ORIGIN

Query Match 14.4%; Score 19; DB 2; Length 166606;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GGCCACAGAGATGCAGAAG 75

|||||

Db 70573 GGCCACAGAGATGCAGAAG 70591

|||||

RESULT 37

AC126443/c

```

LOCUS      AC126443      168766 bp      DNA      linear      HTG 06-JUL-2002
DEFINITION Mus musculus chromosome UNK clone RP23-464J8, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
ACCESSION  AC126443
VERSION     AC126443.1  GI:21699723
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 168766)
            McPherson,J.D. and Waterston,R.H.
            The sequence of Mus musculus clone
            Unpublished
            2 (bases 1 to 168766)
            McPherson,J.D. and Waterston,R.H.
            Direct Submission
            McPherson,J.D. and Waterston,R.H.
            Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
            3 (bases 1 to 168766)
            McPherson,J.D. and Waterston,R.H.
            Direct Submission
            Submitted (06-JUL-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0464J08
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165197 bases at least Q40
Consensus quality: 166166 bases at least Q30
Consensus quality: 166509 bases at least Q20
Insert size: 186000; agarose-fp
Insert size: 168200; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; agarose-fp
Quality coverage: 0.38 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1585: contig of 1585 bp in length
* 1586: gap of unknown length
* 1686: contig of 1870 bp in length
* 3555: gap of unknown length
* 3556: contig of 2875 bp in length
* 6530: gap of unknown length
* 6531: contig of 3975 bp in length
* 6631: gap of unknown length
* 10606: contig of 5084 bp in length
* 10705: gap of unknown length
* 15789: contig of 5084 bp in length
* 15889: gap of unknown length
* 15890: contig of 6359 bp in length
* 22248: gap of unknown length
* 22249: contig of 6709 bp in length
* 22349: gap of unknown length
* 29057: contig of 8406 bp in length
* 29158: gap of unknown length
* 37663: gap of unknown length
* 37664: contig of 5359 bp in length
* 43023: gap of unknown length
* 43023: gap of unknown length

* 43123 48872: contig of 5750 bp in length
* 48873 48972: gap of unknown length
* 48973 67906: contig of 18934 bp in length
* 67907 68006: gap of unknown length
* 68007 79307: contig of 11301 bp in length
* 79308 79408: gap of unknown length
* 103115 103214: contig of 23707 bp in length
* 103215 116372: contig of 13058 bp in length
* 116373 134688: gap of unknown length
* 134689 134788: contig of 23747 bp in length
* 134789 158535: gap of unknown length
* 158536 168766: contig of 10132 bp in length.
* 158635 Location/Qualifiers
* 1..168766
* /organism="Mus musculus"
* /db_xref="taxon:10090"
* /chromosome="UNK"
* /clone="RP23-464J8"
* 1..1585
* /note="assembly_name:Contig10"
* 1686..3555
* /note="assembly_name:Contig11"
* 3556..6530
* /note="assembly_name:Contig12"
* 6531..10605
* /note="assembly_name:Contig13"
* 10606..15789
* /note="assembly_name:Contig14"
* 15790..22248
* /note="assembly_name:Contig15"
* 22249..29057
* /note="assembly_name:Contig16"
* 29058..37663
* /note="assembly_name:Contig17"
* 37664..43022
* /note="assembly_name:Contig18"
* 43023..48872
* /note="assembly_name:Contig19"
* 48873..67906
* /note="assembly_name:Contig20"
* 67907..79307
* /note="assembly_name:Contig21"
* 79308..103114
* /note="assembly_name:Contig22"
* 103115..116372
* /note="assembly_name:Contig23"
* 116373..134688
* /note="assembly_name:Contig24"
* 134689..158535
* /note="assembly_name:Contig25"
* 158536..168766
* /note="assembly_name:Contig26"

BASE COUNT 52459 a 32388 c 33335 g 48916 t 1668 others
ORIGIN
Query Match 14.4%; Score 19; DB 2; Length 168766;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGCCCAAGCTGAAGGCCA 61
    |||||
Db 109635 AAGCCCAAGCTGAAGGCCA 109617

RESULT 38
AL845505/c 172191 bp DNA linear HTG 16-AUG-2002
LOCUS Mus musculus chromosome X clone RP23-115D12, *** SEQUENCING IN
DEFINITION PROGRESS ***, 21 unordered pieces.
ACCESSION AL845505

```

```

VERSTON
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL845505.1 GI:22316235
HTG: HTGS_PHASE1; HTGS_DRAFT.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 172191)
Mclay,K.
Direct Submission
Submitted (14-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM115D12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 165696 bases at least Q40
Consensus quality: 168114 bases at least Q30
Consensus quality: 169326 bases at least Q20
Insert size: 170191; sum-of-contigs
Insert size: 180458; 5.0% error; agarose-fp
Quality coverage: 4.12x in Q20 bases; sum-of-contigs Quality
coverage: 4.03x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
*
* 1
* 2795 2894: contig of 2794 bp in length
* 2895 14660: contig of 11766 bp in length
* 14661 14760: gap of 100 bp
* 14761 18145: contig of 3385 bp in length
* 18146 18245: gap of 100 bp
* 18246 44830: contig of 26585 bp in length
* 44831 44930: gap of 100 bp
* 44931 48269: contig of 3339 bp in length
* 48270 48369: gap of 100 bp
* 48370 69198: contig of 20829 bp in length
* 69199 69298: gap of 100 bp
* 69299 74022: contig of 4724 bp in length
* 74023 74122: gap of 100 bp
* 74123 90268: contig of 16146 bp in length
* 90269 90368: gap of 100 bp
* 90369 107301: contig of 16933 bp in length
* 107302 107401: gap of 100 bp
* 107402 121227: contig of 13826 bp in length
* 121228 121327: gap of 100 bp
* 121328 123613: contig of 2286 bp in length
* 123614 123713: gap of 100 bp
* 123714 128972: contig of 5259 bp in length
* 128973 129072: gap of 100 bp
* 129073 134995: contig of 5923 bp in length
* 134996 140357: gap of 100 bp
* 140358 140457: contig of 5262 bp in length
* 140458 146939: contig of 6482 bp in length
* 146940 147039: gap of 100 bp
* 147040 152260: contig of 5221 bp in length
* 152261 152360: gap of 100 bp
* 152361 154448: contig of 2088 bp in length
* 154449 154548: gap of 100 bp
* 154549 159704: contig of 5156 bp in length
*
*
* 159705 159804: gap of 100 bp
* 159805 163480: contig of 3676 bp in length
* 163481 163580: gap of 100 bp
* 163581 169430: contig of 5850 bp in length
* 169431 169530: gap of 100 bp
* 169531 172191: contig of 2661 bp in length.
*
*
* Location/Qualifiers
* 1..172191
* /organism="Mus musculus"
* /db_xref="taxon:10090"
* /chromosome="X"
* /clone_lib="RPC1-23"
* 1..2794
* /note="assembly_fragment:00354
* fragment_chain:1"
* 2895..14660
* /note="assembly_fragment:00181
* fragment_chain:1"
* 14761..18145
* /note="assembly_fragment:00410
* fragment_chain:1"
* 18246..44830
* /note="assembly_fragment:00227
* fragment_chain:1"
* 44931..48269
* /note="assembly_fragment:01244
* fragment_chain:1"
* 48370..69198
* /note="assembly_fragment:00235
* fragment_chain:1"
* 69299..74022
* /note="assembly_fragment:00471
* fragment_chain:1"
* 74123..90268
* /note="assembly_fragment:01240
* fragment_chain:1"
* 90369..107301
* /note="assembly_fragment:00063
* fragment_chain:1"
* 107402..121227
* /note="assembly_fragment:00158
* fragment_chain:2"
* 121328..123613
* /note="assembly_fragment:01145
* fragment_chain:2"
* 123714..128972
* /note="assembly_fragment:00902
* fragment_chain:2"
* 129073..134995
* /note="assembly_fragment:01186
* fragment_chain:2"
* 135096..140357
* /note="assembly_fragment:01115
* fragment_chain:2"
* 140458..146939
* /note="assembly_fragment:00956
* fragment_chain:2"
* 147040..152260
* /note="assembly_fragment:00080
* fragment_chain:3"
* 152361..154448
* /note="assembly_fragment:00305
* fragment_chain:3"
* 154549..159704
* /note="assembly_fragment:00655
* fragment_chain:3"
* 159805..163480
* /note="assembly_fragment:00651"
* 163581..169430
* /note="assembly_fragment:00660
* fragment_chain:4"
* 169531..172191

```

/note="assembly_fragment:01013

fragment_chain:4

clone_end:t7

vector_side:right"

BASE COUNT 49464 a 32131 c 32707 g 55878 t 2011 others

ORIGIN

Query Match 14.4%; Score 19; DB 2; Length 172191;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61

Db 79245 AAGGCCAAGCTGAAGGCCA 79227

RESULT 39

AC122629

LOCUS

DEFINITION Rattus norvegicus clone CH230-102A4, *** SEQUENCING IN PROGRESS

AC122629

ACCESSION

VERSION AC122629.2 GI:21731433

KEYWORDS

SOURCE HTGS-PHASE1

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

AUTHORS

1 (bases 1 to 172797)
 Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman F.R., Allen C.,
 Albrooks S.L., Amarantunge H.C., Are J.R., Ayala M., Banks T.,
 Barbara J., Benton J., Bimaga K., Blankenburg K., Bonnin D.,
 Bouck J., Bowler S., Brileva M., Brown E., Brown M., Bryant N.P.,
 Buhay C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
 Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,
 Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C.,
 Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
 Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
 Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H.,
 Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
 Eathart C., Edgar D., Edwards C.C., Elhaj C., Escotto M.,
 Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P.,
 Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R.,
 Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K.,
 Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J.,
 Hernandez O., Hodgson A., Hognes M., Holloway C., Hollins B.,
 Jacobson B., Jia Y., Johnson R., Jolivet S., Hume J., Jackson L.E.,
 Karlsson E., Kelly S., Khan U., King L., Korvah J., Kovar C.,
 Kratovic J., Kureshi A., Landry N., Leal B., Lewis L.C., Lewis L.,
 Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Louisedge H.,
 Lozano R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J.,
 Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E.,
 Massey E., Mahoney E., McLeod M.P., Meador M., Mei G., Metzker M.,
 Miner G., Miner Z., Mitchell T., Mohabbat K., Morgan M., Morris S.,
 Moser M., Neal D., Newton J., Newton N., Nguyen A., Nguyen N.,
 Nguyen N., Nickerson E., Nwokenwo S., Ogih M., Okuwonu G.,
 Oragunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L.,
 Peters L., Pickens R., Primus E., Pu L.L., Quiles M., Ren Y.,
 Rives M., Rojas A., Rojubokan I., Rolfe M., Ruiz S., Savary G.,
 Scherer S., Scott G., Shen H., Shoohtari N., Sisson I.,
 Sodergren E., Sonaika T., Sparks A., Stanley H., Stone H.,
 Sutton A., Svatek A., Tabor P., Tamerisa A., Tamerisa K., Tang H.,
 Tansey J., Taylor C., Taylor T., Telford B., Thomas N., Thomas S.,
 Usmani K., Vasquez L., Vera V., Villalón D., Vinson R., Wang Q.,
 Wang S., Ward-Moore S., Warren R., Washington C., Watlington S.,
 Williams G., Williamson A., Wleczyk R., Wooden S., Worley K.,
 Wu C., Wu Y., Wu Y.F., Zhou J., Zorrilla S., Nelson D.,
 Weinstein G. and Gibbs R.
 Direct Submission
 Unpublished
 2 (bases 1 to 172797)

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Worley K.C.

Direct Submission

Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 172797)

Worley K.C.

Direct Submission

Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:21205946.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GKCM

Center clone name: CH230-102A4

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 113756 bases at least Q40

Consensus quality: 118828 bases at least Q30

Consensus quality: 123024 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
 consists of 67 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1758: contig of 1758 bp in length
 1759 1858: gap of unknown length
 1859 2964: contig of 1106 bp in length
 2965 3064: gap of unknown length
 3065 4560: contig of 1496 bp in length
 4561 4660: gap of unknown length
 4661 5819: contig of 1159 bp in length
 5820 7366: contig of unknown length
 7367 7466: contig of 1447 bp in length
 7467 8958: gap of unknown length
 8959 9058: contig of 1492 bp in length
 9059 10424: gap of unknown length
 10425 10524: contig of 1366 bp in length
 10525 12064: gap of unknown length
 12065 12164: gap of unknown length
 12165 13615: contig of 1451 bp in length
 13616 13715: gap of unknown length
 13716 15101: contig of 1386 bp in length
 15102 16254: gap of unknown length
 16255 16354: gap of unknown length
 16355 17443: contig of 1089 bp in length
 17444 17543: gap of unknown length
 17544 18862: contig of 1319 bp in length
 18863 18962: gap of unknown length
 18963 20482: contig of 1520 bp in length
 20483 20582: gap of unknown length
 20583 22101: contig of 1519 bp in length
 22102 22201: gap of unknown length
 22202 23489: contig of 1288 bp in length
 23490 23589: gap of unknown length
 23590 25078: contig of 1489 bp in length
 25079 25178: gap of unknown length
 25179 26268: contig of 1090 bp in length


```
*
* 26269 26368: gap of unknown length
* 26369 27550: contig of 1182 bp in length
* 27551 27650: gap of unknown length
* 29238 29238: contig of 1588 bp in length
* 29239 29338: gap of unknown length
* 29339 30567: contig of 1229 bp in length
* 30568 30667: gap of unknown length
* 30668 31946: contig of 1279 bp in length
* 31947 32046: gap of unknown length
* 32047 33276: contig of 1230 bp in length
* 33277 33376: gap of unknown length
* 33377 34712: contig of 1336 bp in length
* 34713 34812: gap of unknown length
* 34813 36059: contig of 1247 bp in length
* 36060 36159: gap of unknown length
* 36160 38183: contig of 2024 bp in length
* 38184 38283: gap of unknown length
* 38284 40179: contig of 1896 bp in length
* 40180 40279: gap of unknown length
* 40280 42485: contig of 2206 bp in length
* 42486 42585: gap of unknown length
* 42586 44371: contig of 1786 bp in length
* 44372 44471: gap of unknown length
* 44472 46629: contig of 2158 bp in length
* 46630 46729: gap of unknown length
* 46730 48613: contig of 1884 bp in length
* 48614 48713: gap of unknown length
* 48714 50116: contig of 1403 bp in length
* 50117 50216: gap of unknown length
* 50217 52877: contig of 2661 bp in length
* 52878 52977: gap of unknown length
* 52978 54957: contig of 1980 bp in length
* 54958 55057: gap of unknown length
* 55058 57019: contig of 1962 bp in length
* 57020 57119: gap of unknown length
* 57120 59360: contig of 2241 bp in length
* 59361 59460: gap of unknown length
* 59461 61172: contig of 1712 bp in length
* 61173 61272: gap of unknown length
* 62405 62405: contig of 1133 bp in length
* 62406 64814: gap of unknown length
* 62505 64814: contig of 2309 bp in length
* 64815 64914: gap of unknown length
* 64915 67708: contig of 2794 bp in length
* 67709 67808: gap of unknown length
* 67809 69632: contig of 1824 bp in length
* 69633 69732: gap of unknown length
* 69733 72062: contig of 2330 bp in length
* 72063 72162: gap of unknown length
* 72163 73921: contig of 1759 bp in length
* 73922 74021: gap of unknown length
* 74022 76561: contig of 2540 bp in length
* 76562 76661: gap of unknown length
* 76662 79481: contig of 2820 bp in length
* 79482 79581: gap of unknown length
* 79582 83000: contig of 3419 bp in length
* 83001 83100: gap of unknown length
* 83101 87071: contig of 3971 bp in length
* 87072 87171: gap of unknown length
* 87172 89546: contig of 2375 bp in length
* 89547 89646: gap of unknown length
* 89647 92393: contig of 2747 bp in length
* 92394 92493: gap of unknown length
* 92494 96986: contig of 4493 bp in length
* 96987 97086: gap of unknown length
* 97087 101666: contig of 4580 bp in length
* 101667 101766: gap of unknown length
* 101767 105032: contig of 3266 bp in length
* 105033 105132: gap of unknown length
* 105133 107532: contig of 2400 bp in length
* 107533 112074: contig of 4442 bp in length
* 107633
```

```
Query Match 14.4%; Score 19; DB 2; Length 172737;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GGAGAAATGCCAGCTTG 39
    |||
Db 112772 GGAAGAAATGCCAGCTTG 112790
    |||

RESULT 40
AC008871/c 174138 bp DNA linear PRI 06-DEC-2001
LOCUS Homo sapiens chromosome 5 clone CTD-2197111, complete sequence.
DEFINITION AC008871
ACCESSION AC008871
VERSION AC008871.5 GI:17386232
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 174138)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 174138)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 174138)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 6, 2001 this sequence version replaced gi:9256065.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.

FEATURES
    source
    1..174138
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="5"
        /clone="CTD-2197111"

BASE COUNT 49893 a 31309 c 33213 g 59723 t
ORIGIN

Query Match 14.4%; Score 19; DB 9; Length 174138;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CAAGAGACCACAGAGCAG 108
    |||
Db 35324 CAAGAGACCACAGAGCAG 35306
    |||

RESULT 41
AC112933 174670 bp DNA linear HTG 21-AUG-2002
LOCUS Mus musculus clone RP24-418J2, WORKING DRAFT SEQUENCE, 8 ordered
pieces
DEFINITION AC112933
ACCESSION AC112933
VERSION AC112933.4 GI:22381912
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 174670)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
```

TITLE
JOURNAL
REFERENCE
AUTHORS

Mus musculus, clone RP24-418J2
Unpublished
2 (bases 1 to 174670)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehozsky,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McWenig,V., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Noren,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,R., Rise,C., Rogov,P., Roman,J.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Svally,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 174670)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,R., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE
JOURNAL
COMMENT

Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 21, 2002 this sequence version replaced gi:21591839.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20144
Center clone name: 418_J_2
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 172471 bases at least Q40
Consensus quality: 173097 bases at least Q30
Consensus quality: 173390 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 173970; sum-of-contigs
Quality coverage: 11.6 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 1991: contig of 1991 bp in length
* 1992 2091: gap of 100 bp
* 2092 4608: contig of 2517 bp in length
* 4609 4708: gap of 100 bp
* 4709 10380: contig of 5672 bp in length
* 10381 10480: gap of 100 bp
* 10481 19423: contig of 8943 bp in length
* 19424 19523: gap of 100 bp
* 19524 47741: contig of 28218 bp in length
* 47742 47841: gap of 100 bp
* 47842 76804: contig of 28963 bp in length
* 76805 76904: gap of 100 bp
* 76905 122708: contig of 45804 bp in length
* 122709 122808: gap of 100 bp
* 122809 174670: contig of 51862 bp in length.

FEATURES
source

1. 174670
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-418J2"
/clone_lib="RPCI-24 Male Mouse BAC"
1. 1991
misc_feature
/note="assembly_fragment"
2092..4608
misc_feature
/note="assembly_fragment"
4709..10380
misc_feature
/note="assembly_fragment"
10481..19423
misc_feature
/note="assembly_fragment"
19524..47741
misc_feature
/note="assembly_fragment"
47842..76804
misc_feature
/note="assembly_fragment"
76905..122708
misc_feature
/note="assembly_fragment"
122809..174670
/note="assembly_fragment"
BASE COUNT 50336 a 37369 c 36806 g 49456 t
ORIGIN

Query Match 14.4%; Score 19; DB 2; Length 174670;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGCCCAAGCTGAAGGCCA 61
|||||

Db 40130 AAGCCCAAGCTGAAGGCCA 40148

RESULT 42

AC118879
LOCUS AC118879 175037 bp DNA linear HTG 14-JUL-2002
DEFINITION Rattus norvegicus clone CH230-472K2, *** SEQUENCING IN PROGRESS
ACCESSION AC118879
VERSION AC118879.2 GI:21747356
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 175037)

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaraturung, H.C., Are, J.R., Ayele, M., Banks, T., Barbarella, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, F., Johnson, R., Jollivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseg, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraqunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, R., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vaquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE

REFERENCE
JOURNAL
Unpublished
2 (bases 1 to 175037)
Worley, K.C.

AUTHORS

TITLE

JOURNAL
Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 175037)
Worley, K.C.

REFERENCE

AUTHORS

TITLE

JOURNAL
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20258343.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project information
Center project name: GVYO
Center clone name: CH230-472K2
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.90329
Consensus quality: 138521 bases at least Q40
Consensus quality: 142923 bases at least Q30
Consensus quality: 146010 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1007: contig of 1007 bp in length
1008 1107: gap of unknown length
1108 2149: contig of 1042 bp in length
2150 2249: gap of unknown length
2250 3370: contig of 1121 bp in length
3371 3470: gap of unknown length
3471 4646: contig of 1176 bp in length
4647 4746: gap of unknown length
4747 5876: contig of 1130 bp in length
5877 5976: gap of unknown length
5977 7629: contig of 1553 bp in length
7630 9006: contig of 1377 bp in length
9007 9106: gap of unknown length
9107 10780: contig of 1674 bp in length
10781 10880: gap of unknown length
10881 12444: contig of 1564 bp in length
12445 12544: gap of unknown length
12545 14109: contig of 1565 bp in length
14110 14209: gap of unknown length
14210 15653: contig of 1444 bp in length
15654 15753: gap of unknown length
15754 16877: contig of 1024 bp in length
16878 19235: contig of 2358 bp in length
19236 19335: gap of unknown length
19336 20455: contig of 1120 bp in length
20456 21738: contig of 1183 bp in length
21739 21838: gap of unknown length
21839 23653: contig of 1815 bp in length
23654 23753: gap of unknown length
23754 25302: contig of 1549 bp in length
25303 25402: gap of unknown length
25403 26614: contig of 1212 bp in length
26615 26714: gap of unknown length
26715 28514: contig of 1800 bp in length
28515 28614: gap of unknown length
28615 30443: contig of 1829 bp in length
30444 30543: gap of unknown length
30544 32375: contig of 1832 bp in length
32376 32475: gap of unknown length
32476 34037: contig of 1562 bp in length
34038 34137: gap of unknown length
34138 35998: contig of 1861 bp in length
35999 36098: gap of unknown length
36099 37996: contig of 1898 bp in length
37997 40345: contig of 2249 bp in length
40346 40445: gap of unknown length
40446 42372: contig of 1927 bp in length
42373 42472: gap of unknown length
42473 45396: contig of 2924 bp in length
45397 45496: gap of unknown length
45497 48748: contig of 3252 bp in length
48749 48848: gap of unknown length
48849 51292: contig of 2444 bp in length
51293 51392: gap of unknown length
51393 54376: contig of 2984 bp in length
54377 54476: gap of unknown length
54477 57758: contig of 3282 bp in length
57759 57858: gap of unknown length
57859 60723: contig of 2865 bp in length
60724 60823: gap of unknown length
60824 63425: contig of 2602 bp in length

```

* 63426 63525: gap of unknown length
* 63526 66201: contig of 2676 bp in length
* 66202 66301: gap of unknown length
* 66302 69653: contig of 3352 bp in length
* 69654 72975: gap of unknown length
* 72976 73025: contig of 3172 bp in length
* 73026 75411: gap of unknown length
* 75412 75511: contig of 2386 bp in length
* 75512 78885: contig of 3374 bp in length
* 78886 82987: contig of 4012 bp in length
* 82988 83097: gap of unknown length
* 83098 86339: contig of 3242 bp in length
* 86340 89385: gap of unknown length
* 89386 89485: contig of 2946 bp in length
* 89486 93482: gap of unknown length
* 93483 96259: contig of 2777 bp in length
* 96260 99359: gap of unknown length
* 99360 100087: contig of 3628 bp in length
* 100088 103824: gap of unknown length
* 103825 109269: contig of 5345 bp in length
* 109270 109369: gap of unknown length
* 109370 112382: contig of 3013 bp in length
* 112383 112482: gap of unknown length
* 112483 116027: contig of 3545 bp in length
* 116028 116127: gap of unknown length
* 116128 121318: contig of 5191 bp in length
* 121319 121418: gap of unknown length
* 121419 125277: contig of 3859 bp in length
* 125278 125377: gap of unknown length
* 125378 129404: contig of 4027 bp in length
* 129405 129504: gap of unknown length
* 129505 135160: contig of 5656 bp in length
* 135161 135260: gap of unknown length
* 135261 141525: contig of 6265 bp in length
* 141526 141625: gap of unknown length
* 141626 147453: contig of 5828 bp in length

Query Match          14.4%: Score 19; DB 2; Length 175037;
Best Local Similarity 100.08; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AGCAGGAGAGTGGAGTGA 122
Db 19685 AGCAGGAGAGTGGAGTGA 19703
|||||
***, 67 unordered pieces.

AC097955 176409 bp DNA linear HTG 11-JUL-2002
Rattus norvegicus clone CH230-110B17, *** SEQUENCING IN PROGRESS
AC097955
AC097955.3 GI:21723867
HTG; HTGS_PHASE1.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 176409)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

```

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
 Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lounseged,H.,
 Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
 Ogunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,
 Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.

TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 176409)
 Worley,K.C.

Direct Submission
 Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 176409)
 Worley,K.C.

Direct Submission
 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Jul 10, 2002 this sequence version replaced gi:17949462.
 ----- Genome Center of Medicine
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFSE
 Center clone name: CH230-110B17
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 123062 bases at least Q40
 Consensus quality: 126575 bases at least Q30
 Consensus quality: 129664 bases at least Q20

***** NOTE: Estimated insert size may differ from sequence length
 * (see <http://www.hgsc.bcm.tmc.edu/docs/genbank/draft.data.html>).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 67 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.

```

1 1050: contig of 1050 bp in length
* 1051: gap of unknown length
* 1151: contig of 1062 bp in length
* 2212: gap of unknown length
* 2213: contig of 1222 bp in length
* 3534: gap of unknown length
* 3535: contig of 1065 bp in length
* 3635: gap of unknown length
* 4799: contig of 1070 bp in length
* 4800: gap of unknown length
* 5870: contig of 1208 bp in length
* 5970: gap of unknown length
* 7177: contig of 1216 bp in length
* 7278: gap of unknown length
* 8493: contig of 1206 bp in length
* 8594: gap of unknown length
* 9799: contig of 1206 bp in length
* 9800: gap of unknown length
* 11347: contig of 1448 bp in length
* 11447: gap of unknown length
* 11448: contig of 1249 bp in length
* 12697: gap of unknown length
* 12797: contig of 1596 bp in length
* 14393: gap of unknown length
* 14992: contig of 1188 bp in length
* 15880: gap of unknown length
* 15881: contig of 1167 bp in length
* 16948: gap of unknown length
* 17047: contig of 1173 bp in length
* 18221: gap of unknown length
* 18321: contig of 1001 bp in length
* 19421: gap of unknown length
* 19422: contig of 1161 bp in length
* 20582: gap of unknown length
* 20683: contig of 1569 bp in length
* 22252: gap of unknown length
* 22351: contig of 1018 bp in length
* 23369: gap of unknown length
* 23469: contig of 1659 bp in length
* 25128: gap of unknown length
* 25228: contig of 1971 bp in length
* 27199: gap of unknown length
* 27200: contig of 1507 bp in length
* 28806: gap of unknown length
* 28907: contig of 1667 bp in length
* 30573: gap of unknown length
* 30674: contig of 1398 bp in length
* 32071: gap of unknown length
* 32171: contig of 1668 bp in length
* 33839: gap of unknown length
* 33940: contig of 2399 bp in length
* 36338: gap of unknown length
* 36439: contig of 1575 bp in length
* 38013: gap of unknown length
* 38113: contig of 2267 bp in length
* 40380: gap of unknown length
* 40381: contig of 2539 bp in length
* 40481: gap of unknown length
* 43119: contig of 1523 bp in length
* 43200: gap of unknown length
* 44642: contig of 1857 bp in length
* 44643: gap of unknown length
* 46599: contig of 1857 bp in length
* 46600: gap of unknown length
* 48620: contig of 1921 bp in length
* 48720: gap of unknown length
* 50348: contig of 1628 bp in length
* 50448: gap of unknown length
* 52707: contig of 2259 bp in length
* 52807: gap of unknown length
* 52808: contig of 2308 bp in length
* 55115: gap of unknown length
* 55216: contig of 1533 bp in length
* 56748: gap of unknown length
* 56849: contig of 3107 bp in length
* 59555: gap of unknown length
* 60055: gap of unknown length

```

```

* 60056 61804: contig of 1749 bp in length
* 61805: gap of unknown length
* 61905: contig of 2173 bp in length
* 64078 64177: gap of unknown length
* 64178 67094: contig of 2917 bp in length
* 67095 67194: gap of unknown length
* 67195 68690: contig of 1496 bp in length
* 68691 68790: gap of unknown length
* 68791 71790: contig of 3000 bp in length
* 71791 71890: gap of unknown length
* 71891 75304: contig of 3414 bp in length
* 75305 75405: gap of unknown length
* 75406 78445: contig of 3041 bp in length
* 78446 78545: gap of unknown length
* 81392: contig of 2847 bp in length
* 81393 81492: gap of unknown length
* 81493 83766: contig of 2274 bp in length
* 83767 83866: gap of unknown length
* 83867 86812: contig of 2946 bp in length
* 86813 86912: gap of unknown length
* 86913 88777: contig of 1965 bp in length
* 88778 88978: gap of unknown length
* 88979 91962: contig of 2985 bp in length
* 91963 92062: gap of unknown length
* 92063 95558: contig of 3496 bp in length
* 95559 95658: gap of unknown length
* 95659 99330: contig of 3672 bp in length
* 99331 99430: gap of unknown length
* 99431 103014: contig of 3584 bp in length
* 103015 103115: gap of unknown length
* 103116 106384: contig of 3270 bp in length
* 106385 106484: gap of unknown length
* 106485 109913: contig of 3429 bp in length
* 109914 110013: gap of unknown length
* 110014 113006: contig of 2993 bp in length

```

Query Match 14.4%; Score 19; DB 2; Length 176409;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 ACCAGGAGAGTGGAGTGA 122
 Db 66235 ACCAGGAGAGTGGAGTGA 66217
 |||||

RESULT 44

AC022742 AC022742 176967 bp DNA linear HTG 09-MAY-2001
 DEFINITION Homo sapiens chromosome 15 clone RP11-762A1 map 15, WORKING DRAFT
 SEQUENCE, 4 unordered pieces.

ACCESSION AC022742 GI:13123383

VERSION AC022742.4 HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS HTGS; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 176967)

JOURNAL Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

REFERENCE 2 (bases 1 to 176967)

AUTHORS Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenesor, J.,

Feireira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lechoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

McPheeters, R., Meldrim, J., Mcneus, L., Morrow, J., Naylor, J.,

Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
 Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 25, 2001 this sequence version replaced gi:11990718.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L5677
 Center clone name: 762_A1
 ----- Summary Statistics

Sequencing vector: M13; M7815; 2% of reads
 Chemistry: Plasmid; n/a; 98% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 176032 bases at least Q40
 Consensus quality: 176449 bases at least Q30
 Consensus quality: 176615 bases at least Q20
 Insert size: 186000; agarose-fp
 Insert size: 176667; sum-of-contigs
 Quality coverage: 9.0 in Q20 bases; agarose-fp
 Quality coverage: 9.5 in Q20 bas.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 14400: contig of 14400 bp in length
 * 14401 14500: gap of 100 bp
 * 14501 61165: contig of 46665 bp in length
 * 61166 61265: gap of 100 bp
 * 61266 112521: contig of 51256 bp in length
 * 112522 112621: gap of 100 bp
 * 112622 176967: contig of 64346 bp in length.

FEATURES

source
 1. .176967
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
 /map="15"
 /clone="RP11-762A1"
 /clone_lib="RPC1-11 Human Male BAC"
 1. .14400
 /note="assembly_fragment"
 /clone_end:SP6
 vector_side:left
 14501..61165
 /note="assembly_fragment"
 61266..112521
 /note="assembly_fragment"
 112622..176967
 /note="assembly_fragment"
 /clone_end:R7
 vector_side:right

BASE COUNT 53791 a 35746 c 36226 g 50904 t 300 others
 ORIGIN

Query Match 14.4%; Score 19; DB 2; Length 176967;
 Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 57 GCCACACAGATGCAGAG 75
 Db 69605 GCCACACAGATGCAGAG 69623
 |||||||||||||||||||
 |||||||||||||||||||

RESULT 45

AC102783
 LOCUS
 DEFINITION
 Mus musculus clone RP23-390K3, WORKING DRAFT SEQUENCE, 24 unordered
 pieces.
 AC102783.2 GI:22381794
 VERSION
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS
 house mouse.
 SOURCE
 Mus musculus
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 1 (bases 1 to 177033)
 Mus musculus, clone RP23-390K3
 Unpublished
 2. (bases 1 to 177033)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
 Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
 Lamazares, R., Landers, T., Lebecky, J., Levine, R., Liu, G.,
 MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,
 Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 177033)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 21, 2002 this sequence version replaced gi:17060893.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information

Center project name: L19655
 Center clone name: 390_K_3
 ----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 170563 bases at least Q40
 Consensus quality: 173449 bases at least Q30
 Consensus quality: 174139 bases at least Q20
 Insert size: 183000; agarose-fp
 Insert size: 174733; sum-of-contigs
 Quality coverage: 6.1 in Q20 bases; agarose-fp
 Quality coverage: 6.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 24 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1
4612 4711: contig of 4611 bp in length
4612 4711: gap of 100 bp
4712 5577: contig of 866 bp in length
5578 5677: gap of 100 bp
5678 6686: contig of 1009 bp in length
6687 6786: gap of 100 bp
6787 7249: contig of 463 bp in length
7250 7349: gap of 100 bp
7350 8617: contig of 1268 bp in length
8618 8717: gap of 100 bp
8718 10292: contig of 1575 bp in length
10293 10392: gap of 100 bp
10393 11672: contig of 1280 bp in length
11673 11772: gap of 100 bp
11773 13066: contig of 1294 bp in length
13067 13166: gap of 100 bp
13167 14607: contig of 1441 bp in length
14608 14707: gap of 100 bp
14708 17503: contig of 2796 bp in length
17504 17603: gap of 100 bp
17604 21653: contig of 4050 bp in length
21654 21753: gap of 100 bp
21754 25974: contig of 4221 bp in length
25975 26074: gap of 100 bp
26075 29880: contig of 3806 bp in length
29881 33369: contig of 3389 bp in length
33370 33469: gap of 100 bp
33470 70307: contig of 36838 bp in length
70308 70407: gap of 100 bp
70408 75527: contig of 5120 bp in length
75528 75627: gap of 100 bp
75628 84901: contig of 9274 bp in length
84902 85001: gap of 100 bp
85002 94921: contig of 9920 bp in length
94922 95021: gap of 100 bp
95022 100827: contig of 5806 bp in length
100828 100927: gap of 100 bp
100928 114503: contig of 13576 bp in length
114504 114603: gap of 100 bp
114604 135326: contig of 20723 bp in length
135327 135426: gap of 100 bp
135427 152074: contig of 16648 bp in length

```

```

* 152075 152174: gap of 100 bp
* 152175 174449: contig of 22275 bp in length
* 174450 174549: gap of 100 bp
* 174550 177033: contig of 2484 bp in length.

```

FEATURES

```

source
1. .177033
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-390K3"
/clone_lib="RPCI-23 Female Mouse BAC"
1. .4611
/misc_feature
clone_end:SP6
vector_side:left
4712..5577
/note="assembly_fragment"
5678..6686
/note="assembly_fragment"
6787..7249
/note="assembly_fragment"
7350..8617
/note="assembly_fragment"
8718..10292
/note="assembly_fragment"
10393..11672
/note="assembly_fragment"
11773..13066
/note="assembly_fragment"
13167..14607
/note="assembly_fragment"
14708..17503
/note="assembly_fragment"
17604..21653
/note="assembly_fragment"
21754..25974
/note="assembly_fragment"
26075..29880
/note="assembly_fragment"
29981..33369
/note="assembly_fragment"
33470..70307
/note="assembly_fragment"
70408..75527
/note="assembly_fragment"
75628..84901
/note="assembly_fragment"
85002..94921
/note="assembly_fragment"
95022..100827
/note="assembly_fragment"
100928..114503
/note="assembly_fragment"
114604..135326
/note="assembly_fragment"
135427..152074
/note="assembly_fragment"
152175..174449
/note="assembly_fragment"
174550..177033
/note="assembly_fragment
clone_end:T7
vector_side:right"

```

BASE COUNT 52386 a .33924 c 32870 g 55548 t 2305 others

Query Match 14.4%; Score 19; DB 2; Length 177033;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AAGCTGAAGGCCACAGAGA 67

Db 138688 AAGCTGAAGGCCACAGAGA 138706

RESULT 46

AC018623

LOCUS

DEFINITION

AC018623

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC018623 180019 bp DNA linear HTG 01-APR-2000
Homo sapiens chromosome 8 clone RP11-444C21 map 8, WORKING DRAFT
SEQUENCE, 12 unordered pieces.

AC018623

HTG: HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 180019)

Birken, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 8, clone RP11-444C21

Unpublished

2 (bases 1 to 180019)

Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bida, F.,

Boguslavsky, L., Bouhgaier, B., Brown, A., Burkett, G., Castle, A.,

Choepe, Y., Collangelo, M., Collins, S., Collamore, A., Cooke, P.,

Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lehoczy, J., Levine, R., Liu, G., Locke, K.,

Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

Meidrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H.,

O'Connor, T., O'Donnell, P., Olivari, T.M., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A.,

Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,

Vasilev, H., Vlei, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A.

and Zody, W.

Direct Submission

Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 1, 2000 this sequence version replaced gi:6653305.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L5243

Center clone name: 444_C_21

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 168843 bases at least Q40

Consensus quality: 173972 bases at least Q30

Consensus quality: 176111 bases at least Q20

Insert size: 180000; agarose-fp

Insert size: 178919; sum-of-contigs

Quality coverage: 4.8 in Q20 bases; agarose-fp

Quality coverage: 4.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1358: contig of 1358 bp in length

* 1359 1458: gap of 100 bp

* 1459 3021: contig of 1563 bp in length

* 3022 3121: gap of 100 bp

* 3122 7480: contig of 4359 bp in length

* 7481 7580: gap of 100 bp

* 7581 15678: contig of 12098 bp in length

* 15679 19778: gap of 100 bp

* 19779 27895: contig of 8117 bp in length

* 27896 27995: gap of 100 bp

* 27996 44261: contig of 16266 bp in length

* 44262 44361: gap of 100 bp

* 44362 60303: contig of 15942 bp in length

* 60304 60403: gap of 100 bp

* 60404 77029: contig of 16626 bp in length

* 77030 77129: gap of 100 bp

* 77130 95870: contig of 18741 bp in length

* 95871 95970: gap of 100 bp

* 95971 118453: contig of 22489 bp in length

* 118460 118559: gap of 100 bp

* 118560 145068: contig of 26509 bp in length

* 145069 145168: gap of 100 bp

* 145169 180019: contig of 34851 bp in length.

FEATURES

source

1..180019

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="8"

/clone="RP11-444C21"

/clone_lib="RPC1-11 Human Male BAC"

1..1358

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

/note="assembly_fragment"

BASE COUNT 58626 a 30783 c 32284 g 57225 t 1101 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 19; DB 2; Length 180019;

Mismatches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 AAGTGGAGTGAATTCCT 130

Db 12396 AAGTGGAGTGAATTCCT 12414

RESULT 47

AC110005

LOCUS

DEFINITION

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

AC110005

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE 1 (bases 1 to 184157)
JOURNAL Direct Submission
REFERENCE 2 (bases 1 to 184157)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 184157)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 24, 2002 this sequence version replaced gi:18642729.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
FEATURES
 source
 Location/Qualifiers
 1. .184157
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="RP11-265K23"
BASE COUNT 51799 a 43222 c 41962 g 47174 t
ORIGIN
 Query Match 14.4%; Score 19; DB 9; Length 184157;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 AGGAGAAGTGGAGTGAAT 125
 |||||
Db 136030 AGGAGAAGTGGAGTGAAT 136048
RESULT 48
AC116851
LOCUS AC116851 185027 bp DNA linear HTG 18-AUG-2002
DEFINITION Mus musculus clone RP24-396N7, WORKING DRAFT SEQUENCE, 9 unordered
 pieces.
ACCESSION AC116851
VERSION AC116851.2 GI:22297003
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 185027)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-396N7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185027)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhgalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
 Landers, T., Lechoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,

Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
 Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 185027)
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
 Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 18, 2002 this sequence version replaced gi:19882105.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L25617
 Center clone name: 396_N.7
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 182377 bases at least Q40
 Consensus quality: 183576 bases at least Q30
 Consensus quality: 183998 bases at least Q20
 Insert size: 182000; agarose-ftp
 Insert size: 184227; sum-of-contigs
 Quality coverage: 7.7 in Q20 bases; agarose-ftp
 Quality coverage: 7.6 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 2482: contig of 2482 bp in length
 * 2483 2582: gap of 100 bp
 * 2583 13026: contig of 10444 bp in length
 * 13027 13126: gap of 100 bp
 * 13127 25566: contig of 12440 bp in length
 * 25567 25666: gap of 100 bp

```

* 25667 34242: contig of 8576 bp in length
* 34243 34342: gap of 100 bp
* 34343 98429: contig of 64087 bp in length
* 98430 98529: gap of 100 bp
* 98530 117192: contig of 18663 bp in length
* 117193 117292: gap of 100 bp
* 117293 133546: contig of 16254 bp in length
* 133547 133646: gap of 100 bp
* 133647 177342: contig of 43696 bp in length
* 177343 177442: gap of 100 bp
* 177443 185027: contig of 7585 bp in length.

```

FEATURES

```

source
1. .185027
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-396N7"
/clone_lib="RPCi-24 Male Mouse BAC"
1. .2482
/note="assembly_fragment"
clone_end:SP6
vector_side:left
2583. .13026
/note="assembly_fragment"
13127. .25566
/note="assembly_fragment"
25667. 34242
/note="assembly_fragment"
34343. .98429
/note="assembly_fragment"
98530. .117192
/note="assembly_fragment"
117293. .133546
/note="assembly_fragment"
133647. .177342
/note="assembly_fragment"
177443. .185027
/note="assembly_fragment"
clone_end:T7
vector_side:right
59027 a 33873 c 33903 g 57424 t 800 others
ORIGIN

```

Query Match 14.4%; Score 19; DB 2; Length 185027;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGAGATGCGAGAGAACACT 81

Db 122180 AGAGATGCGAGAGAACACT 122198

```

RESULT 49
AC116058/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-204F1, *** SEQUENCING IN PROGRESS
*** 70 unordered pieces.

```

AC116058 185828 bp DNA linear HTG 13-JUL-2002

AC116058.2 Gi:21732014

HTG; HTGS_PHASE1.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 185828)

REFERENCE
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimaye,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.B., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H., Lozadó,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,S., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Ozagunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 185828)

Worley,K.C.

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:19698585.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLKJ

Center clone name: CH230-204F1

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 127424 bases at least Q40

Consensus quality: 131027 bases at least Q30

Consensus quality: 133711 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 70 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1
1433: contig of 1433 bp in length
1533: gap of unknown length
1534: contig of 1390 bp in length
1535: gap of unknown length
2923: gap of unknown length
3023: contig of 1441 bp in length
4464: gap of unknown length
4564: gap of unknown length
5999: contig of 1435 bp in length
6000: gap of unknown length
6100: contig of 1704 bp in length
7803: gap of unknown length
7903: contig of 1162 bp in length
9065: gap of unknown length
9165: gap of unknown length
10363: contig of 1198 bp in length
10463: gap of unknown length
11640: contig of 1177 bp in length
11641: gap of unknown length
11740: gap of unknown length
11741: contig of 1021 bp in length
12761: gap of unknown length
12861: gap of unknown length
14266: contig of 1405 bp in length
14366: gap of unknown length
15835: contig of 1469 bp in length
15935: gap of unknown length
16949: contig of 1014 bp in length
17049: gap of unknown length
18237: contig of 1188 bp in length
18337: gap of unknown length
18338: contig of 1450 bp in length
18339: gap of unknown length
19887: gap of unknown length
21086: contig of 1199 bp in length
21186: gap of unknown length
22879: contig of 1693 bp in length
22880: gap of unknown length
22979: gap of unknown length
24058: contig of 1079 bp in length
24158: gap of unknown length
25441: contig of 1283 bp in length
25541: gap of unknown length
26933: contig of 1392 bp in length
27033: gap of unknown length
28060: contig of 1027 bp in length
28160: gap of unknown length
29434: contig of 1274 bp in length
29534: gap of unknown length
30838: contig of 1304 bp in length
30938: gap of unknown length
32455: contig of 1517 bp in length
32555: gap of unknown length
34004: contig of 1449 bp in length
34104: gap of unknown length
35351: contig of 1247 bp in length
35451: gap of unknown length
36813: contig of 1362 bp in length
36913: gap of unknown length
37961: contig of 1048 bp in length
38061: gap of unknown length
40261: contig of 2200 bp in length
40361: gap of unknown length
42219: contig of 1858 bp in length
42319: gap of unknown length
44732: contig of 2413 bp in length
44832: gap of unknown length
45994: contig of 1162 bp in length
46094: gap of unknown length
47638: contig of 1544 bp in length
47738: gap of unknown length
50033: contig of 2295 bp in length
50133: gap of unknown length
51982: contig of 1849 bp in length
52082: gap of unknown length
54517: gap of unknown length
54617: gap of unknown length
55793: contig of 1176 bp in length
55893: gap of unknown length
57369: contig of 1476 bp in length

57370 57469: gap of unknown length
57470 60281: contig of 2812 bp in length
60282 60381: gap of unknown length
60382 63015: contig of 2634 bp in length
63016 63115: gap of unknown length
63116 64232: contig of 1117 bp in length
64233 64332: gap of unknown length
64333 66937: gap of unknown length
66938 68774: gap of unknown length
68775 68874: gap of unknown length
70650 70650: contig of 1776 bp in length
70750 70750: gap of unknown length
72860 72860: contig of 2110 bp in length
72961 74772: contig of 1812 bp in length
74773 74872: gap of unknown length
74873 77156: contig of 2284 bp in length
77157 77256: gap of unknown length
77257 79711: contig of 2455 bp in length
79712 79811: gap of unknown length
79812 82322: contig of 2511 bp in length
82323 82422: gap of unknown length
82423 85227: contig of 2805 bp in length
85228 85327: gap of unknown length
85328 87271: contig of 1944 bp in length
87272 87371: gap of unknown length
87372 90074: contig of 2703 bp in length
90075 90174: gap of unknown length
90175 93369: contig of 3195 bp in length
93370 93469: gap of unknown length
93470 96888: contig of 3419 bp in length
96889 96988: gap of unknown length
96989 100692: contig of 3704 bp in length

Query Match 14.4%; Score 19; DB 2; Length 185828;
Best Local Similarity 100.0%; Pred. NO. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 ACCACAGCAGGAGAGT 115
|||||

Db 9198 ACCACAGCAGGAGAGT 9180
|||||

RESULT 50

AC020892

LOCUS Homo sapiens chromosome 15 clone RP11-313P18 map 15q21.2, complete
DEFINITION Homo sapiens

ACCESSION AC020892

VERSION AC020892.7 GI:13540717

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 186253)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,

Pate, D. and Hood, L.

Sequencing of human chromosome 15 D15S146-D15S117 region

Unpublished

2 (bases 1 to 186253)

Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,

Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G.,

James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T.

and Hood, L.

Direct Submission

Submitted (12-JAN-2000) Multimegabase Sequencing Center, University

of Washington, PO BOX 357730, Seattle, WA 98195, USA

3 (bases 1 to 186253)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,

TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
COMMENT On Apr. 4, 2001 this sequence version replaced gi:13162486.

----- Genome Center
Center: Multimegabase Sequencing Center
Center code: UWMSC
Web site: <http://chroma.mbt.washington.edu/msg.www>
Contact: leerowen@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399

Note: Data from overlapping BACs AC066613 [drafting center UWMSC],
AC020685 [drafting center WIBR], and AC026770 [drafting center
UWMSC] was added for finishing.

FEATURES
Source
1..186253
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15q21.2"
/clone="RP11-313P18"
/clone.lib="RPC1 human BAC library 11"
/note="Note: Data from overlapping BACs #RP11-707P17,
RP11-414J1, and CTD-2308G16 was added and the consensus
sequence was determined from RP11-313P18 to the extent
possible"
misc_feature
1..2529
/note="Overlap with RP11-707P17 AC066613"
9006..9025
/note="low quality data"
9945..9950
/note="low quality data"
14447
/note="low quality data"
14690..14695
/note="low quality data"
23515..23525
/note="low quality data"
24918..24925
/note="low quality data"
49155..49160
/note="low quality data"
90499..90505
/note="low quality data"
91255..91350
/note="low quality data"
93480..186253
/note="Overlap with clone RP11-414J1 AC020685"
176791..186253
/note="Overlap with clone CTD-2308G16 AC026770"
BASE COUNT 60025 a 36875 c 35294 g 54059 t
ORIGIN

Query Match 14.48; Score 19; DB 9; Length 186253;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GGCCACAGATGCAGAG 75
|||||
Db 163450 GGCCACAGATGCAGAG 163468

Search completed: June 2, 2003, 16:15:05
Job time : 1159 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 15:39:40 ; Search time 1428 Seconds
(without alignments)
1497.062 Million cell updates/sec

Title: US-09-915-178-1

Perfect score: 132

Sequence: 1 atggcacacaaactagacct.....agtggagtgaatttctga 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2551178

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	18.9	374	10	AW620090 852 MARC
2	21	15.9	382	12	BG410966 EM1_28_B0
3	21	15.9	418	13	BM125588
4	20	15.2	608	17	AZ098162
5	20	15.2	732	17	AG012646 Homo sapi
6	20	15.2	997	13	B1524256

19	14.4	198	14	N88692	N88692 K5134F Huma
19	14.4	203	12	BF800160	BF800160 PMO-CI004
19	14.4	354	17	A2808724	A2808724 PMO0072624
19	14.4	509	17	A2250549	A2250549 RCI-23-1
19	14.4	530	13	B084935	B084935 B084935
19	14.4	629	17	A2769784	A2769784 IM0570M13
19	14.4	655	14	BQ803203	BQ803203 WHE2834_H
19	14.4	678	12	BF317304	BF317304 G01904069
19	14.4	724	12	BE882559	BE882559 G01507007
19	14.4	1058	17	CN8052GR	AL318132 Tetraodon
19	14.4	135	9	AA096439	AA096439 19794.seq
19	14.4	144	9	AA623585	AA623585 vn73d02.r
19	14.4	154	9	AA1156792	AA1156792 ue54f03.r
20	18	157	9	AA967821	AA967821 uh05f03.r
21	18	157	14	D76516	D76516 MUS70C08 mo
22	18	158	9	AA792584	AA792584 vs88e04.r
23	18	158	14	W91170	W91170 mf71f03.r1
24	18	160	9	AA270923	AA270923 va70f05.r
25	18	161	9	AA207933	AA207933 mv92c01.r
26	18	162	9	AA792947	AA792947 vp28e01.r
27	18	162	9	AA220778	AA220778 mv69c04.r
28	18	162	9	AA591963	AA591963 v150b08.r
29	18	163	14	BM843852	BM843852 K-EST0121
30	18	164	14	BM686528	BM686528 UI-E-CO0-
31	18	169	9	AA144770	AA144770 mr68a05.r
32	18	169	12	BE774336	BE774336 MRI-UM000
33	18	170	14	R57257	R57257 F2310 Fetal
34	18	171	9	AA375556	AA375556 ES987853
35	18	172	14	W18665	W18665 mb98604.r1
36	18	173	9	AA692385	AA692385 vt21a10.r
37	18	174	14	T27818	T27818 EST17484 Hu
38	18	179	12	BE774172	BE774172 MRI-UM000
39	18	180	9	AA068081	AA068081 mm56e02.r
40	18	180	10	AW647096	AW647096 EST325639
41	18	181	9	AA566472	AA566472 vm48b04.r
42	18	182	9	AA316715	AA316715 EST188545
43	18	184	14	N83763	N83763 KK2711F Hum
44	18	187	10	AW211038	AW211038 uc90d11.y
45	18	189	9	AA072898	AA072898 mm72d12.r
46	18	195	9	AA087727	AA087727 mol3e09.r
47	18	195	9	AA454807	AA454807 zx77f10.r
48	18	198	9	AV044717	AV044717 AV044717
49	18	198	10	BE168674	BE168674 QV1-HT051
50	18	201	9	AA302441	AA302441 EST15672
51	18	201	14	W16355	W16355 mb56c07.r1
52	18	203	9	AA403933	AA403933 va32a01.r
53	18	203	9	AA467283	AA467283 vf06e09.r
54	18	203	9	AA538208	AA538208 vj50h09.r
55	18	205	14	H92399	H92399 ys86a06.r1
56	18	207	9	AA312784	AA312784 EST183467
57	18	209	9	AA416035	AA416035 vf40h12.r
58	18	210	9	AA301761	AA301761 EST14990
59	18	210	9	AA623434	AA623434 vn33a11.r
60	18	212	9	AA445744	AA445744 vf09e09.r
61	18	212	9	AA472510	AA472510 vho7d12.r
62	18	213	9	AA140326	AA140326 mr66e10.r
63	18	213	9	AA207455	AA207455 mv87c04.r
64	18	213	14	F26549	F26549 HSPD14071 H
65	18	214	14	W89298	W89298 mf63c09.r1
66	18	215	9	AA666996	AA666996 vq87h04.r
67	18	215	9	AA546784	AA546784 vq02d02.r
68	18	215	10	AW369977	AW369977 ILO-BT023
69	18	216	14	T92656	T92656 ye22e05.r1
70	18	216	17	AQ545403	AQ545403 CITBI-E1-
71	18	217	12	BF041410	BF041410 BP250008B
72	18	217	12	BF083159	BF083159 QV0-CS001
73	18	217	14	D53771	D53771 HUM119F07B
74	18	218	9	AA137562	AA137562 mq37c10.r
75	18	221	10	AW886615	AW886615 RCI-OT008
76	18	223	14	N85757	N85757 L0512F Huma
77	18	226	10	AW800960	AW800960 MR3-UM006
78	18	227	14	T60895	T60895 yb72f05.r1
79	18	229	9	AA091048	AA091048 cchn1095.

80 18 13.6 230 9 AA382739
81 18 13.6 230 14 C06531
82 18 13.6 232 9 AA095816
83 18 13.6 234 12 BF924141
84 18 13.6 237 9 AA372460
85 18 13.6 239 9 AA340512
86 18 13.6 239 9 AA366141
87 18 13.6 239 10 AW800966
88 18 13.6 240 9 AA302239
89 18 13.6 240 14 T25985
90 18 13.6 241 9 AA302528
91 18 13.6 241 10 AW998269
92 18 13.6 241 10 AW998418
93 18 13.6 242 10 AW998418
94 18 13.6 243 9 AU059537
95 18 13.6 243 10 AW797675
96 18 13.6 243 10 AW797688
97 18 13.6 244 12 BF012761
98 18 13.6 244 14 BQ840431
99 18 13.6 245 14 W14700
100 18 13.6 247 9 AA358097
101 18 13.6 247 9 AA362157
102 18 13.6 247 13 BG997026
103 18 13.6 251 9 AA301772
104 18 13.6 252 14 H40563
105 18 13.6 252 10 AW797680
106 18 13.6 254 14 N85477
107 18 13.6 255 9 AL118094
108 18 13.6 255 9 AA617515
109 18 13.6 257 10 AW800885
110 18 13.6 258 9 AA307117
111 18 13.6 258 9 AA339727
112 18 13.6 258 10 AW794138
113 18 13.6 258 13 BG994832
114 18 13.6 260 9 AA365696
115 18 13.6 260 10 AW998455
116 18 13.6 261 10 AW797742
117 18 13.6 261 9 AA316198
118 18 13.6 263 12 BG814678
119 18 13.6 264 12 BF378584
120 18 13.6 266 10 AW801054
121 18 13.6 266 14 W11112
122 18 13.6 267 12 BE714634
123 18 13.6 268 9 AA685446
124 18 13.6 269 10 AW998366
125 18 13.6 270 9 AA304229
126 18 13.6 271 9 AA354636
127 18 13.6 271 14 BQ309112
128 18 13.6 272 14 W01438
129 18 13.6 273 9 AA301890
130 18 13.6 273 10 AW797766
131 18 13.6 273 10 AW800972
132 18 13.6 274 9 AA308404
133 18 13.6 274 10 AW797701
134 18 13.6 274 13 B1496663
135 18 13.6 274 14 D54136
136 18 13.6 276 9 AA365522
137 18 13.6 276 14 BM855353
138 18 13.6 279 9 AA352157
139 18 13.6 279 9 AA362030
140 18 13.6 280 9 AA022711
141 18 13.6 280 10 AW797700
142 18 13.6 282 9 AA301934
143 18 13.6 285 12 BE714668
144 18 13.6 287 10 AW793109
145 18 13.6 288 9 AA338821
146 18 13.6 289 9 AA374209
147 18 13.6 289 9 AA616956
148 18 13.6 289 9 AA070672
149 18 13.6 290 9 A1265376
150 18 13.6 290 9 AA380802
151 18 13.6 291 10 BB564596
152 18 13.6 291 10 BB564596
153 18 13.6 292 9 AA304555
154 18 13.6 292 14 D56366
155 18 13.6 293 9 AA301999
156 18 13.6 293 10 AW619458
157 18 13.6 295 9 AA384610
158 18 13.6 296 13 BM125864
159 18 13.6 296 14 D53023
160 18 13.6 297 9 AA073962
161 18 13.6 297 9 AV136898
162 18 13.6 299 9 AA340452
163 18 13.6 299 14 BM855208
164 18 13.6 300 9 AU098753
165 18 13.6 300 9 AA316498
166 18 13.6 300 9 AA373192
167 18 13.6 300 10 AW325404
168 18 13.6 301 14 R11297
169 18 13.6 302 9 A1157676
170 18 13.6 302 9 AA309673
171 18 13.6 302 10 AW800956
172 18 13.6 303 9 AA316425
173 18 13.6 303 9 AA615691
174 18 13.6 303 14 D55279
175 18 13.6 304 9 AA657158
176 18 13.6 304 9 AA686446
177 18 13.6 304 9 AA745537
178 18 13.6 304 14 F29410
179 18 13.6 305 9 AA840447
180 18 13.6 306 12 BF884106
181 18 13.6 307 9 AA371161
182 18 13.6 307 9 AV120605
183 18 13.6 309 9 AA360865
184 18 13.6 309 9 AA372704
185 18 13.6 309 9 AA661462
186 18 13.6 310 9 AA303888
187 18 13.6 310 14 BQ367731
188 18 13.6 311 14 F32364
189 18 13.6 312 14 F36325
190 18 13.6 312 14 H23750
191 18 13.6 313 9 AL034856
192 18 13.6 313 9 AA304699
193 18 13.6 313 14 W19791
194 18 13.6 314 9 AA138347
195 18 13.6 314 9 AA304702
196 18 13.6 314 14 C17724
197 18 13.6 314 14 D55359
198 18 13.6 317 10 AW801124
199 18 13.6 318 9 AA340143
200 18 13.6 318 12 BE863715
201 18 13.6 318 14 BM855196
202 18 13.6 319 9 AA304443
203 18 13.6 319 10 AW619459
204 18 13.6 321 9 AA092043
205 18 13.6 321 9 AA686035
206 18 13.6 322 14 BQ400156
207 18 13.6 322 14 D54437
208 18 13.6 322 14 F24677
209 18 13.6 323 14 AA870213
210 18 13.6 323 9 AA352586
211 18 13.6 324 9 AA590964
212 18 13.6 324 14 W25668
213 18 13.6 325 14 W25668
214 18 13.6 326 9 AA307549
215 18 13.6 326 14 W82636
216 18 13.6 327 10 AW945234
217 18 13.6 327 9 A1048068
218 18 13.6 329 14 H41377
219 18 13.6 330 9 AA315972
220 18 13.6 330 9 AA316512
221 18 13.6 330 10 AW869624
222 18 13.6 331 9 AL363867
223 18 13.6 331 9 AL363867
224 18 13.6 333 14 BQ324259
225 18 13.6 335 9 AA062353
AA382739 EST96282
C06531 C06531 Rat
AA095816 16004.seq
BF924141 MR4-NT014
AA372460 EST84358
AA340512 EST45729
AA366141 EST77049
AW800966 MR3-UM006
AA302239 EST15348
T25985 ATH467 HTCD
AA302528 EST15689
AW998269 PM2-BN006
AW998418 PM2-BN006
AU059537 AU059537
AW797675 CM0-UM004
AW797688 CM0-UM004
BF012761 ux73C01.y
BQ840431 mah67g10.
W14700 mb34c04.r1
AA358097 EST66956
AA362157 EST71636
BG997026 MR4-HT105
AA301772 EST14827
AA374250 EST86362
H40563 yn87c12.r1
AW797680 CM0-UM004
N85477 J3657F Huma
AL118094 r225a26
AA617515 v177g01.r
AA354418 EST62702
AW800885 MR3-UM006
AA307117 EST17803
AA339727 EST44841
AW794138 MR1-UM000
BG994832 PM0-HT116
AA365696 EST76526
AW998455 PM2-BN006
AW797742 CM2-UM004
AA316198 EST187913
BG814678 dab05f10.
BF378584 CM0-UM004
AW801054 MR3-UM006
W11112 ma78h09.r1
BE714634 PM2-HT072
AA685446 EST107195
AA304229 EST16960
AA354636 EST62927
BQ309112 MR0-BT600
W01438 za73c04.r1
AA301890 EST14940
AW797766 CM2-UM004
AW800972 MR3-UM006
AA308404 EST179234
AW797701 CM0-UM004
B1496663 df127b03.
D54136 HDM129G11B
AA365522 EST76310
BM855353 K-EST0138
AA352157 EST60371
AA362030 EST1374
AA022711 ze71f08.r
AW797700 CM0-UM004
AA301934 EST15013
BE714668 PM2-HT072
AW793109 CM4-UM000
AA338821 EST43818
AA374209 EST86338
AA616956 v120f03.r
AA070672 zm53g03.r
A1265376 uk03h11.y
AA380802 EST93797
BB564596 BB564596

c 226 18 13.6 337 10 AW415710
227 18 13.6 339 9 AL117845
228 18 13.6 339 14 D55927
229 18 13.6 340 9 AA108087
230 18 13.6 340 9 AA305923
231 18 13.6 340 9 AA316779
232 18 13.6 340 12 BF583502
233 18 13.6 342 14 W11627
234 18 13.6 344 9 AA945733
235 18 13.6 344 9 AA352601
236 18 13.6 344 14 F28066
237 18 13.6 344 14 H35100
238 18 13.6 345 9 AI952139
239 18 13.6 348 14 D51057
240 18 13.6 349 9 AA317870
241 18 13.6 349 10 AW824021
242 18 13.6 350 9 AA089668
243 18 13.6 350 14 F27686
244 18 13.6 350 14 W83798
245 18 13.6 352 14 T62988
246 18 13.6 353 9 AA709866
247 18 13.6 353 10 AW619828
248 18 13.6 354 9 AA313946
249 18 13.6 354 14 W62142
250 18 13.6 355 9 AA821726
251 18 13.6 355 14 D52330
252 18 13.6 357 12 BF934709
253 18 13.6 357 14 T51439
254 18 13.6 358 9 AA675439
255 18 13.6 358 9 AA843392
256 18 13.6 358 9 AA486145
257 18 13.6 358 14 T49877
258 18 13.6 359 9 AA821760
259 18 13.6 359 9 AI626080
260 18 13.6 359 10 BE178823
261 18 13.6 360 9 AI718100
262 18 13.6 360 9 AO097775
263 18 13.6 360 9 AA407170
264 18 13.6 361 9 AI122585
265 18 13.6 361 10 AW415709
266 18 13.6 361 14 T81560
267 18 13.6 362 9 AI468234
268 18 13.6 362 14 H56367
269 18 13.6 363 12 BE833110
270 18 13.6 364 9 AA869404
271 18 13.6 364 9 AA410037
272 18 13.6 364 14 BM855238
273 18 13.6 365 9 AA051064
274 18 13.6 366 13 BA499546
275 18 13.6 366 14 T49863
276 18 13.6 366 14 T59199
277 18 13.6 368 9 AA746615
278 18 13.6 368 12 BF687930
279 18 13.6 368 14 W10194
280 18 13.6 369 13 BG982434
281 18 13.6 369 14 F28020
282 18 13.6 370 9 AI707460
283 18 13.6 370 14 BM768418
284 18 13.6 370 14 BM768693
285 18 13.6 371 9 AI024403
286 18 13.6 371 9 AA407038
287 18 13.6 371 9 AA523332
288 18 13.6 372 9 AI761042
289 18 13.6 372 9 AA410036
290 18 13.6 372 9 AA574047
291 18 13.6 373 9 AA644882
292 18 13.6 373 10 BE620722
293 18 13.6 373 12 BE833193
294 18 13.6 374 9 AI718994
295 18 13.6 375 9 AA500732
296 18 13.6 375 10 AW262820
297 18 13.6 376 9 AI153298
298 18 13.6 376 9 AI708841
300 18 13.6 376 14 D54297
301 18 13.6 376 14 F30615
302 18 13.6 377 9 AL022660
303 18 13.6 377 14 H96057
304 18 13.6 378 9 AI084693
305 18 13.6 378 9 AA265400
306 18 13.6 378 9 AA864159
307 18 13.6 378 14 BQ549781
308 18 13.6 379 14 AA138321
309 18 13.6 379 12 BF581235
310 18 13.6 379 13 BI522159
311 18 13.6 380 9 AA737823
312 18 13.6 380 9 AI707617
313 18 13.6 380 14 BM785046
314 18 13.6 381 10 AV663919
315 18 13.6 381 10 AW545053
316 18 13.6 381 10 AW884474
317 18 13.6 381 14 D55058
318 18 13.6 382 9 AI000237
319 18 13.6 383 9 AI719778
320 18 13.6 383 12 BF808578
321 18 13.6 384 9 AA181280
322 18 13.6 384 9 AA559927
323 18 13.6 384 10 AW619405
324 18 13.6 384 12 BE738436
325 18 13.6 385 14 BQ319759
326 18 13.6 386 9 AI206275
327 18 13.6 386 9 AA581000
328 18 13.6 386 14 BM850736
329 18 13.6 386 14 D54613
330 18 13.6 387 9 AA871154
331 18 13.6 387 9 AI911108
332 18 13.6 387 12 BF615106
333 18 13.6 387 13 BM661927
334 18 13.6 387 14 BM855608
335 18 13.6 387 14 BQ784063
336 18 13.6 388 9 AA592421
337 18 13.6 388 14 T63133
338 18 13.6 389 9 AA973422
339 18 13.6 389 9 AI473863
340 18 13.6 389 9 AI830918
341 18 13.6 389 9 AA529989
342 18 13.6 389 10 AW020063
343 18 13.6 390 9 AA849000
344 18 13.6 390 9 AA614380
345 18 13.6 390 13 BE182256
346 18 13.6 391 9 AA723043
347 18 13.6 391 9 AI814223
348 18 13.6 391 10 AW163413
349 18 13.6 391 13 BG964620
350 18 13.6 391 14 R31298
351 18 13.6 392 9 AA637703
352 18 13.6 392 9 AI203929
353 18 13.6 392 9 AA083624
354 18 13.6 392 9 AA266123
355 18 13.6 392 14 F24712
356 18 13.6 392 14 D54589
357 18 13.6 393 9 AA915912
358 18 13.6 393 9 AI761022
359 18 13.6 393 9 AA160388
360 18 13.6 393 10 AV697652
361 18 13.6 393 12 BF447868
362 18 13.6 394 9 AA727844
363 18 13.6 394 9 AA871058
364 18 13.6 394 9 AI582139
365 18 13.6 394 9 AI707776
366 18 13.6 394 9 AA590481
367 18 13.6 394 10 AW619016
368 18 13.6 395 9 AA649497
369 18 13.6 395 9 AI832679
370 18 13.6 395 10 BE138303
371 18 13.6 395 14 D54570
AW884466 QV3-OT006
D54297 HSPD135B09B
F30615 HSPD211778 H
AL022660 57827B40
H96057 yw61906.r1
AI084693 oz79b02.x
AA265400 mz48c05.r
AW884159 QV3-OT006
BQ549781 ik91h08.x
AA138321 mq96c09.r
BF581235 602100449
BI522159 603081565
AA737823 nx14e12.s
AI707617 as31e10.x
BM785046 K-EST0063
AV663919 AV663919
AW545053 C0190B11-
AW884474 QV3-OT006
D55058 HUM163F01B
AI000237 ct04c05.s
AI719778 as41q12.x
BF808578 CM1-CI009
AA181280 zp68d10.s
AA559927 ni60b08.s
AW619405 7456 MARC
BE738436 601572460
BQ319759 PM4-CT081
AI206275 qr22h11.x
AA581000 vi23b05.r
BM850736 K-EST0131
D54613 HUM146A07B
AA871154 vq31q08.r
AI911108 qe18b05.x
BF615106 d881d06.x
BM661927 UI-E-Ck1-
BM855608 K-EST0138
BQ784063 SdEST4a83
AA592421 v035d07.r
T63133 yb99a01.s1
AA973422 0044d02.s
AI473863 tal1h03.x
AI830918 wj61h04.x
AA529989 vj13h08.r
AW020063 df03f07.y
AA849000 EST191762
AA614380 dp46c04.s
BI518226 603042056
AA723043 z983a06.s
AI814223 wk54h06.x
AW163413 au83e01.y
BG964620 602831809
R31298 yb76a02.r1
AA637703 vr21b10.r
AI203929 qd79g02.x
AA083624 zn39a02.r
AA266123 mz49a05.r
D54589 HUM145B02B
F24712 HSPD11231 H
AA915912 oh86d07.s
AI761022 w110c02.x
AA160388 zo64a07.r
AV697652 AV697652
BF447868 7q96e04.x
AA727844 vp33e12.r
AA871058 vq29g09.r
AI582139 as03c07.x
AI707776 as35d01.x
AA590481 vm24d06.r
AW619016 353 MARC
AA649497 ns44b09.s
AI832679 at71b07.x
BE138303 ug51a05.y
D54570 HUM144D01B

c 372 18 13.6 396 9 A1718322 A1718322 as53b08.x 445 18 13.6 410 9 AA816138 AA816138 VP44c06.i
c 373 18 13.6 396 9 AA483076 AA483076 ne71e11.s 446 18 13.6 410 9 A1120749 A1120749 mp73c09.i
c 374 18 13.6 396 10 A1762048 A1762048 ne71e11.s 447 18 13.6 410 9 A1499000 A1499000 tn01g11.x
c 375 18 13.6 396 13 B1032602 B1032602 PM3-NN117 448 18 13.6 410 9 A1719722 A1719722 as92b02.x
c 376 18 13.6 396 14 BM991466 BM991466 UI-H-DHO- 449 18 13.6 410 9 AA403689 AA403689 m255g05.i
c 377 18 13.6 397 9 A1515341 A1515341 zo42h06.s 450 18 13.6 410 9 AA590198 AA590198 vns56a09.i
c 378 18 13.6 398 14 BM687860 BM687860 UI-E-CKI- 451 18 13.6 410 9 AA600887 AA600887 np56d10.s
c 379 18 13.6 398 9 A1087406 A1087406 oz72f11.x 452 18 13.6 410 9 AA615404 AA615404 v069f02.i
c 380 18 13.6 398 9 AA221676 AA221676 mv28b04.i 453 18 13.6 410 10 AA649210 AA649210 hc79c11.x
c 381 18 13.6 398 9 AA470085 AA470085 zt98g07.s 454 18 13.6 410 12 BE854595 BE854595 ux31f10.y
c 382 18 13.6 398 10 A1746756 A1746756 AV746756 455 18 13.6 410 13 BM505632 BM505632 ih14h07.x
c 383 18 13.6 398 10 A1746756 A1746756 AV746756 456 18 13.6 410 14 BQ129534 BQ129534 ih30h11.x
c 384 18 13.6 398 13 B1496662 B1496662 df127b03. 457 18 13.6 411 9 AA673311 AA673311 vns69g12.i
c 385 18 13.6 398 14 BM988447 BM988447 UI-H-DHO- 458 18 13.6 411 9 AA870153 AA870153 vq12e02.i
c 386 18 13.6 399 14 F24867 F24867 HSPD11526 H 459 18 13.6 411 9 A1880646 A1880646 at05f11.x
c 387 18 13.6 400 9 AA946832 AA946832 qg43e03.s 460 18 13.6 411 9 AA208486 AA208486 mv85c05.i
c 388 18 13.6 400 9 AA946832 AA946832 qg43e03.s 461 18 13.6 411 9 AA527683 AA527683 nh86d05.s
c 389 18 13.6 400 9 A1001091 A1001091 e9h4b03.s 462 18 13.6 411 9 AA619410 AA619410 v087h12.i
c 390 18 13.6 400 13 B1518034 B1518034 6030411715 463 18 13.6 411 10 AW189058 AW189058 xk99c08.x
c 391 18 13.6 400 14 W05321 W05321 za84e05.r1 464 18 13.6 411 14 BM855519 BM855519 K-EST0138
c 392 18 13.6 401 9 AA864455 AA864455 OH01907.s 465 18 13.6 412 9 AA605114 AA605114 mj68b09.i
c 393 18 13.6 401 9 A1429236 A1429236 ml58d08.x 466 18 13.6 412 9 AA871729 AA871729 vq40c12.i
c 394 18 13.6 401 9 A1670720 A1670720 wc28d04.x 467 18 13.6 412 9 A1355270 A1355270 qt79e09.x
c 395 18 13.6 401 9 A1872025 A1872025 vm54e11.x 468 18 13.6 412 9 A1924655 A1924655 wa57h09.x
c 396 18 13.6 401 9 AA597004 AA597004 vol1h05.i 469 18 13.6 412 10 AW619959 AW619959 8045 MARC
c 397 18 13.6 401 10 A1739443 A1739443 AV739443 470 18 13.6 412 10 AW951791 AW951791 BBT363861
c 398 18 13.6 401 10 AW305108 AW305108 xv99f06.x 471 18 13.6 412 12 BG579192 BG579192 df24f01.y
c 399 18 13.6 401 12 BE833078 BE833078 QV3-OT006 472 18 13.6 413 9 AA734426 AA734426 v79e0e7.i
c 400 18 13.6 401 14 BM749826 BM749826 K-EST0025 473 18 13.6 413 9 AA929515 AA929515 v440c07.i
c 401 18 13.6 402 9 AA674528 AA674528 vt38f03.i 474 18 13.6 413 9 A1084619 A1084619 o278b10.x
c 402 18 13.6 402 9 AA793944 AA793944 vt38f03.i 475 18 13.6 413 9 AA590717 AA590717 v059f12.i
c 403 18 13.6 402 9 AA855175 AA855175 aj02c02.s 476 18 13.6 413 10 AV663360 AV663360 4603360
c 404 18 13.6 402 9 A1707686 A1707686 as32a08.x 477 18 13.6 413 12 BG036404 BG036404 602326530
c 405 18 13.6 402 9 AU042227 AU042227 478 18 13.6 414 9 A1749958 A1749958 at34d01.x
c 406 18 13.6 402 9 AA411834 AA411834 zt67f01.s 479 18 13.6 414 9 AA582794 AA582794 nn35b08.s
c 407 18 13.6 402 14 BM991448 BM991448 UI-H-DHO- 480 18 13.6 414 13 B1084746 B1084746 602869757
c 408 18 13.6 403 9 AA774770 AA774770 se87e06.s 481 18 13.6 415 9 AA792197 AA792197 v045c06.i
c 409 18 13.6 403 9 A1080144 A1080144 mj99f01.i 482 18 13.6 415 9 AA824266 AA824266 aj29e08.s
c 410 18 13.6 403 9 A1708863 A1708863 ss27h03.x 483 18 13.6 415 9 AA870311 AA870311 vq14d05.i
c 411 18 13.6 403 10 A1760430 A1760430 AV760430 484 18 13.6 415 14 AA147960 AA147960 zc48d12.s
c 412 18 13.6 403 10 A1749111 A1749111 xy21e07.x 485 18 13.6 415 14 BM850366 BM850366 K-EST0130
c 413 18 13.6 403 14 BM841476 BM841476 K-EST0118 486 18 13.6 415 14 BM855515 BM855515 4603360
c 414 18 13.6 404 9 AA636867 AA636867 vt20g07.i 487 18 13.6 416 9 AA937247 AA937247 OJ02f01.s
c 415 18 13.6 404 9 A1718269 A1718269 as51d08.x 488 18 13.6 416 9 AA308305 AA308305 EST179135
c 416 18 13.6 404 9 A1749969 A1749969 ac34e02.x 489 18 13.6 416 10 BE217903 BE217903 vt31d08.x
c 417 18 13.6 404 9 A1832625 A1832625 ac70h07.x 490 18 13.6 416 14 BM856279 BM856279 K-EST0139
c 418 18 13.6 404 9 A1985951 A1985951 wt79b02.x 491 18 13.6 416 14 W91744 W91744 MTA.G01.080
c 419 18 13.6 404 12 BG688032 BG688032 335437 BA 492 18 13.6 417 9 AA755328 AA755328 vq2e09.i
c 420 18 13.6 405 9 AA308256 AA308256 EST179106 493 18 13.6 417 9 A1184617 A1184617 qf46c03.x
c 421 18 13.6 405 9 AA417155 AA417155 zu04e11.i 494 18 13.6 417 9 A1879910 A1879910 ar99d03.x
c 422 18 13.6 405 9 AA590590 AA590590 vm59f02.i 495 18 13.6 417 9 A1884379 A1884379 wm31f04.x
c 423 18 13.6 405 10 A189208 A189208 x102g08.x 496 18 13.6 417 9 AA63174 AA63174 vq85h06.i
c 424 18 13.6 406 9 AA871000 AA871000 vq29a05.i 497 18 13.6 417 9 AA623014 AA623014 np79h12.s
c 425 18 13.6 406 9 AA245555 AA245555 mv50a05.i 498 18 13.6 417 10 BF435945 BF435945 nab75d05.
c 426 18 13.6 406 12 BG100882 BG100882 uy16e08.y 499 18 13.6 417 12 BE906510 BE906510 601498575
c 427 18 13.6 407 9 AA823363 AA823363 vp36b10.i 500 18 13.6 417 12 BE906510 BE906510 601498575
c 428 18 13.6 407 9 AA583191 AA583191 nm45b04.s 501 18 13.6 417 12 BF034316 BF034316 601455334
c 429 18 13.6 407 10 AW542557 AW542557 C0159A06- 502 18 13.6 417 13 B1276078 B1276078 UI-R-CW0-
c 430 18 13.6 408 9 A1718723 A1718723 as95e10.x 503 18 13.6 418 9 AA057636 AA057636 601498575
c 431 18 13.6 408 9 AA615456 AA615456 vq78e03.i 504 18 13.6 418 9 AA846825 AA846825 aj99h02.s
c 432 18 13.6 408 10 A1770926 A1770926 h193d10.x 505 18 13.6 418 9 A1333875 A1333875 qp99d04.x
c 433 18 13.6 408 14 W54335 W54335 md05c05.r1 506 18 13.6 418 9 A132464 A132464 z007h09.i
c 434 18 13.6 408 14 W54335 W54335 md05c05.r1 507 18 13.6 418 9 A1735492 A1735492 at12c08.x
c 435 18 13.6 409 9 AA637951 AA637951 vt22c10.i 508 18 13.6 418 9 A1749009 A1749009 601498575
c 436 18 13.6 409 9 AA665053 AA665053 nu73g12.s 509 18 13.6 418 10 BE629242 BE629242 nu35b06.y
c 437 18 13.6 409 9 A1755337 A1755337 vq62f09.i 510 18 13.6 419 9 AA758513 AA758513 ah66c02.s
c 438 18 13.6 409 9 A1333615 A1333615 qp91b04.x 511 18 13.6 419 9 AA421628 AA421628 zt98g07.i
c 439 18 13.6 409 10 A1761739 A1761739 AV761739 512 18 13.6 419 9 AA421628 AA421628 zt98g07.i
c 440 18 13.6 409 10 AW619537 AW619537 7602 MARC 513 18 13.6 419 9 AA506282 AA506282 nh10f05.s
c 441 18 13.6 409 13 BG982683 BG982683 ILS-CN006 514 18 13.6 419 9 AA574728 AA574728 vms1e07.i
c 442 18 13.6 409 14 BM704129 BM704129 UI-E-CKI- 515 18 13.6 419 12 BF036306 BF036306 601459489
c 443 18 13.6 410 9 AA691901 AA691901 vt14g02.i 516 18 13.6 420 9 AA630236 AA630236 ab96f06.s
c 444 18 13.6 410 9 AA770789 AA770789 vt12a11.i 517 18 13.6 420 10 AW619764 AW619764 7831 MARC


```

518 18 13.6 420 10 AW619801
c 519 18 13.6 420 10 AW9898270 PM2-BN006
520 18 13.6 420 12 BF426632
c 521 18 13.6 421 9 A1142610
522 18 13.6 421 9 AA097362
c 523 18 13.6 421 10 AV662697
524 18 13.6 421 10 AW784283
525 18 13.6 421 14 T28934
c 526 18 13.6 422 9 AA546118
527 18 13.6 422 14 BM988129
c 528 18 13.6 423 9 A1190309
529 18 13.6 423 9 AA445072
c 530 18 13.6 423 10 AV592009
531 18 13.6 423 12 BF525063
c 532 18 13.6 424 9 A1718016
533 18 13.6 424 13 BM429376
c 534 18 13.6 424 14 BM987456
535 18 13.6 425 9 AA070874
c 536 18 13.6 425 9 A1085716
537 18 13.6 425 9 A1085902
c 538 18 13.6 425 9 A1192730
539 18 13.6 425 9 AA081417
c 540 18 13.6 425 10 AW711964
541 18 13.6 425 10 AW619595
c 542 18 13.6 426 9 A1282536
543 18 13.6 426 14 BM853886
c 544 18 13.6 427 9 AA961747
545 18 13.6 427 9 AA098544
546 18 13.6 427 12 BF751572
547 18 13.6 427 13 BF848878
548 18 13.6 427 13 BM125857
549 18 13.6 427 14 BM768493
550 18 13.6 428 9 AA314732
551 18 13.6 428 9 AA483378
552 18 13.6 428 9 AA463456
553 18 13.6 428 10 AW463456
554 18 13.6 428 12 BF452590
555 18 13.6 428 12 BF867472
556 18 13.6 428 12 BF907243
557 18 13.6 428 13 BM055733
558 18 13.6 429 9 AA261583
559 18 13.6 429 10 AW823999
560 18 13.6 429 12 BF715155
561 18 13.6 429 12 BF715155
562 18 13.6 429 12 BF467061
563 18 13.6 429 12 BF710616
564 18 13.6 430 10 AW912908
565 18 13.6 430 14 W07728
c 566 18 13.6 431 9 A1346709
567 18 13.6 431 10 AW619277
568 18 13.6 431 12 BF253202
569 18 13.6 431 12 BF889330
c 570 18 13.6 431 14 N70636
571 18 13.6 431 14 R28160
c 572 18 13.6 432 9 AA059707
573 18 13.6 432 9 AA633937
574 18 13.6 432 9 AA082482
575 18 13.6 432 9 A1720365
576 18 13.6 432 9 AA188050
577 18 13.6 432 9 AA316182
578 18 13.6 432 9 AA529971
c 579 18 13.6 432 10 AV618094
580 18 13.6 432 10 AV618095
c 581 18 13.6 432 10 AV664771
582 18 13.6 432 10 AV712821
583 18 13.6 432 10 BF254902
584 18 13.6 432 14 BM738252
585 18 13.6 432 14 BM738720
586 18 13.6 433 9 AA730441
c 587 18 13.6 433 9 A1740739
588 18 13.6 433 9 AA484097
589 18 13.6 433 12 BG223174
590 18 13.6 433 13 BF304896
591 18 13.6 433 13 AW619801 7869 MARC
592 18 13.6 434 9 AW9898270 PM2-BN006
593 18 13.6 434 9 BF426632 dF71b06.Y
594 18 13.6 434 9 A1142610 OK35e04.s
595 18 13.6 434 9 AA097362 mk16a11.r
596 18 13.6 434 10 AV662697 AV662697
597 18 13.6 434 10 AW784283 zB60g12.g
598 18 13.6 434 14 T28934 EST61003 Hu
599 18 13.6 434 9 AA546118 VK04f05.r
600 18 13.6 434 9 BM988129 UT-H-CO0-
601 18 13.6 434 9 A1190309 qd57g03.x
602 18 13.6 435 9 AA445072 V959b08.r
603 18 13.6 435 10 AV592009 AV592009
604 18 13.6 435 12 BF525063 UT-R-AD0-
605 18 13.6 435 14 A1718016 as93c12.x
606 18 13.6 435 14 BM429376 1A20C04a
607 18 13.6 436 9 BM987456 UT-H-CO0-
608 18 13.6 436 9 AA070874 zM54C08.r
609 18 13.6 436 9 A1085716 oz75e01.x
610 18 13.6 436 9 A1085902 oz74e03.x
611 18 13.6 436 9 A1192730 qe62e02.x
612 18 13.6 436 9 AA081417 zn39a02.s
613 18 13.6 436 9 AV711964 AV711964
614 18 13.6 436 9 AW619595 7663 MARC
615 18 13.6 436 14 A1282536 qv21b06.x
616 18 13.6 436 14 BM853886 K-EST0136
617 18 13.6 436 9 AA961747 or60d01.s
618 18 13.6 436 9 AA098544 mk18c12.r
619 18 13.6 436 9 BE751572 203745 MA
620 18 13.6 436 9 BI848878 471431 MA
621 18 13.6 436 9 BM125857 1076b07.Y
622 18 13.6 436 9 BM768493 K-EST0051
623 18 13.6 437 9 AA314732 EST186638
624 18 13.6 437 9 AA483378 ne74c10.s
625 18 13.6 437 9 AA463456 BF230012B
626 18 13.6 437 10 AW463456 BF230021A
627 18 13.6 437 12 BF452590 maa01h04.
628 18 13.6 437 10 BF867472 601442561.
629 18 13.6 437 12 BF907243 601500936
630 18 13.6 437 13 BM055733 1482d05.Y
631 18 13.6 437 9 AA261583 mz87c10.r
632 18 13.6 438 9 AW823999 uf62d02.Y
633 18 13.6 438 9 BF715155 mab05h05.
634 18 13.6 438 13 BF467061 1A03C10a
635 18 13.6 438 13 BF710616 QV3-HT063
636 18 13.6 438 9 AW912908 uf46d09.Y
637 18 13.6 438 14 W07728 zb03b08.r1
638 18 13.6 439 9 A1346709 qp47c06.x
639 18 13.6 439 9 AW619277 6356 MARC
640 18 13.6 439 12 BF253202 602364159
641 18 13.6 439 12 BF889330 601513219
642 18 13.6 439 14 N70636 za84f10.s1
643 18 13.6 439 14 R28160 yh65c09.s1
644 18 13.6 439 9 AA059707 mj74b02.r
645 18 13.6 439 9 AA633937 ac73e08.s
646 18 13.6 439 9 AA082482 zn40c04.r
647 18 13.6 439 9 A1720365 as75g05.x
648 18 13.6 439 9 AA188050 zp52c05.r
649 18 13.6 439 9 AA316182 ESP188040
650 18 13.6 439 9 AA529971 vj12h12.r
651 18 13.6 440 9 AV618094 AV618094
652 18 13.6 440 9 AV618095 AV618095
653 18 13.6 440 9 AV664771 AV664771
654 18 13.6 440 9 AV712821 AV712821
655 18 13.6 440 9 BE254902 601111843
656 18 13.6 440 14 BM738252 K-EST0002
657 18 13.6 440 14 BM738720 K-EST0006
658 18 13.6 441 9 AA730441 nw47f04.s
659 18 13.6 441 9 A1740739 wg17f04.x
660 18 13.6 441 9 AA484097 ne73d10.s
661 18 13.6 441 12 BG223174 nah65c07.
662 18 13.6 441 13 BF304896 AR066A061
663 18 13.6 441 14 W52576
664 18 13.6 441 14 W52576
665 18 13.6 441 14 W52576
666 18 13.6 441 14 W52576
667 18 13.6 441 14 W52576
668 18 13.6 441 14 W52576
669 18 13.6 441 14 W52576
670 18 13.6 441 14 W52576
671 18 13.6 441 14 W52576
672 18 13.6 441 14 W52576
673 18 13.6 441 14 W52576
674 18 13.6 441 14 W52576
675 18 13.6 441 14 W52576
676 18 13.6 441 14 W52576
677 18 13.6 441 14 W52576
678 18 13.6 441 14 W52576
679 18 13.6 441 14 W52576
680 18 13.6 441 14 W52576
681 18 13.6 441 14 W52576
682 18 13.6 441 14 W52576
683 18 13.6 441 14 W52576
684 18 13.6 441 14 W52576
685 18 13.6 441 14 W52576
686 18 13.6 441 14 W52576
687 18 13.6 441 14 W52576
688 18 13.6 441 14 W52576
689 18 13.6 441 14 W52576
690 18 13.6 441 14 W52576
691 18 13.6 441 14 W52576
692 18 13.6 441 14 W52576
693 18 13.6 441 14 W52576
694 18 13.6 441 14 W52576
695 18 13.6 441 14 W52576
696 18 13.6 441 14 W52576
697 18 13.6 441 14 W52576
698 18 13.6 441 14 W52576
699 18 13.6 441 14 W52576
700 18 13.6 441 14 W52576
701 18 13.6 441 14 W52576
702 18 13.6 441 14 W52576
703 18 13.6 441 14 W52576
704 18 13.6 441 14 W52576
705 18 13.6 441 14 W52576
706 18 13.6 441 14 W52576
707 18 13.6 441 14 W52576
708 18 13.6 441 14 W52576
709 18 13.6 441 14 W52576
710 18 13.6 441 14 W52576
711 18 13.6 441 14 W52576
712 18 13.6 441 14 W52576
713 18 13.6 441 14 W52576
714 18 13.6 441 14 W52576
715 18 13.6 441 14 W52576
716 18 13.6 441 14 W52576
717 18 13.6 441 14 W52576
718 18 13.6 441 14 W52576
719 18 13.6 441 14 W52576
720 18 13.6 441 14 W52576
721 18 13.6 441 14 W52576
722 18 13.6 441 14 W52576
723 18 13.6 441 14 W52576
724 18 13.6 441 14 W52576
725 18 13.6 441 14 W52576
726 18 13.6 441 14 W52576
727 18 13.6 441 14 W52576
728 18 13.6 441 14 W52576
729 18 13.6 441 14 W52576
730 18 13.6 441 14 W52576
731 18 13.6 441 14 W52576
732 18 13.6 441 14 W52576
733 18 13.6 441 14 W52576
734 18 13.6 441 14 W52576
735 18 13.6 441 14 W52576
736 18 13.6 441 14 W52576
737 18 13.6 441 14 W52576
738 18 13.6 441 14 W52576
739 18 13.6 441 14 W52576
740 18 13.6 441 14 W52576
741 18 13.6 441 14 W52576
742 18 13.6 441 14 W52576
743 18 13.6 441 14 W52576
744 18 13.6 441 14 W52576
745 18 13.6 441 14 W52576
746 18 13.6 441 14 W52576
747 18 13.6 441 14 W52576
748 18 13.6 441 14 W52576
749 18 13.6 441 14 W52576
750 18 13.6 441 14 W52576
751 18 13.6 441 14 W52576
752 18 13.6 441 14 W52576
753 18 13.6 441 14 W52576
754 18 13.6 441 14 W52576
755 18 13.6 441 14 W52576
756 18 13.6 441 14 W52576
757 18 13.6 441 14 W52576
758 18 13.6 441 14 W52576
759 18 13.6 441 14 W52576
760 18 13.6 441 14 W52576
761 18 13.6 441 14 W52576
762 18 13.6 441 14 W52576
763 18 13.6 441 14 W52576
764 18 13.6 441 14 W52576
765 18 13.6 441 14 W52576
766 18 13.6 441 14 W52576
767 18 13.6 441 14 W52576
768 18 13.6 441 14 W52576
769 18 13.6 441 14 W52576
770 18 13.6 441 14 W52576
771 18 13.6 441 14 W52576
772 18 13.6 441 14 W52576
773 18 13.6 441 14 W52576
774 18 13.6 441 14 W52576
775 18 13.6 441 14 W52576
776 18 13.6 441 14 W52576
777 18 13.6 441 14 W52576
778 18 13.6 441 14 W52576
779 18 13.6 441 14 W52576
780 18 13.6 441 14 W52576
781 18 13.6 441 14 W52576
782 18 13.6 441 14 W52576
783 18 13.6 441 14 W52576
784 18 13.6 441 14 W52576
785 18 13.6 441 14 W52576
786 18 13.6 441 14 W52576
787 18 13.6 441 14 W52576
788 18 13.6 441 14 W52576
789 18 13.6 441 14 W52576
790 18 13.6 441 14 W52576
791 18 13.6 441 14 W52576
792 18 13.6 441 14 W52576
793 18 13.6 441 14 W52576
794 18 13.6 441 14 W52576
795 18 13.6 441 14 W52576
796 18 13.6 441 14 W52576
797 18 13.6 441 14 W52576
798 18 13.6 441 14 W52576
799 18 13.6 441 14 W52576
800 18 13.6 441 14 W52576

```

664 18 13.6 442 9 AA929872 VZ44C07.I 737 18 13.6 450 9 AA148023
665 18 13.6 442 9 AT833129 AT75004.X 738 18 13.6 450 9 AA186647
666 18 13.6 442 9 AL022773 87C19P49 739 18 13.6 450 9 AA557805
667 18 13.6 442 9 AA155816 AA15816 Z047002.I 740 18 13.6 450 10 BE613621
668 18 13.6 442 9 AA230554 AA23054 MV73E12.I 741 18 13.6 450 14 BM88223
669 18 13.6 442 9 AA420470 AA420470 NC60F03.I 742 18 13.6 450 14 BM88223
670 18 13.6 442 9 AA590434 AA590434 VM20B07.I 743 18 13.6 451 9 AA574701
671 18 13.6 442 9 AA617744 AA617744 NP51C07.S 744 18 13.6 451 12 BG253383
672 18 13.6 442 9 AA623351 AA623351 VP25B12.I 745 18 13.6 451 13 BM089275
673 18 13.6 442 10 AV615168 AV615168 AV615168 746 18 13.6 451 14 W04856
674 18 13.6 442 10 AV986772 AV986772 UF87E06.Y 747 18 13.6 452 9 AA793069
675 18 13.6 442 12 BG249640 BG249640 602319733 748 18 13.6 452 9 AI679886
676 18 13.6 442 13 BM105914 BM105914 509497 MA 749 18 13.6 452 9 AA480527
677 18 13.6 443 9 AA691560 AA691560 VS16G07.I 750 18 13.6 452 10 AA989988
678 18 13.6 443 9 AIO15078 AIO15078 OV51E04.S 751 18 13.6 452 10 AA989988
679 18 13.6 443 10 BE626900 BE626900 UU04F08.Y 752 18 13.6 452 12 BF614970
680 18 13.6 443 12 BF046634 BF046634 BP250020A 753 18 13.6 452 13 BM431924
681 18 13.6 443 14 BQ129779 BQ129779 1130911.Y 754 18 13.6 452 14 BQ044342
682 18 13.6 443 14 BQ234159 BQ234159 HD41H12.G 755 18 13.6 452 14 C88595
683 18 13.6 443 14 BQ257777 BQ257777 AGENCOURT 756 18 13.6 453 13 BM431970
684 18 13.6 444 9 AA472840 AA472840 V458F09.I 757 18 13.6 453 13 BM431970
685 18 13.6 444 9 AA557716 AA557716 N147B06.S 758 18 13.6 453 14 BM970898
686 18 13.6 444 9 AA597166 AA597166 VC05H05.I 759 18 13.6 453 14 BQ220112
687 18 13.6 444 10 AV664309 AV664309 AV664309 760 18 13.6 454 9 AA675430
688 18 13.6 444 10 AW465087 AW465087 BP230017B 761 18 13.6 454 9 AI103001
689 18 13.6 444 12 BG671616 BG671616 DRNBVE09 762 18 13.6 454 9 AA624249
690 18 13.6 444 14 BM969729 BM969729 UT-CF-DU1 763 18 13.6 454 12 BQ687948
691 18 13.6 444 14 BQ221715 BQ221715 AGENCOURT 764 18 13.6 455 14 BQ050657
692 18 13.6 444 14 BQ563782 BQ563782 G106G04.Y 765 18 13.6 455 9 AA869073
693 18 13.6 445 9 AA104455 AA104455 MC45C09.I 766 18 13.6 455 9 AI049606
694 18 13.6 445 9 AI707865 AI707865 AS26A08.X 767 18 13.6 455 9 AI254343
695 18 13.6 445 9 AA207529 AA207529 MV89C06.I 768 18 13.6 455 9 AA129780
696 18 13.6 445 9 AA208172 AA208172 MV82D11.I 769 18 13.6 455 9 AA624360
697 18 13.6 445 10 AW669799 AW669799 113369 MA 770 18 13.6 455 10 AV762708
698 18 13.6 445 14 BM841330 BM841330 K-EST0118 771 18 13.6 455 10 AW082906
699 18 13.6 445 14 N99549 N99549 ZA0D001.R1 772 18 13.6 455 10 AW619290
700 18 13.6 446 9 AA104283 AA104283 MC45E09.I 773 18 13.6 455 10 AW917430
701 18 13.6 446 9 AI719522 AI719522 AS44D03.X 774 18 13.6 455 10 BE113191
702 18 13.6 446 9 AA245919 AA245919 MX06G06.I 775 18 13.6 455 12 BE908679
703 18 13.6 446 9 AA240699 AA240699 NC62D07.I 776 18 13.6 455 12 BE967731
704 18 13.6 446 10 BE273236 BE273236 601142546 777 18 13.6 455 14 BM763917
705 18 13.6 446 12 BG168277 BG168277 602340814 778 18 13.6 455 14 BQ600351
706 18 13.6 446 13 B1327377 B1327377 AR07E002T 779 18 13.6 456 9 AA659067
707 18 13.6 446 14 BM760559 BM760559 K-EST0041 780 18 13.6 456 9 AA437971
708 18 13.6 446 14 BQ028237 BQ028237 UI-H-COO- 781 18 13.6 456 10 AV662449
709 18 13.6 446 14 R11502 R11502 YF28F11.S1 782 18 13.6 456 10 AW619874
710 18 13.6 446 14 T59161 T59161 YB50F09.S1 783 18 13.6 456 12 BF339067
711 18 13.6 446 14 W37054 W37054 MB72H10.R1 784 18 13.6 456 13 BM542700
712 18 13.6 446 14 W44429 W44429 ZC28G02.S1 785 18 13.6 456 14 BM766933
713 18 13.6 447 9 AI200768 AI200768 QF67B10.X 786 18 13.6 456 14 BQ085873
714 18 13.6 447 9 AI749605 AI749605 AT25B06.X 787 18 13.6 456 14 W29255
715 18 13.6 447 9 AA622812 AA622812 NP77C11.S 788 18 13.6 456 14 W29917
716 18 13.6 447 14 BM738093 BM738093 K-EST0002 789 18 13.6 457 9 AA65306
717 18 13.6 447 14 BM888592 BM888592 FMW271 HU 790 18 13.6 457 9 AA538207
718 18 13.6 448 9 AA844493 AA844493 AJ21B03.S 791 18 13.6 457 10 AV663920
719 18 13.6 448 9 AI313428 AI313428 QP80D09.X 792 18 13.6 457 12 BG150602
720 18 13.6 448 9 AA417156 AA417156 ZU04E12.I 793 18 13.6 457 12 BG778264
721 18 13.6 448 10 AW161076 AW161076 AU78F08.Y 794 18 13.6 457 13 B1521153
722 18 13.6 448 13 BM424102 BM424102 AGENCOURT 795 18 13.6 457 13 B1838135
723 18 13.6 448 14 W61175 W61175 ZD31B01.R1 796 18 13.6 457 14 BM818373
724 18 13.6 449 9 AI327405 AI327405 MQ37C10.X 797 18 13.6 457 14 BQ234689
725 18 13.6 449 12 BF034546 BF034546 601455457 798 18 13.6 458 9 AA822935
726 18 13.6 449 13 B1848716 B1848716 471229 MA 799 18 13.6 458 9 AI249439
727 18 13.6 449 13 B1848728 B1848728 471246 MA 800 18 13.6 458 9 AA606682
728 18 13.6 449 13 BM015450 BM015450 603641643 801 18 13.6 458 12 BG506360
729 18 13.6 449 13 BM088974 BM088974 502602 MA 802 18 13.6 459 9 AI180916
730 18 13.6 449 14 BQ674882 BQ674882 AGENCOURT 803 18 13.6 459 9 AI679377
731 18 13.6 449 14 W08781 W08781 MB51E12.R1 804 18 13.6 459 9 AA409574
732 18 13.6 449 14 W09113 W09113 MA70C04.R1 805 18 13.6 459 12 BF526927
733 18 13.6 450 9 AA869790 AA869790 VQ15H03.I 806 18 13.6 459 12 BF726605
734 18 13.6 450 9 AA881962 AA881962 VX30H08.I 807 18 13.6 459 12 BG059103
735 18 13.6 450 9 AI000052 AI000052 OS50A03.S 808 18 13.6 459 12 BG113182
736 18 13.6 450 9 AI081185 AI081185 OR32D11.X 809 18 13.6 459 12 BE904152

AA148023 ZO48D12.I
AA186647 ZP64G03.I
AA557805 N162G09.S
BE613621 601504410
BM88223 TMM137 HU
BQ717613 AGENCOURT
AA574701 VM31D09.I
BG253383 602362987
BG961429 MR4-CT053
BM089275 502986 MA
W04856 ZAT5A12.R1
AA793069 VP21C12.I
AI679886 TU67A08.X
AA480527 NE63B09.S
AA989988 UF31G08.Y
BF614970 QD80C03.X
BM431924 LJEJ14B5
BQ044342 UI-M-EF0-
C88595 C88595 Mous
BM117611 L0853H05-
BM431970 LJEJ14G2
BM970898 UI-CF-EC1
BQ220112 AGENCOURT
AA675430 V101C07.I
AI103001 EST121290
AA624249 VM98E10.I
BG687948 335289 BA
BQ050657 AGENCOURT
AA869073 VQ30D08.I
AI049606 AN38B03.X
AI254343 QUS5B10.X
AA129780 ZN51A04.I
AA624360 VM02E02.I
AV762708 AV762708
AW082906 XC04C01.X
AW619290 652 MARC
AW917430 EST348734
BE113191 UI-R-BJ1-
BE908679 601499520
BE967731 601648704
BM763917 K-EST0045
BQ600351 MI-P-E7-a
AA659067 NU81D01.S
AA437971 VE32H08.I
AA662449 AV662449
AW619874 7954 MARC
BF339067 602034860
BM542700 AGENCOURT
BM766933 K-EST0048
BQ085873 I11B07.Y
W29255 MC18G02.R1
W29917 MC08C04.R1
AA65306 NT88G03.S
AA538207 VJ56H08.I
AA663920 AV663920
BG150602 NA132C09
BG778264 602666852
B1521153 603081565
B1838135 603083637
BM818373 K-EST0085
BQ234689 HD48G02.G
AA822935 VP30F10.I
AA124939 QX04E11.X
AA606682 VM93G02.I
BG506360 601860425
AI180916 UB77C03.I
AI679377 TU67A08.X
AA409574 EST01315
BF526927 602070201
BF726605 BY09B10.Y
BG059103 NAH45B12
BG113182 602283853
BE904152 601494365

c 810	18	13.6	459	13	BI281171	BI281171	UI-R-CTOS	c 883	18	13.6	469	14	BM994578	UI-H-DH0-
811	18	13.6	459	14	BQ668952	BQ668952	AGENCYCOURT	884	18	13.6	469	14	BQ050650	AGENCYCOURT
812	18	13.6	459	14	BQ669786	BQ669786	AGENCYCOURT	885	18	13.6	470	14	BM840001	K-EST0116
c 813	18	13.6	460	9	AI057027	OY75D02.x		886	18	13.6	470	14	BM842129	K-EST0119
c 814	18	13.6	460	9	AI057027	OY75D02.x		887	18	13.6	470	14	BM842129	K-EST0119
815	18	13.6	460	12	BQ807231	WY71C02.x		c 888	18	13.6	470	14	BQ222029	AGENCYCOURT
816	18	13.6	460	12	BQ807231	WY71C02.x		888	18	13.6	470	14	BQ222029	AGENCYCOURT
817	18	13.6	460	14	BM062524	BM062524	AGENCYCOURT	c 889	18	13.6	471	9	AA420669	nc62d06.s
818	18	13.6	460	14	BM062524	BM062524	AGENCYCOURT	c 890	18	13.6	471	9	AA420669	nc62d06.s
c 819	18	13.6	461	9	AI024383	OY52A10.x		891	18	13.6	471	9	AA420669	nc62d06.s
c 820	18	13.6	461	9	AI024383	OY52A10.x		c 892	18	13.6	471	10	AV591224	AV591224
821	18	13.6	461	9	AA510551	AA510551	AGENCYCOURT	c 893	18	13.6	471	10	AV591224	AV591224
822	18	13.6	461	10	AW913388	AW913388	AGENCYCOURT	894	18	13.6	471	10	AV591224	AV591224
823	18	13.6	461	10	BF012437	UX56C09.y		895	18	13.6	472	10	BE262403	BE262403
824	18	13.6	461	14	BM739041	K-EST0008		896	18	13.6	472	14	BM840163	K-EST0117
825	18	13.6	461	14	BM739041	K-EST0008		c 897	18	13.6	472	14	BM916572	AGENCYCOURT
826	18	13.6	461	14	BM739041	K-EST0008		c 898	18	13.6	472	14	BM916572	AGENCYCOURT
827	18	13.6	461	14	BM739041	K-EST0008		c 899	18	13.6	472	14	BM916572	AGENCYCOURT
828	18	13.6	461	14	BM739041	K-EST0008		900	18	13.6	473	14	BQ044034	UI-M-EFO-
829	18	13.6	461	14	BM739041	K-EST0008		901	18	13.6	473	14	BQ044034	UI-M-EFO-
830	18	13.6	463	9	AA684524	AA684524	AGENCYCOURT	902	18	13.6	473	14	BQ044034	UI-M-EFO-
831	18	13.6	463	9	AA684524	AA684524	AGENCYCOURT	903	18	13.6	473	14	BQ044034	UI-M-EFO-
832	18	13.6	463	9	AA684524	AA684524	AGENCYCOURT	904	18	13.6	473	14	BQ044034	UI-M-EFO-
c 833	18	13.6	463	10	AW664772	AW664772		905	18	13.6	473	14	BQ044034	UI-M-EFO-
c 834	18	13.6	463	10	AW664772	AW664772		906	18	13.6	473	14	BQ044034	UI-M-EFO-
c 835	18	13.6	463	10	AW664772	AW664772		c 907	18	13.6	473	14	BQ044034	UI-M-EFO-
c 836	18	13.6	463	10	AW664772	AW664772		908	18	13.6	473	14	BQ044034	UI-M-EFO-
c 837	18	13.6	463	10	AW664772	AW664772		c 909	18	13.6	473	14	BQ044034	UI-M-EFO-
c 838	18	13.6	463	10	AW664772	AW664772		910	18	13.6	473	14	BQ044034	UI-M-EFO-
c 839	18	13.6	463	10	AW664772	AW664772		911	18	13.6	473	14	BQ044034	UI-M-EFO-
840	18	13.6	464	9	AA207582	AA207582	AGENCYCOURT	c 912	18	13.6	473	14	BQ044034	UI-M-EFO-
841	18	13.6	464	9	AA207582	AA207582	AGENCYCOURT	913	18	13.6	473	14	BQ044034	UI-M-EFO-
842	18	13.6	464	9	AA207582	AA207582	AGENCYCOURT	914	18	13.6	473	14	BQ044034	UI-M-EFO-
843	18	13.6	464	9	AA207582	AA207582	AGENCYCOURT	915	18	13.6	473	14	BQ044034	UI-M-EFO-
c 844	18	13.6	464	12	BG252807	BG252807	AGENCYCOURT	c 916	18	13.6	473	14	BQ044034	UI-M-EFO-
c 845	18	13.6	464	12	BG252807	BG252807	AGENCYCOURT	917	18	13.6	473	14	BQ044034	UI-M-EFO-
846	18	13.6	464	12	BG252807	BG252807	AGENCYCOURT	918	18	13.6	473	14	BQ044034	UI-M-EFO-
847	18	13.6	464	12	BG252807	BG252807	AGENCYCOURT	919	18	13.6	473	14	BQ044034	UI-M-EFO-
848	18	13.6	464	12	BG252807	BG252807	AGENCYCOURT	920	18	13.6	473	14	BQ044034	UI-M-EFO-
c 849	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	c 921	18	13.6	473	14	BQ044034	UI-M-EFO-
c 850	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	922	18	13.6	473	14	BQ044034	UI-M-EFO-
c 851	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	c 923	18	13.6	473	14	BQ044034	UI-M-EFO-
c 852	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	924	18	13.6	473	14	BQ044034	UI-M-EFO-
c 853	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	c 925	18	13.6	473	14	BQ044034	UI-M-EFO-
c 854	18	13.6	465	9	AI012423	AI012423	AGENCYCOURT	926	18	13.6	473	14	BQ044034	UI-M-EFO-
855	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 927	18	13.6	473	14	BQ044034	UI-M-EFO-
856	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	928	18	13.6	473	14	BQ044034	UI-M-EFO-
857	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	929	18	13.6	473	14	BQ044034	UI-M-EFO-
858	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	930	18	13.6	473	14	BQ044034	UI-M-EFO-
c 859	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	931	18	13.6	473	14	BQ044034	UI-M-EFO-
c 860	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	932	18	13.6	473	14	BQ044034	UI-M-EFO-
861	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	933	18	13.6	473	14	BQ044034	UI-M-EFO-
862	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	934	18	13.6	473	14	BQ044034	UI-M-EFO-
863	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 935	18	13.6	473	14	BQ044034	UI-M-EFO-
864	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 936	18	13.6	473	14	BQ044034	UI-M-EFO-
865	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 937	18	13.6	473	14	BQ044034	UI-M-EFO-
866	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	938	18	13.6	473	14	BQ044034	UI-M-EFO-
867	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	939	18	13.6	473	14	BQ044034	UI-M-EFO-
868	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	940	18	13.6	473	14	BQ044034	UI-M-EFO-
c 869	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	941	18	13.6	473	14	BQ044034	UI-M-EFO-
c 870	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 942	18	13.6	473	14	BQ044034	UI-M-EFO-
871	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	943	18	13.6	473	14	BQ044034	UI-M-EFO-
872	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	944	18	13.6	473	14	BQ044034	UI-M-EFO-
873	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	945	18	13.6	473	14	BQ044034	UI-M-EFO-
874	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	946	18	13.6	473	14	BQ044034	UI-M-EFO-
875	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	947	18	13.6	473	14	BQ044034	UI-M-EFO-
876	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	948	18	13.6	473	14	BQ044034	UI-M-EFO-
877	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	949	18	13.6	473	14	BQ044034	UI-M-EFO-
878	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	950	18	13.6	473	14	BQ044034	UI-M-EFO-
c 879	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 951	18	13.6	473	14	BQ044034	UI-M-EFO-
c 880	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	952	18	13.6	473	14	BQ044034	UI-M-EFO-
881	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 953	18	13.6	473	14	BQ044034	UI-M-EFO-
c 882	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	954	18	13.6	473	14	BQ044034	UI-M-EFO-
	18	13.6	466	13	BM432631	BM432631	AGENCYCOURT	c 955	18	13.6	473	14	BQ044034	UI-M-EFO-

956 18 13.6 485 14 BM904542
 957 18 13.6 486 12 BG029162
 958 18 13.6 486 14 BG025833
 959 18 13.6 486 14 BQ044617
 960 18 13.6 486 14 BQ276900
 961 18 13.6 487 9 AA924288
 962 18 13.6 487 10 BE135516
 963 18 13.6 487 13 BM552487
 964 18 13.6 487 14 BQ015863
 965 18 13.6 487 14 BQ214887
 966 18 13.6 487 14 BQ688840
 967 18 13.6 488 13 BI911020
 968 18 13.6 488 14 BM920153
 969 18 13.6 488 14 BQ044277
 970 18 13.6 489 13 BI907023
 971 18 13.6 489 14 BQ043931
 972 18 13.6 490 12 BF392651
 973 18 13.6 491 9 AV133286
 974 18 13.6 491 14 BQ044155
 975 18 13.6 492 13 BI561941
 976 18 13.6 493 12 BF652397
 977 18 13.6 493 12 BG715095
 978 18 13.6 493 12 BG777915
 979 18 13.6 493 13 BI602996
 980 18 13.6 493 14 BM905815
 981 18 13.6 494 13 BI494623
 982 18 13.6 494 14 BM951454
 983 18 13.6 495 10 AV758795
 984 18 13.6 495 12 BF977790
 985 18 13.6 495 12 BG705343
 986 18 13.6 495 12 BG715004
 987 18 13.6 495 12 BF185700
 988 18 13.6 495 13 BI597542
 989 18 13.6 495 14 BM990169
 990 18 13.6 495 14 BM997291
 991 18 13.6 495 14 BQ434624
 992 18 13.6 496 9 AI386131
 993 18 13.6 496 12 BF436663
 994 18 13.6 496 12 BF688118
 995 18 13.6 496 13 BI602447
 996 18 13.6 496 13 BI669025
 997 18 13.6 496 14 BM989712
 998 18 13.6 497 10 BE368357
 999 18 13.6 497 12 BF439312
 1000 18 13.6 497 12 BG713987

ALIGNMENTS

RESULT 1
 AW620090 374 bp mRNA linear EST 24-MAR-2000
 LOCUS 852 MARC PBE Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION AW620090
 ACCESSION AW620090
 VERSION AW620090.1 GI:7326274
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 374)
 Smith, T.P.D., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad
 , C.E. and Keeler, J.W.
 Mapping of expressed sequence tags from a porcine early embryonic
 cDNA library
 Anim. Genet. 32 (2), 66-72 (2001)
 21314990
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

BM904542 AGENCOURT
 BG029162 602295257
 BM925833 AGENCOURT
 BQ044617 UI-M-EFO-
 BQ276900 AGENCOURT
 AA924288 UI-R-AI-d
 BE135516 uq52a06.Y
 BM552487 AGENCOURT
 BQ015863 UI-H-DTI-
 BQ214887 AGENCOURT
 BQ688840 AGENCOURT
 BI911020 603068742
 BM920153 AGENCOURT
 BQ044277 UI-M-EFO-
 BI907023 603064979
 BQ043931 UI-M-EFO-
 BF392651 UI-R-CAO-
 AV133286 AV133286
 BQ044155 UI-M-EFO-
 BI561941 603254859
 BF652397 275944 NA
 BG715095 602676033
 BG777915 60265666
 BI602996 603251201
 BM905815 AGENCOURT
 BI494623 dfl11f09.
 BM951454 UI-M-EFO-
 AV758795 AV758795
 BF977790 602148622
 BG705343 602687862
 BG715004 602673209
 BF185700 601817273
 BI597542 603247071
 BM990169 UI-H-DHO-
 BM997291 UI-H-DHO-
 BQ434624 AGENCOURT
 AI386131 mq37c10.Y
 BF436663 7p15h09.x
 BF688118 602067344
 BI602447 603252238
 BI669025 603295120
 BM989712 UI-H-DHO-
 BE368357 601220724
 BF439312 nab62g08.
 BG713987 602674389

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt. trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: GGAACAGCTATGACCATG
 BACKWARD: GTAAACGACGGCCAGT
 Seq primer: AATTAACCTCACTAAAGG.
 Location/Qualifiers
 1..374
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC PBE"
 /tissue_type="Day 12 whole embryos"
 /lab_host="XL0LR"
 /note="Vector: pBLUESCRIPT SK-; Site.1: EcoRI; Site.2:
 XhoI; Library made from pool of embryos in spherical and
 filamentous stages of development (7.5% and 92.5%, et al,
 respectively, of each stage) as described in Choi et al,
 Endocrinology 137, 1457-67, 1996."
 BASE COUNT 112 a 86 c 118 g 58 t
 ORIGIN
 Query Match 18.9%; Score 25; DB 10; Length 374;
 Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;
 QY 33 CAGCTTGGATAAGGCCAAGCTGAAG 57
 |||||
 DB 98 CAGCTTGGATAAGGCCAAGCTGAAG 122
 |||||
 RESULT 2
 BG410966 382 bp mRNA linear EST 13-MAR-2001
 LOCUS EML_28_B04_g1_A002 Embryo 1 (EML) Sorghum bicolor cDNA, mRNA
 DEFINITION
 BG410966
 SEQUENCE
 BG410966
 EST.
 KEYWORDS
 SOURCE sorghum.
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 382)
 Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
 An EST database from Sorghum: developing embryos
 Unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: PolyTMix
 High quality sequence start: 75
 High quality sequence stop: 379
 POLYA=Yes.
 Location/Qualifiers
 1..382
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Embryo 1 (EML)"
 /note="Organ: Embryos germinated for 24 hr; Vector:
 pBluescript II from Lambda Zap II; Site.1: XhoI; Site.2:
 EcoRI; The library was made from poly-A RNA in the cloning
 vector lambda Zap II. Clones to be sequenced were
 prepared by mass excision."

BASE COUNT 133 a 77 c 94 g 78 t
 ORIGIN

Query Match 15.9%; Score 21; DB 12; Length 382;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GACCTGGAGAAATGCCAGC 36
 |||||
 Db 227 GACCTGGAGAAATGCCAGC 247

RESULT 3

BMI25588/c

LOCUS

DEFINITION 418 bp mRNA linear EST 12-MAR-2002
 id76b07.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
 P13472 THYMOSIN BETA-10. ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 418)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
 , M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
 Jackson, Y., and Bowers, Y.

TITLE

JOURNAL

COMMENT

Endocrine Pancreas Consortium
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)

MGI:1955282 This sequence now available from the IMAGE consortium,
 for clone orders contact: info@image.llnl.gov
 High quality sequence stop: 66.

FEATURES

source

1. .418

Location/Qualifiers

/organism="Mus musculus"

/strain="ICR"

/db_xref="taxon:10090"

/clone="IMAGE:5668956"

/clone_lib="Melton Normalized Mixed Mouse Pancreas 1

N1-MMS1"

/sex="Both for embryonic and newborn, male for adult and

adult islet"

/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,

adult, mixed"

/lab_host="DH10B"

/note="Vector: pSPORT1; Site.1: Not I; Site.2: Sal I; Five
 libraries representing E10.5/12.5 pancreatic bud, E16.5
 pancreas, newborn pancreas, adult pancreas, and adult
 islets of Langerhans were separately constructed using
 Superscript Plasmid Library kit (Life Technologies). cDNA
 was made by oligo-dT priming and size-selected by column
 fractionation. Libraries were amplified once on solid
 support and plasmid DNA from each library was prepared
 and mixed in equal amounts. The mixed library DNA was
 normalized by method #4 from Bonaldo, Lennon, and Soares
 1996 Genome Research 6:791-806; 0.5 microgram

single-stranded mixed library plasmid DNA was mixed with
 5 micrograms PCR product representing mixed library
 inserts and hybridized to an EcoT of 6. Single-stranded
 (unhybridized) plasmids were isolated by hydroxyapatite
 chromatography and used to make this library."

BASE COUNT 68 a 98 c 116 g 133 t
 ORIGIN

Query Match 15.9%; Score 21; DB 13; Length 418;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TTGGATAAGCCCAAGCTGAAG 57

|||||

Db 385 TTGGATAAGCCCAAGCTGAAG 365

RESULT 4

AZ098162

LOCUS

DEFINITION 608 bp DNA linear GSS 09-MAY-2001
 RPCI-23-15E12-TV RPCI-23 Mus musculus genomic clone RPCI-23-15E12,
 DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 608)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.

TITLE

JOURNAL

COMMENT

Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-15E12.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (inforesgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 15 row: E column: 12
 Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .608

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-15E12"

/clone_lib="RPCI-23"

/sex="Female"

/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site.1:
 EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT

ORIGIN

198 a 97 c 143 g 170 t

Query Match

Best Local Similarity

15.2%; Score 20; DB 17; Length 608;

100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 GAGACCACAGCAGGAGAA 113
|||||
Db 201 GAGACCACAGCAGGAGAA 220

AG012646 732 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f50C10X10, genomic
survey sequence.

AG012646
AG012646 1 GI:3419975
GSS.
Homo sapiens DNA, clone:f50C10X10.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
1 (bases 1 to 732)
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1998)

JOURNAL
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
2 (bases 1 to 732)
Direct Submission
Submitted (15-AUG-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgsc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
source
1..732
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="f50C10X10"
BASE COUNT 141 a 162 c 200 g 224 t 5 others
ORIGIN

Query Match 15.2%; Score 20; DB 17; Length 732;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 AATGCCAGCTTGGATAAGG 46
|||||
Db 71 AATGCCAGCTTGGATAAGG 90

BI524256 997 bp mRNA linear EST 29-AUG-2001
603052058R1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201607 3',
mRNA sequence.

BI524256
BI524256 1 GI:15349048
EST.
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaphs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

BASE COUNT 63 a 44 c 60 g 31 t
ORIGIN

Query Match 14.4%; Score 19; DB 14; Length 198;

http://image.llnl.gov
Plate: LLAM11505 row: c column: 16
High quality sequence stop: 68.

FEATURES
source
1..997
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5201607"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC library."

BASE COUNT 381 a 213 c 207 g 196 t
ORIGIN

Query Match 15.2%; Score 20; DB 13; Length 997;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 AGAGACCACAGCAGGAGAGA 112
|||||
Db 629 AGAGACCACAGCAGGAGAGA 648

RESULT 7
N88692
LOCUS
DEFINITION
K5134F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone K5134 5' similar to THYMOSIN BETA-10, mRNA sequence.

ACCESSION
N88692
VERSION
N88692.1 GI:1442022
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 198)
Liaw, C.C.
cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 617/7328915
Fax: 617/9750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GAAATTAACCTCTACTAAAGG.

FEATURES
source
1..198
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="K5134"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

BASE COUNT 63 a 44 c 60 g 31 t
ORIGIN

Query Match 14.4%; Score 19; DB 14; Length 198;

Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCAAGCTGAAGG 58
|||||
Db 87 GATAGGCCAAGCTGAAGG 105

RESULT 8

BF800160/c

LOCUS

BF800160 203 bp mRNA linear EST 12-JAN-2001

PM0-C10046-181000-001-H07 C10046 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF800160

VERSION

BF800160.1 GI:12129149

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&st2=PM0-C10046-

181000-001-H07&ts=2000-10-18&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 203.

Location/Qualifiers

1..203

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="C10046"

/dev_stage="Adult"

/note="Organ: colon; ins: Vector: puc18; Site: 1; SmaI;

Site: 2; SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT

39 a 57 c 68 g 39 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 27;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AAGAGACCACAGCAGGAGGA 110

|||||

Db 66 AAGAGACCACAGCAGGAGGA 48

|||||

RESULT 9

Az808724

LOCUS

354 bp DNA linear GSS 20-FEB-2001

Az808724

Query Match

Best Local Similarity 100.0%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61

|||||

Db 113 AAGGCCAAGCTGAAGGCCA 131

|||||

RESULT 10

Az250549/c

LOCUS

509 bp DNA linear GSS 15-JUN-2000

Az250549

Query Match

Best Local Similarity 100.0%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61

|||||

Db 113 AAGGCCAAGCTGAAGGCCA 131

|||||

DEFINITION

2M0072G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0072G24 F, DNA sequence.

ACCESSION

AZ808724

VERSION

AZ808724.1 GI:12974345

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

High quality sequence stop: 354.

Insert Length: 10000

Plate: 0072

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 354.

Location/Qualifiers

1..354

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0072G24"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT

104 a 71 c 62 g 117 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61

|||||

Db 113 AAGGCCAAGCTGAAGGCCA 131

|||||

RESULT 10

Az250549/c

LOCUS

509 bp DNA linear GSS 15-JUN-2000

Az250549

Query Match

Best Local Similarity 100.0%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61

|||||

Db 113 AAGGCCAAGCTGAAGGCCA 131

|||||

```

DEFINITION  RPCI-23-18017.TJB RPCI-23 Mus musculus genomic clone RPCI-23-18017,
DNA sequence.
ACCESSION   A2250549
VERSION     A2250549.1 GI:8563752
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 509)
AUTHORS     Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,
            B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
TITLE       Mouse BAC End Sequences from Library RPCI-23
JOURNAL     Unpublished (1999)
COMMENT     Other GSSs: RPCI-23-18017.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tldb/bac\_ends/mouse/bac\_end\_intro.html
            Plate: 18 row: 0 column: 17
            Seq primer: SP6
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..509
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-18017"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested
                     with a combination of EcoRI and EcoRI Methylase. Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI sites. The ligation products were transformed into
                     DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  164 a 92 c 110 g 143 t
ORIGIN
Query Match      14.4%; Score 19; DB 17; Length 509;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  43 AAGGCCAAGCTGAAGGCCA 61
    |||||||
Db  202 AAGGCCAAGCTGAAGGCCA 184

RESULT 11
BJ084935/c
LOCUS      BJ084935
DEFINITION BJ084935 NIBB Mochii normalized xenopus tailbud library Xenopus
            laevis cDNA clone XL102a03 3', mRNA sequence.
ACCESSION   BJ084935
VERSION     BJ084935.1 GI:17580703
KEYWORDS    EST.
SOURCE      African clawed frog.
ORGANISM    Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
            Xenopodinae; Xenopus.

REFERENCE   1 (bases 1 to 530)
AUTHORS     Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            Y.
TITLE       Expressed genes in X. laevis embryo
JOURNAL     Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
     source           1..530
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XL102a03"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /note="vector: pBSRM3; Site_1: NotI; Site_2: EcoRI; cDNAs
                     were oligo-dT primed and directionally cloned. Staging
                     according to Nieuwkoop and Faber. Library is subtracted
                     and was constructed by N. Garrett and A.M. Zorn,
                     (Wellcome/CRC Institute)."

BASE COUNT  137 a 101 c 98 g 194 t
ORIGIN
Query Match      14.4%; Score 19; DB 13; Length 530;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  39 GGATAGGCCCAAGCTGAAG 57
    |||||||
Db  530 GGATAGGCCCAAGCTGAAG 512

RESULT 12
AZ769784/c
LOCUS      AZ769784
DEFINITION 1M0570M13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0570M13 R, DNA sequence.
ACCESSION   AZ769784
VERSION     AZ769784.1 GI:12890286
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 629)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0570 row: M column: 13
            Seq primer: CACACGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 629.
            Location/Qualifiers
     source           1..629

```


/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0570M13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gll4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 186 a 131 c 134 g 178 t
 ORIGIN

Query Match 14.4%; Score 19; DB 17; Length 629;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCCA 61
 |||||
 Db 582 AAGGCCAAGCTGAAGGCCA 564

RESULT 13
 BQ803203
 LOCUS
 DEFINITION WHE2834_H05_O10ZS Triticum monococcum vernalized apex cDNA library
 Triticum monococcum cDNA clone WHE2834_H05_O10, mRNA sequence.
 BQ803203
 BQ803203.1 GI:22018172
 EST.
 SOURCE Triticum monococcum.
 ORGANISM Triticum monococcum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
 REFERENCE 1 (bases 1 to 655)
 AUTHORS Anderson, O.D., Chao, S., Crossman, C., Dubcovsky, J., Echenique, V., Lazo, G.R., Pham, J., Rausch, C.J., Stamova, B., Wilson, C. and Woo, J.
 TITLE The structure and function of the expressed portion of the wheat genomes - Vernalized apex cDNA library from Triticum monococcum Unpublished (2002)
 JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: candersn@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
 Seq primer: SK primer.
 Location/Qualifiers
 1. .655
 /organism="Triticum monococcum"
 /cultivar="G3116"
 /db_xref="taxon:4568"
 /clone="WHE2834_H05_O10"

/clone_lib="Triticum monococcum vernalized apex cDNA library"
 /tissue_type="vernalized apex"
 /dev_stage="One month old plants"
 /lab_host="E. coli XL0LR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; One-month old plants were subjected to vernalization treatment by placing them in the cold room at 6 C, under 15hr light/9hr dark condition. Total RNA was prepared from apex tissue extracted from plants with no cold treatment; and from plants with 2-week, 4-week and 6-week cold treatment separately. Equal amount of total RNA was pooled from all four samples, a cDNA library was made using pooled polyA RNA and CDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova, J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 159 a 154 c 178 g 164 t
 ORIGIN

Query Match 14.4%; Score 19; DB 14; Length 655;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CTGATGACCAAGAGACCA 100
 |||||
 Db 535 CTGATGACCAAGAGACCA 553

RESULT 14
 BF317304
 LOCUS
 DEFINITION 601904069F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136561 5', mRNA sequence.
 BF317304
 BF317304.1 GI:11265629
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 678)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapps-f@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCMI042 row: j column: 18
 High quality sequence stop: 651.
 Location/Qualifiers
 1. .678
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4136561"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 120 a 178 c 255 g 125 t

ORIGIN

Query Match 14.4%; Score 19; DB 12; Length 678;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 GAGACCACAGCAGGAGAGA 112
 |||||
 Db 611 GAGACCACAGCAGGAGAGA 629

RESULT 15

BE882559/c
 LOCUS BE882559 724 bp mRNA linear EST 20-OCT-2000
 DEFINITION G01507007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908904 5',
 mRNA sequence.

ACCESSION BE882559
 VERSION BE882559.1 GI:10331335
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 724)
 TITLE NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone Sequencing by: Incyte Genomics, Inc.
 DNA Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1AM9721 row: m column: 01
 High quality sequence stop: 716.

FEATURES

source

1..724
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3908904"
 /clone_lib="NIH_MGC_71"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: NotI;
 Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb."
 176 a 180 c 228 g 140 t

BASE COUNT

ORIGIN

Query Match 14.4%; Score 19; DB 12; Length 724;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 AGCTGAAGGCCACAGAGAT 68
 |||||
 Db 606 AGCTGAAGGCCACAGAGAT 588

RESULT 16

CNS052GR/c
 LOCUS CNS052GR 1058 bp DNA linear GSS 26-JUL-2000
 DEFINITION Tetraodon nigroviridis genome survey sequence SP6 end of clone
 036F09 of library B from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION AL318132
 VERSION AL318132.1 GI:9551016
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

1 (bases 1 to 1058)
 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetraodon nigroviridis DNA sequence

TITLE

JOURNAL

MEDLINE

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

PUBMED

BACKWARD: 5' CCAGTGAATGTAAACGACCTACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCTCCTAAAGG 3'.

FEATURES

Location/Qualifiers
1..135

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

BASE COUNT 42 a 30 c 44 g 19 t

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

Db 99 GATAGGCCCAAGCTGAAG 116

RESULT 18

AA6233585

LOCUS

DEFINITION vn73d02.r1 Knowles Solter mouse blastocyst B1 Mus musculus CDNA clone IMAGE:1037571 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN); mRNA sequence.

ACCESSION

AA6233585

VERSION

AA6233585.1 GI:2527461

KEYWORDS

EST.

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 144)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:577595

Trace considered overall poor quality

High quality sequence stop: 1.

Location/Qualifiers

1..144

/organism="Mus musculus"

/strain="C57BL/6J x DBA/2J F1"

/db_xref="taxon:10090"

/clone="IMAGE:1037571"

/clone_lib="Knowles Solter mouse blastocyst B1"

/tissue_type="blastocyst"

/dev_stage="embryo (pre-implantation)"

/lab_host="DH10B"

/note="Organ: embryo; Vector: pSPORT; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally from mRNA prepared

from 800 blastocysts. Primer: SalI(dT):

5'-CGGTCACCGTCGACCGCTTTT-3'. cDNAs were

BASE COUNT

56 a 29 c 40 g 19 t

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 144;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

Db 49 GATAGGCCCAAGCTGAAG 66

RESULT 19

AA156792

LOCUS

DEFINITION ue54f03.r1 Soares_mammary_gland_NLMG Mus musculus cDNA clone IMAGE:1494941 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN); mRNA sequence.

AA156792

AA156792.1 GI:3685261

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 154)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:932545

Trace considered overall poor quality

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..154

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:1494941"

/clone_lib="Soares_mammary_gland_NLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="Vector: pT73p-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT73 vector. Library is normalized. Library

was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 60 a 33 c 42 g 19 t

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 154;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
 D76516
 Db 43 GATAAGGCCAAGCTGAAG 60

RESULT 20

AA967821 157 bp mRNA linear EST 19-MAY-1998
 LOCUS un05f03.r1 Soares mouse hypothalamus NMHY Mus musculus cDNA clone
 DEFINITION IMAGE:1617053 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);,
 mRNA sequence.

ACCESSION

AA967821 GI:3141714

VERSION

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1. (bases 1 to 157)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:956353

Trace considered overall poor quality

Seq primer: -28ml3 rev2 Et from Amersham

High quality sequence stop: 1.

FEATURES

source

1. 157

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:1617053"

/clone_lib="Soares mouse hypothalamus NMHY"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCAAGGTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Wolfgang Liedtke. Library went through
 two rounds of normalization, and was constructed by Bento
 Soares and M.Fatima Bonaldo."

63 a 33 c 43 g 18 t

Query Match 13.6%; Score 18; DB 9; Length 157;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

40 GATAAGGCCAAGCTGAAG 57

D76516

Db 46 GATAAGGCCAAGCTGAAG 63

RESULT 21

D76516 157 bp mRNA linear EST 07-OCT-1996
 LOCUS MUS70C08 mouse embryonal carcinoma cell line F9 Mus musculus cDNA
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

clone 70C08, mRNA sequence.

D76516 GI:1596294

EST.

house mouse.

REFERENCE

1 (bases 1 to 157)

AUTHORS

Nishiguchi,S., Sakuma,R., Nomura,M., Zou,Z., Jearanaisilavong,J.,
 Joh,T., Yasunaga,T. and Shimada,K.

TITLE

A catalogue of genes in mouse embryonal carcinoma F9 cells

identified with expressed sequence tags

J. Biochem. 119 (4), 749-767 (1996)

JOURNAL

96337530

MEDLINE

Contact: Kazunori Shimada

Department of Medical Genetics, Division of Molecular Biomedicine

Research Institute for Microbial Diseases, Osaka University

3-1, Yamadaoka, Suita, Osaka, 565, Japan

Tel: 06-879-8325

Fax: 06-879-8326.

FEATURES

source

1. 157

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="70C08"

/clone_lib="mouse embryonal carcinoma cell line F9"

/note="Vector: Uni-Zap XR; Site.1: EcoR I; Site.2: Xho I;

mRNA was purified from 14.7 hybrid MN cells and used to

construct a size- selected unidirectional cDNA library in

Uni-Zap XR vector."

55 a 38 c 46 g 15 t 3 others

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 14; Length 157;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

D76516

Db 90 GATAAGGCCAAGCTGAAG 107

RESULT 22

AA792584

LOCUS

DEFINITION

VS88e04.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone

IMAGE:1153374 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);,

mRNA sequence.

AA792584

VERSION

AA792584.1 GI:2855539

EST.

KEYWORDS

house mouse.

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 158)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.


```

RESULT 27
AA220778
LOCUS
DEFINITION
  AA220778 162 bp mRNA linear EST 10-FEB-1997
  mv9c04.r1 Soares mouse 3NME12.5 Mus musculus cDNA clone
  IMAGE:660294 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);,
  mRNA sequence.
ACCESSION
VERSION
  AA220778
KEYWORDS
  EST.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 162)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of MedicineP
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:406142
  Trace considered overall poor quality
  Seq primer: -28ml3 rev2 ET from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..162
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="IMAGE:660294"
    /clone_lib="Soares mouse 3NME12 5"
    /sex="unknown"
    /tissue_type="fetus"
    /dev_stage="12.5dpc total fetus"
    /lab_host="PH108"
    /note="Organ: whole fetus; Vector: pT73D-Pac (Pharmacia)
    with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
    1st strand cDNA was primed with a Not I - oligo(dT) primer
    [5' TGTTACCAATCTGAAGTGGAGCGCGCTTATTTTATTTTATTTT
    3'], on total mouse RNA [provided by Minoru Ko, Wayne
    State Univ.]; double-stranded cDNA was ligated to Eco RI
    adaptors (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of the modified pT73 vector.
    Library went through one round of normalization, and was
    constructed by Bento Soares and M. Fatima Bonaldo."
  BASE COUNT 63 a 34 c 45 g 20 t
  ORIGIN
    Query Match 13.6%; Score 18; DB 9; Length 162;
    Best Local Similarity 100.0%; Pred. No. 82;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 40 GATAGGCCCAAGCTGAAG 57
    |||||||
    DB 49 GATAGGCCCAAGCTGAAG 66
    |||||||
  RESULT 28
AA591963
LOCUS
DEFINITION
  AA591963 162 bp mRNA linear EST 16-SEP-1997
  v150b08.r1 Beddington mouse embryonic region Mus musculus cDNA
  IMAGE:907191 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN)
  );, mRNA sequence.
ACCESSION
VERSION
  AA591963
KEYWORDS
  EST.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 162)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of MedicineP
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:527855
  Trace considered overall poor quality
  Seq primer: -28ml3 rev1 ET from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..162
    /organism="Mus musculus"
    /strain="C57BL/6 x DBA"
    /db_xref="taxon:10090"
    /clone="IMAGE:907191"
    /clone_lib="Beddington mouse embryonic region"
    /sex="pooled"
    /tissue_type="embryo"
    /dev_stage="7.5dpc"
    /lab_host="DH12S"
    /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
    SalI; Site_2: NotI; Cloned unidirectionally. Primer:
    Oligo dT. Gastrulating embryos were collected at 7.5dpc
    from C57BL6 x DBA matings, excluding embryos that had
    developed head folds and all extraembryonic tissues.
    Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
    Referenced in Development 121, 2479-2489 (1995)"
  BASE COUNT 65 a 38 c 44 g 15 t
  ORIGIN
    Query Match 13.6%; Score 18; DB 9; Length 162;
    Best Local Similarity 100.0%; Pred. No. 82;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 40 GATAGGCCCAAGCTGAAG 57
    |||||||
    DB 49 GATAGGCCCAAGCTGAAG 66
    |||||||
  RESULT 29
BM843852
LOCUS
DEFINITION
  BM843852 163 bp mRNA linear EST 06-MAR-2002
  K-EST0121847 S12SNU216 Homo sapiens cDNA clone S12SNU216-58-D10 5',
  mRNA sequence.
ACCESSION
VERSION
  BM843852
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 163)

```

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 58 row: D column: 10
High quality sequence stop: 163.
Location/Qualifiers

FEATURES

source

1. .163
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S12SN0216-58-D10"
/clone_lib="S12SN0216"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SMU-216"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT

53 a 34 c 52 g 24 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 83;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

40 GATAAGGCCAAGCTGAAG 57

|||||

Db 119 GATAAGGCCAAGCTGAAG 136

RESULT 30

BM686528

LOCUS

UI-E-CQ0-adn-f-08-0-UI.r1 164 bp mRNA linear EST 28-FEB-2002

DEFINITION

UI-E-CQ0-adn-f-08-0-UI 5', mRNA sequence.

ACCESSION

BM686528

VERSION

BM686528.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 164)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

97044477

COMMENT

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. .164

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-CQ0-adn-f-08-0-UI"

/clone_lib="UI-E-CQ0"

/tissue_type="optic nerve"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-CQ0 is a cDNA library containing the following

tissue(s): optic nerve. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is CCATTAAGTG. This library

was created for the program, Gene Discovery in the Visual

System, supported by National Eye Institute (NEI)."

55 a 38 c 52 g 19 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 83;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

40 GATAAGGCCAAGCTGAAG 57

|||||

Db 107 GATAAGGCCAAGCTGAAG 124

RESULT 31

AA144770

LOCUS

DEFINITION

mr68a05.r1 Stratagene mouse testis (#937308) Mus musculus cDNA

clone IMAGE:602576 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN

) ; mRNA sequence.

ACCESSION

AA144770

VERSION

AA144770.1

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 169)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108


```

Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:368008
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 169
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:602576"
/clone_lib="Stratagene mouse testis (#937308)"
/sex="males"
/tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/Note="Organ: testis; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
65 a 41 c 43 g 20 t

BASE COUNT
ORIGIN
Query Match 13.6%; Score 18; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 49 GATAAGGCCAAGCTGAAG 66

RESULT 32
BE774336
LOCUS
DEFINITION 169 bp mRNA linear EST 20-SEP-2000
MRI-UM0009-050600-021-a06 UM0009 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE774336
VERSION BE774336.1 GI:10227991
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsumura,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-mri-UM0009-050
600-021-a06&t3=2000-06-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 169.
Location/Qualifiers
1. 169
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="F2310"
/clone_lib="Fetal heart"
/lab_host="E. coli Y1090"
/Note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
mRNA was purified from human fetal hearts (10-12 weeks).
cDNA was constructed using a NotI-oligo dt adaptor-primer.
SalI adaptors were ligated, followed by digestion with
NotI, for direction cloning into predigested lambda gt22.
Method is described in J. Mol. Cell. Cardiol. (1994) 26,
1329-1333."
55 a 44 c 46 g 24 t 1 others

BASE COUNT
ORIGIN
Query Match 13.6%; Score 18; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAAGGCCAAGCTGAAG 57

```

```

1. 169
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0009"
/dev_stage="Adult"
/Note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
51 a 43 c 48 g 27 t

BASE COUNT
ORIGIN
Query Match 13.6%; Score 18; DB 12; Length 169;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 22 GATAAGGCCAAGCTGAAG 39

RESULT 33
R57257
LOCUS
DEFINITION 170 bp mRNA linear EST 02-MAY-1996
F2310 Fetal heart Homo sapiens cDNA clone F2310 5' end similar to
Thymosin beta-10, mRNA sequence.
ACCESSION R57257
VERSION R57257.1 GI:827315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170)
Hwang,D.M., Fung,Y.W., Wang,R.X., Laurensen,C.M., Ng,S.H., Lam
,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
Analysis of expressed sequence tags from a fetal human heart cDNA
library
Genomics 30 (2), 293-298 (1995)
96163883
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: clliew@rics.bwh.harvard.edu
Seq primer: GTGGCGAGCACTCCTGGAGCC.
Location/Qualifiers
1. 170
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="F2310"
/clone_lib="Fetal heart"
/lab_host="E. coli Y1090"
/Note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
mRNA was purified from human fetal hearts (10-12 weeks).
cDNA was constructed using a NotI-oligo dt adaptor-primer.
SalI adaptors were ligated, followed by digestion with
NotI, for direction cloning into predigested lambda gt22.
Method is described in J. Mol. Cell. Cardiol. (1994) 26,
1329-1333."
55 a 44 c 46 g 24 t 1 others

BASE COUNT
ORIGIN
Query Match 13.6%; Score 18; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAAGGCCAAGCTGAAG 57

```

RESULT 35

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimposeludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR1-UM0009-300
 500-017-e07&t3=2000-05-30&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 179.

FEATURES

Source

1. 179
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UM0009"
 /dev_stage="Adult"
 /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

29 a 47 c 46 g 57 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 12; Length 179;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 148 GATAAGGCCAAGCTGAAG 131

RESULT 39

AA068081

LOCUS

DEFINITION

mm56e02.r1 Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:532442 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. 180
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 180)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:319378
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 50.
 Location/Qualifiers
 1. 180
 /organism="Mus musculus"
 /db_xref="taxon:10090"

FEATURES

source

/clone="IMAGE:532442"
 /clone_lib="Stratagene mouse embryonic carcinoma (#937317)"
 /tissue_type="carcinoma"
 /dev_stage="embryonic"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. P19 cell line. Average insert size: 1.0 kb; Uni-ZAP XR vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

68 a 38 c 52 g 22 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 180;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 69 GATAAGGCCAAGCTGAAG 86

RESULT 40

AW647096

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1994)

Other ESTs: TC84502

Contact: Julie Earle-Hughes

TIGR

The Institute For Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208.

Location/Qualifiers

1. 180

/organism="Mus musculus"

/cultivar="3T3"

/db_xref="taxon:10090"

/clone="R3DAB96"

/clone_lib="R3DA"

/tissue_type="adipose"

/note="Site_1: EcoRI; Site_2: XhoI"

70 a 37 c 49 g 22 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 10; Length 180;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 69 GATAAGGCCAAGCTGAAG 86

RESULT 41

AA666472

LOCUS

DEFINITION

AA666472

181 bp mRNA linear EST 19-NOV-1997

vm48b04.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone

IMAGE:1001455 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);

mRNA sequence.

AA666472
 AA666472.1 GI:2625173

KEYWORDS

EST.
 house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 181)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, I., Lennon, G., Soares, B., Wilson, R. and Waterson, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565671

Seq primer: -28mi3 rev1 ET from Amersham.

FEATURES

source

1..181

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:1001455"

/clone_lib="Stratagene mouse Tcell 937311"

/tissue.type="Tcell"

/dev.stage="M30 CD4+ cells"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: blood; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

20 a 52 c 40 g 69 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 181;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

|||||

Db 103 GATAGGCCCAAGCTGAAG 86

|||||

RESULT 42

AA316715

LOCUS

DEFINITION

EST188545 HCC cell line (metastasis to liver in mouse) II Homo

sapiens cDNA 5' end similar to similar to thymosin beta-10

(GB:S54005), mRNA sequence.

182 bp mRNA linear EST 19-APR-1997

AA316715

ACCESSION

VERSION

KEYWORDS

SOURCE

human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 182)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, W.C., Hedblom, E., Hinkley, P.S.Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Uitterback, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
 Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
 , M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
 Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl.), 3-174 (1995)

96026280

COMMENT

Bioinformatics

Contact: Kerlavage, AR

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/ngi/ngi.html>)

Seq primer: M3 Reverse.

Location/Qualifiers

1..182

/organism="Homo sapiens"

/db_xref="ATCC (inhost):113617"

/db_xref="taxon:9606"

/clone_lib="HCC cell line (metastasis to liver in mouse)

II"

/tissue.type="colon"

/cell_type="KM12SM"

/cell_line="KM12C(HCC)metastasis into mouse (liver)"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 63 a 39 c 53 g 26 t 1 others

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 182;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

|||||

Db 80 GATAGGCCCAAGCTGAAG 97

|||||

RESULT 43

N83763

LOCUS

DEFINITION

clone KK2711 5' similar to THYMOSIN BETA-10, mRNA sequence.

184 bp mRNA linear EST 01-APR-1996

N83763

ACCESSION

VERSION

KEYWORDS

SOURCE

human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 184)

Liew, C.C.

CDNAs from fetal heart (1996)

Unpublished (1996)

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: clliew@rics.bwh.harvard.edu

Seq primer: GAATTAACCTCCTCAAGG.

FEATURES

source

Location/Qualifiers
1. .184
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KK2711"

/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

63 a 38 c 57 g 26 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 94 GATAAGGCCAAGCTGAAG 111

RESULT 44

AW211038

LOCUS

DEFINITION AW211038 187 bp mRNA linear EST 03-DEC-1999
similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);, mRNA sequence.

ACCESSION AW211038.1 GI:6516978

VERSION EST.

KEYWORDS

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 187)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lohar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

MGI:1030265

Seq primer: -40RP from Gibco

High quality sequence stop: 181.

FEATURES

source

Location/Qualifiers
1. .187

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:2649813"

/clone_lib="NCI-CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lohar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999).

68 a 41 c 57 g 21 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 10; Length 187;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 93 GATAAGGCCAAGCTGAAG 110

RESULT 45

AA072898

LOCUS

DEFINITION AA072898 189 bp mRNA linear EST 07-FEB-1997
mm72d12.l1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:533975 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN
);, mRNA sequence.

ACCESSION AA072898.1 GI:1594628

VERSION EST.

KEYWORDS

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 189)

REFERENCE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMNI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMNI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:320911

Trace considered overall poor quality

Seq primer: -28ml3 revl ET from Amersham

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .189

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:533975"

/clone_lib="Stratagene mouse macrophage (#937306)"

/tissue_type="macrophage"

/dev_stage="WEHI-3 cell line"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: blood; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

69 a 44 c 53 g 23 t

BASE COUNT

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 189;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

Db 69 GATAAGGCCAAGCTGAAG 86

RESULT 46

AA087727

LOCUS
DEFINITION AA087727 195 bp mRNA linear EST 23-OCT-1996
m013e09.r1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus
cDNA clone IMAGE:553480 5' similar to gb:S54005 THYMOSIN BETA-10
(HUMAN);, mRNA sequence.

ACCESSION
VERSION AA087727.1 GI:1630936
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 195)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:334272
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 163.
Location/Qualifiers
FEATURES
source 1..195
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:553480"
/clone_lib="Life Tech mouse embryo 10 5dpc 10665016"
/tissue_type="embryo"
/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
/note="Organ: whole embryo; Vector: PCMV-SPORT2; Site_1:
Salt; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 10.5dpc embryos. PCMV-SPORT2 vector."
BASE COUNT 71 a 43 c 57 g 24 t
ORIGIN
Query Match 13.6%; Score 18; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 84 GATAAGGCCAAGCTGAAG 101
|||||
RESULT 47
AA454807
LOCUS 195 bp mRNA linear EST 06-JUN-1997
DEFINITION Zx77f10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:809803 5' similar to gb:S54005 THYMOSIN BETA-10 (HUMAN);,
mRNA sequence.
ACCESSION
VERSION AA454807.1 GI:2177583
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie

T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source 1..195
/organism="Homo sapiens"
/db_xref="GDB:6039563"
/db_xref="taxon:9606"
/clone="IMAGE:809803"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."
BASE COUNT 64 a 45 c 53 g 33 t
ORIGIN
Query Match 13.6%; Score 18; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 73 GATAAGGCCAAGCTGAAG 90
|||||
RESULT 48
AV044717/c
LOCUS 198 bp mRNA linear EST 23-NOV-1999
DEFINITION AV044717 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
1700038G19, mRNA sequence.
ACCESSION
VERSION AV044717.2 GI:4864382
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 198)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigenoto,Y., Shiraki,T., Sogabe,Y., Sugahara
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-resercto.riken.go.jp
Thermotransformation and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

```

Location/Qualifiers
1..198
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1700038G19"
/clone_lib="Mus musculus adult C57BL/6J testis"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/notes="Organ: mammary gland; Vector: p7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTATCAATCTGAAGTGGGCGCGCGAATGCTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
23 a 46 c 50 g 79 t

```

BASE COUNT
ORIGIN

```

Query Match 13.6%; Score 18; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 132 GATAAGGCCAAGCTGAAG 115

```

```

RESULT 49
BE168674/c
LOCUS
DEFINITION QVI-HT0516-070300-095-h01 HT0516 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE168674
VERSION BE168674.1 GI:8631395
KEYWORDS EST.
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 198)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

```

```

TITLE
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV1-HT0516-070>)
300-095-h01st3=2000-03-07st4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 198.
Location/Qualifiers

FEATURES
source

```

1..198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0516"
/dev_stage="Adult"
/notes="Organ: head/neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
31 a 53 c 50 g 64 t

```

BASE COUNT
ORIGIN

```

Query Match 13.6%; Score 18; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 168 GATAAGGCCAAGCTGAAG 151

```

RESULT 50
AA302441

LOCUS

DEFINITION

EST15672 Aorta endothelial cells Homo sapiens cDNA 5' end similar

to similar to thymosin beta-10 (GB:S54005), mRNA sequence.

ACCESSION AA302441

VERSION AA302441.1 GI:1954844

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 201)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Frilichman,J.L., Geoghagen,N.S., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.

,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

Venter,J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

COMMENT Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers

1..201
/organism="Homo sapiens"
/db_xref="ATCC (inhost):114687"
/db_xref="taxon:9606"
/clone_lib="Aorta endothelial cells"
/cell_type="endothelial cell"
/dev_stage="adult"

/note="Organ: aorta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

BASE COUNT 66 a 45 c 57 g 30 t 3 others

ORIGIN

Query Match 13.6%; Score 18; DB 9; Length 201;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

|||||

Db 100 GATAAGGCCAAGCTGAAG 117

Search completed: June 2, 2003, 16:39:10

Job time : 1516 secs

THIS PAGE BLANK (CONT)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 15:41:34 ; Search time 66 seconds
(without alignments)
613.354 Million cell updates/sec

Title: US-09-915-178-1

Perfect score: 132

Sequence: 1 atggcacacaaactagacct.....agtggagtgaatttctctga 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 34415

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Issued_Patents_NA.*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	17	12.9	439	4	US-09-397-787-308
c 2	17	12.9	776	4	US-09-484-970B-82
c 3	17	12.9	2090	2	US-08-445-520B-8
c 4	17	12.9	2090	3	US-08-451-946B-7
c 5	17	12.9	2090	3	US-08-446-938B-7
c 6	17	12.9	2090	3	US-08-311-703A-7
c 7	17	12.9	2090	3	US-08-446-939B-7
c 8	17	12.9	2090	3	US-09-183-543-7
c 9	17	12.9	2090	4	US-08-446-936A-7
c 10	17	12.9	2090	4	US-09-239-864A-10
c 11	17	12.9	2090	5	PCT-US92-09326-3
c 12	17	12.9	2095	1	US-08-361-873A-1
c 13	17	12.9	5057	2	US-08-365-486A-12
c 14	17	12.9	5057	4	US-08-880-342-12
c 15	17	12.9	5108	1	US-07-642-002-1
c 16	16	12.1	220	2	US-08-700-637-9
c 17	16	12.1	1232	4	US-09-392-184-4
c 18	16	12.1	3437	3	US-08-704-711A-9
c 19	16	12.1	3437	4	US-09-521-220-9
c 20	16	12.1	3456	3	US-08-704-711A-8
c 21	16	12.1	3456	4	US-09-521-220-8
c 22	16	12.1	4380	1	US-07-582-945-1
c 23	16	12.1	4380	2	US-08-453-141-1
c 24	16	12.1	4380	3	US-08-293-314-1
c 25	16	12.1	8201	1	US-08-253-155A-9
c 26	16	12.1	12848	1	US-09-453-702B-252
c 27	16	12.1	17056	4	US-09-245-041-3

28	16	12.1	38155	4	US-09-453-702B-79	Sequence 79, Appl
c 29	16	12.1	48908	4	US-09-453-702B-137	Sequence 137, Appl
30	15	11.4	75	1	US-08-153-799-9	Sequence 9, Appl
31	15	11.4	460	4	US-09-040-984-83	Sequence 83, Appl
32	15	11.4	460	4	US-09-123-912-83	Sequence 83, Appl
33	15	11.4	460	4	US-09-643-597-83	Sequence 83, Appl
c 34	15	11.4	975	1	US-08-671-525B-9	Sequence 9, Appl
c 35	15	11.4	975	1	US-08-672-109B-9	Sequence 9, Appl
c 36	15	11.4	975	1	US-08-842-045-9	Sequence 9, Appl
c 37	15	11.4	975	2	US-08-842-238-9	Sequence 9, Appl
c 38	15	11.4	975	3	US-08-829-335B-9	Sequence 9, Appl
c 39	15	11.4	978	3	US-08-706-281A-17	Sequence 17, Appl
c 40	15	11.4	978	4	US-09-097-231-17	Sequence 17, Appl
41	15	11.4	1586	4	US-09-152-060-12	Sequence 12, Appl
42	15	11.4	1711	4	US-09-453-702B-105	Sequence 105, Appl
c 43	15	11.4	1897	1	US-08-615-170-18	Sequence 18, Appl
c 44	15	11.4	1964	4	US-09-434-613-2	Sequence 2, Appl
c 45	15	11.4	2012	4	US-09-149-476-132	Sequence 132, Appl
46	15	11.4	3102	4	US-09-336-643A-17	Sequence 17, Appl
47	15	11.4	3876	1	US-08-494-714-1	Sequence 1, Appl
48	15	11.4	3876	5	PCT-US96-107B2-1	Sequence 1, Appl
49	15	11.4	4350	4	US-09-295-593-37	Sequence 37, Appl
c 50	15	11.4	4833	4	US-09-066-047-1	Sequence 1, Appl
c 51	15	11.4	5541	1	US-08-920-812-20	Sequence 20, Appl
c 52	15	11.4	5541	1	US-08-920-827-20	Sequence 20, Appl
c 53	15	11.4	5541	1	US-08-921-177-20	Sequence 20, Appl
c 54	15	11.4	5541	1	US-08-362-577C-20	Sequence 20, Appl
c 55	15	11.4	5541	2	US-08-920-828-20	Sequence 20, Appl
c 56	15	11.4	7676	1	US-08-451-777A-7	Sequence 7, Appl
c 57	15	11.4	7676	2	US-08-451-778A-7	Sequence 7, Appl
c 58	15	11.4	7676	2	US-08-998-208-7	Sequence 7, Appl
c 59	15	11.4	7676	5	PCT-US95-06743-7	Sequence 7, Appl
60	15	11.4	8367	2	US-08-583-562B-7	Sequence 7, Appl
61	15	11.4	8367	2	US-08-779-113-7	Sequence 7, Appl
62	15	11.4	10718	3	US-08-325-426B-1	Sequence 1, Appl
63	15	11.4	12866	4	US-08-961-527-137	Sequence 137, Appl
64	15	11.4	19736	4	US-09-740-035-3	Sequence 3, Appl
c 65	15	11.4	4403765	4	US-09-103-840A-2	Sequence 2, Appl
c 66	15	11.4	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c 67	14	10.6	30	3	US-08-612-973-34	Sequence 34, Appl
c 68	14	10.6	30	4	US-08-927-597-34	Sequence 34, Appl
c 69	14	10.6	50	1	US-08-171-389-426	Sequence 426, Appl
c 70	14	10.6	50	1	US-08-123-936-426	Sequence 426, Appl
c 71	14	10.6	50	2	US-08-475-228A-426	Sequence 426, Appl
c 72	14	10.6	50	3	US-08-482-080A-426	Sequence 426, Appl
c 73	14	10.6	50	4	US-09-354-947-426	Sequence 426, Appl
c 74	14	10.6	50	5	PCT-US93-12388-426	Sequence 426, Appl
c 75	14	10.6	51	1	US-08-171-389-427	Sequence 427, Appl
c 76	14	10.6	51	1	US-08-123-936-427	Sequence 427, Appl
c 77	14	10.6	51	2	US-08-475-228A-427	Sequence 427, Appl
c 78	14	10.6	51	3	US-08-482-080A-427	Sequence 427, Appl
c 79	14	10.6	51	4	US-09-354-947-427	Sequence 427, Appl
c 80	14	10.6	51	5	PCT-US93-12388-427	Sequence 427, Appl
c 81	14	10.6	213	3	US-08-513-974B-37	Sequence 37, Appl
c 82	14	10.6	233	4	US-09-085-199B-24	Sequence 24, Appl
c 83	14	10.6	240	3	US-08-513-974B-318	Sequence 318, Appl
c 84	14	10.6	339	1	US-08-171-718-118	Sequence 118, Appl
c 85	14	10.6	339	3	US-08-478-087-118	Sequence 118, Appl
c 86	14	10.6	372	3	US-09-188-930-60	Sequence 60, Appl
c 87	14	10.6	531	4	US-09-404-879A-138	Sequence 138, Appl
c 88	14	10.6	571	4	US-09-404-879A-106	Sequence 106, Appl
c 89	14	10.6	737	1	US-08-463-115-19	Sequence 19, Appl
c 90	14	10.6	737	1	US-08-465-388-19	Sequence 19, Appl
c 91	14	10.6	798	4	US-08-998-416-463	Sequence 463, Appl
c 92	14	10.6	858	4	US-09-334-938-12	Sequence 12, Appl
c 93	14	10.6	976	1	US-08-266-451B-25	Sequence 25, Appl
c 94	14	10.6	976	2	US-08-748-725-25	Sequence 25, Appl
c 95	14	10.6	1033	4	US-09-171-209-73	Sequence 73, Appl
c 96	14	10.6	1089	4	US-09-513-838-1	Sequence 1, Appl
c 97	14	10.6	1125	3	US-08-591-685-10	Sequence 10, Appl
c 98	14	10.6	1137	4	US-09-045-585-6	Sequence 6, Appl
c 99	14	10.6	1137	4	US-09-534-185-6	Sequence 6, Appl
c 100	14	10.6	1292	4	US-09-198-603C-7	Sequence 7, Appl

101	14	10.6	1336	1	US-08-107-684B-1	Sequence 1, Appl	174	14	10.6	2074	3	US-09-248-137-11	Sequence 11, Appl
102	14	10.6	1337	2	US-08-743-637B-32	Sequence 32, Appl	175	14	10.6	2190	3	US-08-508-761B-5	Sequence 5, Appl
103	14	10.6	1337	3	US-08-526-840B-32	Sequence 32, Appl	176	14	10.6	2241	2	US-08-838-219B-20	Sequence 20, Appl
104	14	10.6	1359	3	US-08-227-496C-17	Sequence 17, Appl	177	14	10.6	2241	3	US-09-233-336A-20	Sequence 20, Appl
105	14	10.6	1364	4	US-08-763-704A-2	Sequence 2, Appl	178	14	10.6	2241	3	US-09-233-752A-20	Sequence 20, Appl
106	14	10.6	1442	1	US-08-247-908A-1	Sequence 1, Appl	179	14	10.6	2241	4	US-09-402-036-20	Sequence 20, Appl
107	14	10.6	1442	1	US-08-453-942-1	Sequence 1, Appl	180	14	10.6	2241	4	US-09-904-226-20	Sequence 20, Appl
108	14	10.6	1442	1	US-08-926-885A-1	Sequence 1, Appl	181	14	10.6	2257	1	US-08-171-718-15	Sequence 15, Appl
109	14	10.6	1442	5	PCT-US94-05290-1	Sequence 1, Appl	182	14	10.6	2257	3	US-08-478-087-15	Sequence 15, Appl
110	14	10.6	1443	1	US-08-443-965B-10	Sequence 10, Appl	183	14	10.6	2328	4	US-09-513-838-5	Sequence 5, Appl
111	14	10.6	1443	2	US-08-425-989B-10	Sequence 10, Appl	184	14	10.6	2370	2	US-08-838-219B-19	Sequence 19, Appl
112	14	10.6	1443	2	US-08-443-966B-10	Sequence 10, Appl	185	14	10.6	2370	3	US-09-233-336A-19	Sequence 19, Appl
113	14	10.6	1452	4	US-09-039-982A-36	Sequence 36, Appl	186	14	10.6	2370	3	US-09-233-752A-19	Sequence 19, Appl
114	14	10.6	1452	4	US-09-039-641-36	Sequence 36, Appl	187	14	10.6	2370	4	US-09-402-036-19	Sequence 19, Appl
115	14	10.6	1452	4	US-09-039-762A-36	Sequence 36, Appl	188	14	10.6	2370	4	US-09-904-226-19	Sequence 19, Appl
116	14	10.6	1452	4	US-09-042-492D-36	Sequence 36, Appl	189	14	10.6	2403	1	US-08-471-033-30	Sequence 30, Appl
117	14	10.6	1452	4	US-08-913-612A-36	Sequence 36, Appl	190	14	10.6	2403	1	US-08-471-044-30	Sequence 30, Appl
118	14	10.6	1515	4	US-09-240-915-4	Sequence 4, Appl	191	14	10.6	2403	2	US-08-463-483A-30	Sequence 30, Appl
119	14	10.6	1515	4	US-09-240-915-5	Sequence 4, Appl	192	14	10.6	2403	2	US-08-471-046A-30	Sequence 30, Appl
120	14	10.6	1515	4	US-09-591-435-4	Sequence 4, Appl	193	14	10.6	2403	2	US-08-470-566B-30	Sequence 30, Appl
121	14	10.6	1515	4	US-09-591-435-5	Sequence 4, Appl	194	14	10.6	2403	2	US-08-838-219B-7	Sequence 7, Appl
122	14	10.6	1518	4	US-09-240-915-1	Sequence 1, Appl	195	14	10.6	2403	2	US-08-469-334-30	Sequence 30, Appl
123	14	10.6	1518	4	US-09-240-915-2	Sequence 2, Appl	196	14	10.6	2403	3	US-09-300-529-30	Sequence 30, Appl
124	14	10.6	1518	4	US-09-591-435-1	Sequence 1, Appl	197	14	10.6	2403	3	US-09-233-336A-7	Sequence 7, Appl
125	14	10.6	1518	4	US-09-591-435-2	Sequence 2, Appl	198	14	10.6	2403	3	US-09-233-752A-7	Sequence 7, Appl
126	14	10.6	1584	1	US-08-247-908A-10	Sequence 10, Appl	199	14	10.6	2403	4	US-09-402-036-7	Sequence 7, Appl
127	14	10.6	1584	1	US-08-453-942-10	Sequence 10, Appl	200	14	10.6	2502	1	US-09-904-228-7	Sequence 7, Appl
128	14	10.6	1584	2	US-08-926-885A-10	Sequence 10, Appl	201	14	10.6	2502	1	US-08-062-472B-2	Sequence 2, Appl
129	14	10.6	1584	5	PCT-US94-05290-10	Sequence 10, Appl	202	14	10.6	2514	4	US-09-144-914-3	Sequence 3, Appl
130	14	10.6	1599	1	US-08-196-003-2	Sequence 2, Appl	203	14	10.6	2574	4	US-09-255-829-21	Sequence 21, Appl
131	14	10.6	1599	2	US-08-689-870-1	Sequence 1, Appl	204	14	10.6	2574	4	US-09-255-829-27	Sequence 27, Appl
132	14	10.6	1599	2	US-08-689-870-1	Sequence 1, Appl	205	14	10.6	2574	4	US-09-255-829-28	Sequence 28, Appl
133	14	10.6	1599	3	US-08-933-824-2	Sequence 2, Appl	206	14	10.6	2700	1	US-08-484-105-5	Sequence 5, Appl
134	14	10.6	1599	4	US-09-264-465-2	Sequence 2, Appl	207	14	10.6	2700	1	US-08-484-106-5	Sequence 5, Appl
135	14	10.6	1611	4	US-09-039-982A-35	Sequence 35, Appl	208	14	10.6	2992	3	US-09-362-123A-3	Sequence 3, Appl
136	14	10.6	1611	4	US-09-039-641-35	Sequence 35, Appl	209	14	10.6	2992	4	US-09-062-416-1	Sequence 1, Appl
137	14	10.6	1611	4	US-09-039-762A-35	Sequence 35, Appl	210	14	10.6	3016	2	US-08-344-155C-97	Sequence 97, Appl
138	14	10.6	1611	4	US-09-042-492D-35	Sequence 35, Appl	211	14	10.6	3016	2	US-09-009-490A-86	Sequence 86, Appl
139	14	10.6	1611	4	US-08-913-612A-35	Sequence 35, Appl	212	14	10.6	3024	6	5284931-1	Patent No. 5284931
140	14	10.6	1644	4	US-09-255-829-23	Sequence 23, Appl	213	14	10.6	3066	2	US-08-142-439A-1	Sequence 1, Appl
141	14	10.6	1656	3	US-08-318-039A-2	Sequence 2, Appl	214	14	10.6	3066	2	US-08-869-477-1	Sequence 1, Appl
142	14	10.6	1656	3	US-08-318-039B-16	Sequence 16, Appl	215	14	10.6	3249	1	US-08-106-493A-1	Sequence 1, Appl
143	14	10.6	1656	3	US-08-227-496C-20	Sequence 20, Appl	216	14	10.6	3249	1	US-08-429-264-1	Sequence 1, Appl
144	14	10.6	1656	3	US-08-435-568A-2	Sequence 2, Appl	217	14	10.6	3486	5	PCT-US91-09784-3	Sequence 3, Appl
145	14	10.6	1664	4	US-09-045-583-4	Sequence 4, Appl	218	14	10.6	3507	2	US-08-775-009-36	Sequence 36, Appl
146	14	10.6	1664	4	US-09-534-185-4	Sequence 4, Appl	219	14	10.6	3509	4	US-09-255-829-19	Sequence 19, Appl
147	14	10.6	1788	2	US-08-559-505-1	Sequence 1, Appl	220	14	10.6	3660	4	US-09-517-467B-3	Sequence 3, Appl
148	14	10.6	1788	2	US-08-749-907-1	Sequence 1, Appl	221	14	10.6	3747	1	US-08-044-618-5	Sequence 5, Appl
149	14	10.6	1788	4	US-09-241-581B-3	Sequence 3, Appl	222	14	10.6	3792	4	US-08-860-886-1	Sequence 1, Appl
150	14	10.6	1788	4	US-08-265-428-3	Sequence 3, Appl	223	14	10.6	3823	4	US-09-453-702B-132	Sequence 132, App
151	14	10.6	1788	5	PCT-US95-0721-3	Sequence 3, Appl	224	14	10.6	4104	1	US-07-998-003A-94	Sequence 94, Appl
152	14	10.6	1811	1	US-08-848-252-1	Sequence 1, Appl	225	14	10.6	4104	1	US-08-453-274B-94	Sequence 94, Appl
153	14	10.6	1825	2	US-08-890-980-3	Sequence 3, Appl	226	14	10.6	4104	1	US-08-453-699A-94	Sequence 94, Appl
154	14	10.6	1825	3	US-08-890-979-3	Sequence 3, Appl	227	14	10.6	4104	1	US-08-268-161A-94	Sequence 94, Appl
155	14	10.6	1825	3	US-09-032-894-3	Sequence 3, Appl	228	14	10.6	4104	2	US-08-453-702A-94	Sequence 94, Appl
156	14	10.6	1825	4	US-09-031-626-3	Sequence 3, Appl	229	14	10.6	4104	4	US-09-099-639-94	Sequence 94, Appl
157	14	10.6	1846	1	US-08-483-389-117	Sequence 117, App	230	14	10.6	4104	5	PCT-US93-12588-94	Sequence 94, Appl
158	14	10.6	1899	4	US-08-965-762-10	Sequence 10, Appl	231	14	10.6	4104	5	PCT-US95-08071-94	Sequence 94, Appl
159	14	10.6	1899	4	US-09-911-927-10	Sequence 10, Appl	232	14	10.6	4342	4	US-09-338-907-107	Sequence 107, App
160	14	10.6	1899	4	US-09-911-927-12	Sequence 12, Appl	233	14	10.6	4342	4	US-09-218-207-107	Sequence 107, App
161	14	10.6	1899	4	US-09-911-882-10	Sequence 10, Appl	234	14	10.6	4582	4	US-09-338-907-118	Sequence 118, App
162	14	10.6	1899	4	US-09-911-882-12	Sequence 12, Appl	235	14	10.6	4582	4	US-09-218-207-118	Sequence 118, App
163	14	10.6	1944	6	5260223-2	Patent No. 5260223	236	14	10.6	4686	4	US-09-338-907-117	Sequence 117, App
164	14	10.6	2000	4	US-09-605-785-374	Sequence 374, App	237	14	10.6	4686	4	US-09-218-207-117	Sequence 117, App
165	14	10.6	2000	4	US-09-439-313-374	Sequence 374, App	238	14	10.6	4823	2	US-08-457-254-5	Sequence 5, Appl
166	14	10.6	2000	4	US-09-352-616A-374	Sequence 374, App	239	14	10.6	4823	3	US-08-484-257-20	Sequence 20, Appl
167	14	10.6	2040	4	US-09-605-785-375	Sequence 375, App	240	14	10.6	4823	3	US-08-999-927-5	Sequence 5, Appl
168	14	10.6	2040	4	US-09-439-313-375	Sequence 375, App	241	14	10.6	4823	4	US-08-461-819-5	Sequence 5, Appl
169	14	10.6	2040	4	US-09-352-616A-375	Sequence 375, App	242	14	10.6	4823	5	PCT-US94-08806-28	Sequence 28, Appl
170	14	10.6	2043	3	US-08-227-496C-14	Sequence 14, Appl	243	14	10.6	4823	5	PCT-US95-01829-5	Sequence 5, Appl
171	14	10.6	2074	2	US-09-018-576-2	Sequence 2, Appl	244	14	10.6	4823	5	PCT-US95-16686-5	Sequence 5, Appl
172	14	10.6	2074	2	US-09-018-576-11	Sequence 11, Appl	245	14	10.6	4853	1	US-08-832-883-1	Sequence 1, Appl
173	14	10.6	2074	3	US-09-248-137-2	Sequence 2, Appl	246	14	10.6	4853	2	US-08-832-877-1	Sequence 1, Appl

c 247	14	10.6	4875	4	US-09-338-907-114	Sequence 114, App	320	13	9.8	90	5	PCT-US96-09388-109	Sequence 109, App
c 248	14	10.6	4875	4	US-09-218-207-114	Sequence 114, App	321	13	9.8	92	1	US-08-487-141B-109	Sequence 109, App
c 249	14	10.6	4958	4	US-09-338-907-116	Sequence 116, App	322	13	9.8	95	4	US-08-952-793-259	Sequence 259, App
c 250	14	10.6	4958	4	US-09-218-207-116	Sequence 116, App	323	13	9.8	95	5	PCT-US96-09455A-259	Sequence 259, App
c 251	14	10.6	4986	4	US-09-338-907-121	Sequence 121, App	324	13	9.8	152	4	US-09-568-816A-15	Sequence 15, Appl
c 252	14	10.6	4986	4	US-09-218-207-121	Sequence 121, App	325	13	9.8	159	4	US-09-461-697-94	Sequence 94, Appl
c 253	14	10.6	5020	4	US-09-338-907-120	Sequence 120, App	326	13	9.8	192	4	US-09-134-001C-49	Sequence 49, Appl
c 254	14	10.6	5020	4	US-09-218-207-120	Sequence 120, App	327	13	9.8	213	3	US-08-513-974B-37	Sequence 37, Appl
c 255	14	10.6	5044	4	US-09-338-907-115	Sequence 115, App	328	13	9.8	213	3	US-08-513-974B-37	Sequence 37, Appl
c 256	14	10.6	5044	4	US-09-218-207-115	Sequence 115, App	329	13	9.8	225	2	US-08-943-731-160	Sequence 160, App
c 257	14	10.6	5057	4	US-09-338-907-123	Sequence 123, App	330	13	9.8	228	2	US-08-604-989A-7	Sequence 7, Appl
c 258	14	10.6	5057	4	US-09-218-207-123	Sequence 123, App	331	13	9.8	239	4	US-08-619-542B-31	Sequence 31, Appl
c 259	14	10.6	5100	4	US-09-338-907-122	Sequence 122, App	332	13	9.8	239	4	US-09-439-261-29	Sequence 29, Appl
c 260	14	10.6	5100	4	US-09-218-207-122	Sequence 122, App	333	13	9.8	240	3	US-09-227-613-28	Sequence 28, Appl
c 261	14	10.6	5148	4	US-09-338-907-112	Sequence 112, App	334	13	9.8	246	4	US-08-513-974B-318	Sequence 318, App
c 262	14	10.6	5148	4	US-09-218-207-112	Sequence 112, App	335	13	9.8	246	4	US-09-397-787-110	Sequence 110, App
c 263	14	10.6	5227	2	US-08-996-306-3	Sequence 3, Appl	336	13	9.8	254	2	US-08-605-163-21	Sequence 21, Appl
c 264	14	10.6	5234	4	US-09-338-907-113	Sequence 113, App	337	13	9.8	288	2	US-08-716-942-17	Sequence 17, Appl
c 265	14	10.6	5234	4	US-09-218-207-113	Sequence 113, App	338	13	9.8	288	4	US-09-130-337A-17	Sequence 17, Appl
c 266	14	10.6	5245	4	US-09-338-907-3	Sequence 3, Appl	339	13	9.8	291	1	US-08-594-031-147	Sequence 147, App
c 267	14	10.6	5245	4	US-09-218-207-3	Sequence 3, Appl	340	13	9.8	295	1	US-08-594-031-128	Sequence 128, App
c 268	14	10.6	5250	4	US-09-338-907-69	Sequence 69, Appl	341	13	9.8	314	4	US-08-651-155B-148	Sequence 148, App
c 269	14	10.6	5250	4	US-09-218-207-69	Sequence 69, Appl	342	13	9.8	337	1	US-08-594-031-167	Sequence 167, App
c 270	14	10.6	5290	4	US-09-338-907-119	Sequence 119, App	343	13	9.8	340	3	US-08-594-031-168	Sequence 168, App
c 271	14	10.6	5290	4	US-09-218-207-119	Sequence 119, App	344	13	9.8	340	4	US-08-441-971-7	Sequence 7, Appl
c 272	14	10.6	5326	4	US-09-338-907-124	Sequence 124, App	345	13	9.8	340	4	US-08-221-653-7	Sequence 7, Appl
c 273	14	10.6	5326	4	US-09-218-207-124	Sequence 124, App	346	13	9.8	340	4	US-08-442-144A-7	Sequence 7, Appl
c 274	14	10.6	5345	1	US-08-044-618-7	Sequence 7, Appl	347	13	9.8	340	4	US-08-441-970-7	Sequence 7, Appl
c 275	14	10.6	6516	4	US-08-961-527-105	Sequence 105, App	348	13	9.8	341	4	US-08-943-731-158	Sequence 158, App
c 276	14	10.6	7568	2	US-08-694-869-2	Sequence 2, Appl	349	13	9.8	355	4	US-09-155-770-1	Sequence 1, Appl
c 277	14	10.6	7568	3	US-09-349-546-2	Sequence 2, Appl	350	13	9.8	356	1	US-08-297-633A-2	Sequence 2, Appl
c 278	14	10.6	8201	1	US-08-253-155A-9	Sequence 9, Appl	351	13	9.8	356	1	US-08-485-721-10	Sequence 10, Appl
c 279	14	10.6	8396	4	US-09-328-174A-1	Sequence 1, Appl	352	13	9.8	356	2	US-08-392-935-10	Sequence 10, Appl
c 280	14	10.6	8409	4	US-09-167-681-37	Sequence 37, Appl	353	13	9.8	356	5	PCT-US93-08325-2	Sequence 2, Appl
c 281	14	10.6	8697	4	US-08-961-527-123	Sequence 123, App	354	13	9.8	386	4	PCT-US93-08326-10	Sequence 10, Appl
c 282	14	10.6	9848	4	US-09-385-222A-3	Sequence 3, Appl	355	13	9.8	428	4	US-09-347-833-7	Sequence 7, Appl
c 283	14	10.6	9836	4	US-08-972-927-2	Sequence 2, Appl	356	13	9.8	428	4	US-09-456-830-32	Sequence 32, Appl
c 284	14	10.6	11236	1	US-09-221-017B-672	Sequence 672, App	357	13	9.8	428	4	US-09-456-830-48	Sequence 48, Appl
c 285	14	10.6	11236	1	US-07-853-913-1	Sequence 1, Appl	358	13	9.8	428	4	US-09-456-830-60	Sequence 60, Appl
c 286	14	10.6	11725	2	US-08-756-506-1	Sequence 1, Appl	359	13	9.8	428	4	US-09-002-285-32	Sequence 32, Appl
c 287	14	10.6	22306	4	US-09-453-702B-251	Sequence 251, App	360	13	9.8	428	4	US-09-002-285-48	Sequence 48, Appl
c 288	14	10.6	43676	3	US-09-356-952-12	Sequence 12, Appl	361	13	9.8	429	4	US-09-002-285-60	Sequence 60, Appl
c 289	14	10.6	43676	3	US-09-356-952-12	Sequence 12, Appl	362	13	9.8	489	4	US-09-397-787-252	Sequence 252, App
c 290	14	10.6	46819	4	US-09-453-702B-72	Sequence 72, Appl	363	13	9.8	496	1	US-09-370-838-109	Sequence 109, App
c 291	14	10.6	50000	4	US-09-146-053-4	Sequence 4, Appl	364	13	9.8	496	1	US-08-263-413-23	Sequence 23, Appl
c 292	14	10.6	56516	2	US-08-996-306-1	Sequence 1, Appl	365	13	9.8	510	4	US-08-263-413-22	Sequence 22, Appl
c 293	14	10.6	56516	4	US-09-338-907-1	Sequence 1, Appl	366	13	9.8	517	4	US-09-461-697-96	Sequence 96, Appl
c 294	14	10.6	56516	4	US-09-218-207-1	Sequence 1, Appl	367	13	9.8	519	2	US-09-404-879A-211	Sequence 211, App
c 295	14	10.6	56520	4	US-09-338-907-179	Sequence 179, App	368	13	9.8	519	3	US-08-503-226B-36	Sequence 36, Appl
c 296	14	10.6	56520	4	US-09-218-207-179	Sequence 179, App	369	13	9.8	536	1	US-08-721-458B-36	Sequence 36, Appl
c 297	14	10.6	70000	4	US-09-851-896-3	Sequence 3, Appl	370	13	9.8	536	1	US-08-887-534A-13	Sequence 13, Appl
c 298	14	10.6	72604	4	US-09-368-992-7	Sequence 7, Appl	371	13	9.8	536	1	US-07-996-772A-5	Sequence 5, Appl
c 299	14	10.6	72604	4	US-09-657-474-7	Sequence 7, Appl	372	13	9.8	536	1	US-08-446-822-5	Sequence 5, Appl
c 300	13	9.8	15	2	US-08-292-620A-110	Sequence 110, App	373	13	9.8	536	5	US-09-328-314-5	Sequence 5, Appl
c 301	13	9.8	15	3	US-09-071-845-110	Sequence 110, App	374	13	9.8	541	2	PCT-US93-12586-5	Sequence 5, Appl
c 302	13	9.8	20	1	US-08-547-182-10	Sequence 10, App	375	13	9.8	541	3	US-08-503-226B-35	Sequence 35, Appl
c 303	13	9.8	27	1	US-08-334-951-44	Sequence 44, Appl	376	13	9.8	541	3	US-08-721-458B-35	Sequence 35, Appl
c 304	13	9.8	27	1	US-08-758-306-50	Sequence 50, Appl	377	13	9.8	566	4	US-09-605-785-393	Sequence 393, App
c 305	13	9.8	27	1	US-08-758-306-64	Sequence 64, Appl	378	13	9.8	566	4	US-09-439-313-393	Sequence 393, App
c 306	13	9.8	27	1	US-08-758-306-1036	Sequence 1036, App	379	13	9.8	566	4	US-09-352-616A-393	Sequence 393, App
c 307	13	9.8	27	3	US-08-722-719-44	Sequence 44, Appl	380	13	9.8	600	1	US-09-328-111-461	Sequence 461, App
c 308	13	9.8	27	4	US-08-584-040-772	Sequence 772, App	381	13	9.8	600	1	US-08-602-262-4	Sequence 4, Appl
c 309	13	9.8	27	4	US-09-334-951-44	Sequence 44, Appl	382	13	9.8	600	1	US-08-602-262-5	Sequence 5, Appl
c 310	13	9.8	30	2	US-08-821-782-32	Sequence 32, Appl	383	13	9.8	600	3	US-09-004-716-4	Sequence 4, Appl
c 311	13	9.8	30	4	US-09-292-435A-32	Sequence 32, Appl	384	13	9.8	600	3	US-09-004-716-5	Sequence 5, Appl
c 312	13	9.8	36	1	US-07-960-510-10	Sequence 10, Appl	385	13	9.8	608	3	US-09-461-697-92	Sequence 92, Appl
c 313	13	9.8	36	1	US-07-960-510-14	Sequence 14, Appl	386	13	9.8	615	1	US-08-115-753-6	Sequence 6, Appl
c 314	13	9.8	38	1	US-08-390-850-967	Sequence 967, App	387	13	9.8	615	1	US-08-247-946A-5	Sequence 5, Appl
c 315	13	9.8	38	1	US-08-435-634-967	Sequence 967, App	388	13	9.8	621	6	PCT-US95-06420-5	Sequence 5, Appl
c 316	13	9.8	50	4	US-09-590-867A-37	Sequence 37, Appl	389	13	9.8	621	6	5175384-1	Patent No. 5175384
c 317	13	9.8	51	4	US-09-548-260-37	Sequence 37, Appl	390	13	9.8	660	1	US-08-233-146-4	Sequence 4, Appl
c 318	13	9.8	51	4	US-09-461-697-98	Sequence 98, Appl	391	13	9.8	660	1	US-08-463-470-4	Sequence 4, Appl
c 319	13	9.8	50	2	US-08-679-645-518	Sequence 518, App	392	13	9.8	675	1	US-07-807-043B-2	Sequence 2, Appl

393	13	9.8	675	1	US-08-299-849B-2	Sequence 2, Appl	c 466	13	9.8	1252	4	US-08-785-271-13	Sequence 13, Appl
394	13	9.8	675	2	US-08-142-368A-2	Sequence 2, Appl	467	13	9.8	1271	1	US-08-464-339A-1	Sequence 1, Appl
395	13	9.8	675	3	US-08-967-727-2	Sequence 2, Appl	468	13	9.8	1271	5	PCT-US94-14388-1	Sequence 1, Appl
396	13	9.8	675	4	US-08-037-230D-2	Sequence 2, Appl	c 469	13	9.8	1279	3	US-08-826-611-5	Sequence 5, Appl
397	13	9.8	676	1	US-08-533-669A-3	Sequence 3, Appl	470	13	9.8	1287	4	US-09-134-001C-48	Sequence 48, Appl
398	13	9.8	676	2	US-08-183-861-3	Sequence 3, Appl	471	13	9.8	1292	4	US-09-198-603C-7	Sequence 7, Appl
399	13	9.8	676	4	US-09-022-765-3	Sequence 3, Appl	472	13	9.8	1294	4	US-09-425-578-1	Sequence 1, Appl
400	13	9.8	700	4	US-09-325-932A-99	Sequence 99, Appl	473	13	9.8	1302	4	US-09-134-001C-828	Sequence 828, App
401	13	9.8	737	1	US-08-602-262-3	Sequence 1, Appl	c 474	13	9.8	1316	1	US-08-446-822-7	Sequence 7, Appl
402	13	9.8	737	1	US-08-602-262-3	Sequence 1, Appl	c 475	13	9.8	1316	1	US-09-328-314-7	Sequence 7, Appl
403	13	9.8	737	3	US-09-004-716-1	Sequence 1, Appl	c 476	13	9.8	1316	5	PCT-US93-12586-7	Sequence 7, Appl
404	13	9.8	737	3	US-09-004-716-3	Sequence 3, Appl	c 477	13	9.8	1319	2	US-08-484-933B-17	Sequence 17, Appl
405	13	9.8	740	4	US-09-221-017B-355	Sequence 355, App	c 478	13	9.8	1319	2	US-08-484-158B-17	Sequence 17, Appl
406	13	9.8	756	4	US-08-413-974-3	Sequence 3, Appl	c 479	13	9.8	1319	2	US-08-484-96A-17	Sequence 17, Appl
407	13	9.8	756	4	US-08-434-418-3	Sequence 3, Appl	c 480	13	9.8	1319	2	US-08-480-150A-17	Sequence 17, Appl
408	13	9.8	756	4	US-08-433-288-3	Sequence 3, Appl	c 481	13	9.8	1319	3	US-08-458-731-17	Sequence 17, Appl
409	13	9.8	756	4	US-08-174-739A-3	Sequence 3, Appl	c 482	13	9.8	1319	3	US-08-149-223A-17	Sequence 17, Appl
410	13	9.8	756	4	US-08-434-256-3	Sequence 3, Appl	483	13	9.8	1320	6	517197-2	Patent No. 517197
411	13	9.8	792	1	US-08-403-545-6	Sequence 6, Appl	484	13	9.8	1323	4	US-08-858-207A-50	Sequence 50, Appl
412	13	9.8	792	1	US-08-446-822-14	Sequence 14, Appl	485	13	9.8	1327	4	US-09-149-476-286	Sequence 286, App
413	13	9.8	792	4	US-08-404-381-6	Sequence 6, Appl	486	13	9.8	1330	2	US-08-933-750C-80	Sequence 80, Appl
414	13	9.8	792	4	US-09-328-314-14	Sequence 14, Appl	487	13	9.8	1330	3	US-09-234-613-80	Sequence 80, Appl
415	13	9.8	792	5	PCT-US93-12586-14	Sequence 14, Appl	c 488	13	9.8	1334	2	US-08-481-658B-44	Sequence 44, Appl
416	13	9.8	801	2	US-08-903-624-5	Sequence 5, Appl	c 489	13	9.8	1334	2	US-08-477-504A-44	Sequence 44, Appl
417	13	9.8	813	4	US-08-961-527-37	Sequence 37, App	c 490	13	9.8	1334	2	US-08-486-756A-44	Sequence 44, Appl
418	13	9.8	844	4	US-09-889-595-2	Sequence 2, Appl	c 491	13	9.8	1334	3	US-08-485-862B-44	Sequence 44, Appl
419	13	9.8	879	4	US-09-221-017B-1041	Sequence 1041, Ap	c 492	13	9.8	1334	3	US-08-787-739-44	Sequence 44, Appl
420	13	9.8	883	4	US-09-171-209-74	Sequence 74, Appl	c 493	13	9.8	1334	3	US-08-487-077A-44	Sequence 44, Appl
421	13	9.8	888	3	US-09-188-930-13	Sequence 13, Appl	c 494	13	9.8	1334	3	US-08-485-863A-44	Sequence 44, Appl
422	13	9.8	909	4	US-08-928-941D-19	Sequence 19, Appl	c 495	13	9.8	1334	4	US-08-485-049D-44	Sequence 44, Appl
423	13	9.8	909	4	US-09-280-590A-19	Sequence 19, Appl	c 496	13	9.8	1334	4	US-09-178-115-44	Sequence 44, Appl
c 424	13	9.8	921	4	US-09-091-952A-7	Sequence 7, Appl	c 497	13	9.8	1334	4	US-09-177-776-44	Sequence 44, Appl
425	13	9.8	952	1	US-09-134-001C-2430	Sequence 2430, Ap	c 498	13	9.8	1335	1	US-08-525-654A-134	Sequence 134, App
426	13	9.8	952	1	US-08-181-271A-38	Sequence 38, Appl	499	13	9.8	1335	1	US-09-149-476-207	Sequence 207, App
427	13	9.8	952	1	US-08-449-315-38	Sequence 38, Appl	500	13	9.8	1365	1	US-07-807-043B-4	Sequence 4, Appl
428	13	9.8	952	1	US-08-444-803-38	Sequence 38, Appl	501	13	9.8	1365	1	US-08-299-849B-4	Sequence 4, Appl
429	13	9.8	952	1	US-08-449-043-38	Sequence 38, Appl	502	13	9.8	1365	2	US-08-143-368A-4	Sequence 4, Appl
c 430	13	9.8	952	1	US-08-456-265A-38	Sequence 38, Appl	503	13	9.8	1365	3	US-08-967-727-4	Sequence 4, Appl
c 431	13	9.8	952	1	US-08-455-416-38	Sequence 38, Appl	504	13	9.8	1365	4	US-08-037-230D-4	Sequence 4, Appl
c 432	13	9.8	952	1	US-08-455-244-38	Sequence 38, Appl	505	13	9.8	1384	4	US-08-729-594A-33	Sequence 33, Appl
c 433	13	9.8	952	1	US-08-454-876-38	Sequence 38, Appl	506	13	9.8	1384	4	US-08-937-993-33	Sequence 33, Appl
c 434	13	9.8	952	2	US-08-457-364-38	Sequence 38, Appl	507	13	9.8	1386	4	US-09-149-476-147	Sequence 147, App
c 435	13	9.8	952	2	US-08-456-262-38	Sequence 38, Appl	c 508	13	9.8	1398	2	US-08-604-989A-9	Sequence 9, Appl
c 436	13	9.8	952	2	US-08-456-240-38	Sequence 38, Appl	c 509	13	9.8	1401	1	US-07-843-945A-3	Sequence 3, Appl
c 437	13	9.8	952	2	US-08-455-736-38	Sequence 38, Appl	510	13	9.8	1401	2	US-08-218-978-3	Sequence 3, Appl
c 438	13	9.8	952	2	US-08-971-217-38	Sequence 38, Appl	c 511	13	9.8	1416	1	US-08-535-237-1	Sequence 1, Appl
c 439	13	9.8	952	4	US-09-350-600-38	Sequence 38, Appl	512	13	9.8	1416	2	US-08-619-542B-29	Sequence 29, Appl
c 440	13	9.8	1001	4	US-09-641-638-314	Sequence 314, App	513	13	9.8	1443	1	US-08-076-089-1	Sequence 1, Appl
441	13	9.8	1050	1	US-08-599-252-81	Sequence 81, Appl	514	13	9.8	1443	2	US-08-707-200-1	Sequence 1, Appl
442	13	9.8	1050	1	US-08-436-074-54	Sequence 54, Appl	515	13	9.8	1443	4	US-08-996-565-1	Sequence 1, Appl
443	13	9.8	1050	5	PCT-US96-06352-81	Sequence 81, Appl	516	13	9.8	1443	5	PCT-US93-05643-1	Sequence 1, Appl
444	13	9.8	1050	5	PCT-US96-06583-81	Sequence 81, Appl	517	13	9.8	1446	3	US-08-787-091-1	Sequence 1, Appl
445	13	9.8	1092	4	US-09-461-697-80	Sequence 80, Appl	518	13	9.8	1474	4	US-08-858-207A-144	Sequence 144, App
446	13	9.8	1123	1	US-07-971-096-3	Sequence 3, Appl	519	13	9.8	1486	4	US-09-149-476-23	Sequence 23, Appl
447	13	9.8	1123	1	US-08-175-096-3	Sequence 3, Appl	c 520	13	9.8	1508	3	US-08-867-381A-48	Sequence 48, Appl
c 448	13	9.8	1161	1	US-08-086-439C-1	Sequence 1, Appl	c 521	13	9.8	1508	4	US-09-521-144-48	Sequence 48, Appl
c 449	13	9.8	1161	1	US-08-434-877-1	Sequence 1, Appl	c 522	13	9.8	1521	2	US-08-604-989A-10	Sequence 10, Appl
c 450	13	9.8	1168	4	US-09-149-476-79	Sequence 79, Appl	c 523	13	9.8	1535	1	US-08-480-510-1	Sequence 1, Appl
c 451	13	9.8	1180	3	US-08-897-236-10	Sequence 10, Appl	c 524	13	9.8	1535	5	PCT-US94-01780-1	Sequence 1, Appl
c 452	13	9.8	1180	4	US-09-167-874-10	Sequence 10, Appl	c 525	13	9.8	1537	4	US-09-149-476-311	Sequence 311, App
453	13	9.8	1200	1	US-08-592-126-125	Sequence 125, App	c 526	13	9.8	1547	4	US-09-356-818A-1	Sequence 1, Appl
c 454	13	9.8	1206	2	US-08-666-367B-2	Sequence 2, Appl	527	13	9.8	1554	1	US-08-469-486-1	Sequence 1, Appl
c 455	13	9.8	1206	4	US-09-143-438-2	Sequence 2, Appl	528	13	9.8	1554	2	US-08-469-658-1	Sequence 1, Appl
456	13	9.8	1224	1	US-08-574-942-1	Sequence 1, Appl	c 529	13	9.8	1601	3	US-08-817-188-3	Sequence 3, Appl
457	13	9.8	1225	1	US-08-547-182-1	Sequence 1, Appl	530	13	9.8	1603	4	US-08-065-844A-1	Sequence 1, Appl
458	13	9.8	1239	4	US-09-461-697-76	Sequence 76, Appl	c 531	13	9.8	1605	4	US-09-149-476-187	Sequence 187, App
459	13	9.8	1246	4	US-09-651-656-30	Sequence 30, Appl	c 532	13	9.8	1622	1	US-07-996-772A-3	Sequence 3, Appl
460	13	9.8	1246	4	US-09-650-855-30	Sequence 30, Appl	c 533	13	9.8	1622	1	US-08-446-822-3	Sequence 3, Appl
c 461	13	9.8	1251	4	US-09-242-095-1	Sequence 1, Appl	c 534	13	9.8	1622	4	US-09-328-314-3	Sequence 3, Appl
c 462	13	9.8	1252	2	US-08-588-983-43	Sequence 43, Appl	c 535	13	9.8	1622	5	PCT-US93-12586-3	Sequence 3, Appl
c 463	13	9.8	1252	3	US-08-588-976-43	Sequence 43, Appl	c 536	13	9.8	1642	1	US-07-996-772A-1	Sequence 1, Appl
c 464	13	9.8	1252	3	US-08-589-028-13	Sequence 13, Appl	c 537	13	9.8	1642	1	US-08-446-822-1	Sequence 1, Appl
c 465	13	9.8	1252	3	US-08-784-582-13	Sequence 13, Appl	c 538	13	9.8	1642	4	US-09-328-314-1	Sequence 1, Appl

c 539	13	9.8	1642	5	PCT-US93-12586-1	Sequence 1, Appli	13	612	13	9.8	2073	4	US-09-173-300-3	Sequence 3, Appli
c 540	13	9.8	1645	2	US-08-461-812-1	Sequence 1, Appli	13	613	13	9.8	2089	4	US-09-155-770-6	Sequence 6, Appli
c 541	13	9.8	1673	4	US-09-426-568A-1	Sequence 1, Appli	13	c 614	13	9.8	2098	2	US-08-937-931-5	Sequence 5, Appli
c 542	13	9.8	1679	4	US-09-271-437-3	Sequence 3, Appli	13	c 615	13	9.8	2098	4	US-09-285-502-5	Sequence 5, Appli
c 543	13	9.8	1683	2	US-08-838-543-1	Sequence 1, Appli	13	c 616	13	9.8	2098	4	US-09-709-126-5	Sequence 5, Appli
c 544	13	9.8	1704	4	US-09-608-917A-3	Sequence 3, Appli	13	c 617	13	9.8	2098	4	US-09-871-388A-5	Sequence 5, Appli
c 545	13	9.8	1713	4	US-09-741-154-1	Sequence 1, Appli	13	618	13	9.8	2105	4	US-09-088-425-3	Sequence 3, Appli
c 546	13	9.8	1730	2	US-08-687-080-114	Sequence 11A, App	13	619	13	9.8	2114	4	US-09-568-816A-1	Sequence 3, Appli
c 547	13	9.8	1734	2	US-08-948-569A-7	Sequence 7, Appli	13	c 620	13	9.8	2127	2	US-08-832-883-54	Sequence 54, Appl
c 548	13	9.8	1734	2	US-08-663-808-1	Sequence 1, Appli	13	c 621	13	9.8	2127	2	US-08-832-877-54	Sequence 54, Appl
c 549	13	9.8	1734	2	US-09-188-469-7	Sequence 7, Appli	13	c 622	13	9.8	2148	4	US-09-620-412C-320	Sequence 320, App
c 550	13	9.8	1734	3	US-09-332-740-1	Sequence 1, Appli	13	c 623	13	9.8	2155	2	US-08-031-538-3	Sequence 3, Appli
c 551	13	9.8	1734	3	US-09-188-496-1	Sequence 1, Appli	13	624	13	9.8	2156	2	US-08-899-514-1	Sequence 1, Appli
c 552	13	9.8	1734	4	US-09-397-238A-7	Sequence 7, Appli	13	625	13	9.8	2172	4	US-08-030-410-2	Sequence 2, Appli
c 553	13	9.8	1734	4	US-09-368-282-1	Sequence 1, Appli	13	626	13	9.8	2172	4	US-09-357-251-9	Sequence 9, Appli
c 554	13	9.8	1734	4	US-09-566-708A-1	Sequence 1, Appli	13	627	13	9.8	2184	1	US-07-815-333A-1	Sequence 1, Appli
c 555	13	9.8	1762	1	US-08-105-483-300	Sequence 300, App	13	628	13	9.8	2220	4	US-08-997-251-1	Sequence 1, Appli
c 556	13	9.8	1762	1	US-08-709-209-300	Sequence 300, App	13	629	13	9.8	2244	4	US-09-354-151-1	Sequence 1, Appli
c 557	13	9.8	1762	1	US-08-458-101-300	Sequence 300, App	13	630	13	9.8	2264	2	US-08-149-097D-26	Sequence 26, Appl
c 558	13	9.8	1786	1	US-07-920-430-19	Sequence 19, Appl	13	631	13	9.8	2272	3	US-08-147-592A-3	Sequence 3, Appli
c 559	13	9.8	1786	1	US-08-066-299-9	Sequence 9, Appli	13	632	13	9.8	2272	4	US-08-292-694A-3	Sequence 3, Appli
c 560	13	9.8	1786	1	US-08-265-047-1	Sequence 1, Appli	13	633	13	9.8	2277	1	US-08-369-796-7	Sequence 7, Appli
c 561	13	9.8	1786	1	US-08-251-464-19	Sequence 19, Appl	13	634	13	9.8	2277	2	US-08-852-091-7	Sequence 7, Appli
c 562	13	9.8	1786	4	US-08-926-522-20	Sequence 20, Appl	13	635	13	9.8	2277	3	US-08-820-754-7	Sequence 7, Appli
c 563	13	9.8	1786	5	PCT-US92-01368A-19	Sequence 19, Appl	13	636	13	9.8	2277	3	US-08-956-652-7	Sequence 7, Appli
c 564	13	9.8	1810	1	US-07-755-573C-7	Sequence 7, Appli	13	637	13	9.8	2277	3	US-08-956-869-7	Sequence 7, Appli
c 565	13	9.8	1820	4	US-09-530-212A-1	Sequence 1, Appli	13	638	13	9.8	2277	3	US-08-948-547-7	Sequence 7, Appli
c 566	13	9.8	1825	4	US-09-461-697-75	Sequence 75, Appl	13	639	13	9.8	2277	4	US-08-956-653A-7	Sequence 7, Appli
c 567	13	9.8	1829	2	US-08-411-859-1	Sequence 1, Appli	13	640	13	9.8	2277	4	US-09-347-878-53	Sequence 53, Appl
c 568	13	9.8	1829	4	US-08-387-707-7	Sequence 7, Appli	13	641	13	9.8	2277	5	PCT-US95-17025-7	Sequence 7, Appli
c 569	13	9.8	1829	4	US-08-405-271A-7	Sequence 7, Appli	13	642	13	9.8	2278	4	US-09-442-055-1	Sequence 1, Appli
c 570	13	9.8	1838	3	US-08-948-564-1	Sequence 1, Appli	13	643	13	9.8	2288	1	US-08-290-937B-4	Sequence 4, Appli
c 571	13	9.8	1839	3	US-08-152-019A-44	Sequence 44, Appl	13	644	13	9.8	2289	1	US-07-838-410-2	Sequence 2, Appli
c 572	13	9.8	1839	3	US-08-482-677-1	Sequence 1, Appli	13	c 645	13	9.8	2339	4	US-09-268-140-11	Sequence 11, Appl
c 573	13	9.8	1851	4	US-09-149-476-62	Sequence 62, Appl	13	646	13	9.8	2348	4	US-09-393-554-10	Sequence 10, Appl
c 574	13	9.8	1858	2	US-08-909-965C-11	Sequence 11, Appl	13	647	13	9.8	2352	4	US-08-997-251-3	Sequence 3, Appli
c 575	13	9.8	1886	1	US-07-980-526-1	Sequence 1, Appli	13	648	13	9.8	2408	2	US-08-870-827-5	Sequence 5, Appli
c 576	13	9.8	1890	4	US-09-134-001C-1557	Sequence 1557, Ap	13	649	13	9.8	2408	4	US-09-317-179-5	Sequence 1, Appli
c 577	13	9.8	1900	4	US-09-468-265-2	Sequence 2, Appli	13	c 650	13	9.8	2410	2	US-08-780-835B-1	Sequence 1, Appli
c 578	13	9.8	1909	4	US-09-431-099-3	Sequence 3, Appli	13	c 651	13	9.8	2410	4	US-09-303-268-1	Sequence 1, Appli
c 579	13	9.8	1910	1	US-08-247-902A-1	Sequence 1, Appli	13	c 652	13	9.8	2410	4	US-09-116-049-1	Sequence 1, Appli
c 580	13	9.8	1910	5	PCT-US93-10541-1	Sequence 1, Appli	13	c 653	13	9.8	2412	4	US-09-072-596-345	Sequence 345, App
c 581	13	9.8	1915	3	US-08-369-046-1	Sequence 1, Appli	13	654	13	9.8	2424	1	US-08-821-119-16	Sequence 16, Appl
c 582	13	9.8	1925	3	US-08-669-378-1	Sequence 1, Appli	13	655	13	9.8	2424	4	US-09-149-476-228	Sequence 228, App
c 583	13	9.8	1925	3	US-08-669-378-3	Sequence 3, Appli	13	656	13	9.8	2430	1	US-08-062-368-3	Sequence 3, Appli
c 584	13	9.8	1925	3	US-08-669-378-5	Sequence 5, Appli	13	657	13	9.8	2430	1	US-08-233-146-8	Sequence 8, Appli
c 585	13	9.8	1925	3	US-08-669-378-7	Sequence 7, Appli	13	658	13	9.8	2456	1	US-08-463-470-8	Sequence 8, Appli
c 586	13	9.8	1925	3	US-08-669-378-9	Sequence 9, Appli	13	c 659	13	9.8	2456	1	US-08-858-207A-51	Sequence 51, Appl
c 587	13	9.8	1925	3	US-08-669-378-11	Sequence 11, Appl	13	c 660	13	9.8	2483	1	US-08-464-340A-3	Sequence 3, Appli
c 588	13	9.8	1932	4	US-08-604-989A-11	Sequence 11, Appl	13	c 661	13	9.8	2483	5	PCT-US94-08449A-3	Sequence 3, Appli
c 589	13	9.8	1942	2	US-08-996-441B-57	Sequence 57, Appl	13	c 662	13	9.8	2505	4	US-09-268-140-1	Sequence 7, Appli
c 590	13	9.8	1956	3	US-08-993-722A-57	Sequence 57, Appl	13	c 663	13	9.8	2517	4	US-09-534-407-5	Sequence 5, Appli
c 591	13	9.8	1956	3	US-08-993-170A-57	Sequence 57, Appl	13	664	13	9.8	2526	1	US-07-912-952-1	Sequence 1, Appli
c 592	13	9.8	1956	3	US-08-993-775B-57	Sequence 57, Appl	13	665	13	9.8	2556	1	US-08-208-887A-48	Sequence 48, Appl
c 593	13	9.8	1959	3	US-08-996-441B-1	Sequence 1, Appli	13	666	13	9.8	2556	1	US-08-699-103B-9	Sequence 9, Appli
c 594	13	9.8	1959	3	US-08-993-722A-1	Sequence 1, Appli	13	667	13	9.8	2556	4	US-09-229-059-9	Sequence 9, Appli
c 595	13	9.8	1959	3	US-08-993-170A-1	Sequence 1, Appli	13	668	13	9.8	2556	4	US-09-280-598-17	Sequence 17, Appli
c 596	13	9.8	1959	3	US-08-993-775B-1	Sequence 1, Appli	13	669	13	9.8	2556	6	5175384-10	Patent No. 5175384
c 597	13	9.8	1962	4	US-09-072-596-349	Sequence 349, App	13	670	13	9.8	2625	3	US-08-949-386-26	Sequence 26, Appl
c 598	13	9.8	1974	2	US-09-291-541-9	Sequence 9, Appli	13	671	13	9.8	2634	3	US-08-450-562-26	Sequence 26, Appl
c 599	13	9.8	1987	2	US-08-876-882-1	Sequence 1, Appli	13	672	13	9.8	2634	4	US-08-984-709A-26	Sequence 26, Appl
c 600	13	9.8	1987	4	US-09-315-928-1	Sequence 1, Appli	13	673	13	9.8	2634	4	US-08-450-272-26	Sequence 26, Appl
c 601	13	9.8	1987	4	US-08-818-111-152	Sequence 152, App	13	674	13	9.8	2644	2	US-07-728-215-26	Sequence 26, Appl
c 602	13	9.8	1993	4	US-08-818-111-147	Sequence 147, App	13	675	13	9.8	2644	4	US-08-938-085A-26	Sequence 26, Appl
c 603	13	9.8	1993	4	US-09-056-556-152	Sequence 152, App	13	676	13	9.8	2671	2	US-08-666-367B-1	Sequence 1, Appli
c 604	13	9.8	1993	4	US-09-056-556-152	Sequence 152, App	13	c 677	13	9.8	2671	4	US-09-143-438-1	Sequence 1, Appli
c 605	13	9.8	1993	4	US-09-056-556-152	Sequence 152, App	13	c 678	13	9.8	2671	4	US-09-143-438-1	Sequence 1, Appli
c 606	13	9.8	1993	4	US-09-072-596-147	Sequence 147, App	13	679	13	9.8	2704	6	5434340-6	Patent No. 5434340
c 607	13	9.8	1993	4	US-09-072-596-149	Sequence 149, App	13	680	13	9.8	2712	3	US-08-949-386-38	Sequence 38, Appl
c 608	13	9.8	2000	4	US-08-426-509A-1	Sequence 1, Appli	13	681	13	9.8	2712	3	US-08-450-562-38	Sequence 38, Appl
c 609	13	9.8	2000	5	PCT-US95-05008-1	Sequence 1, Appli	13	682	13	9.8	2712	4	US-08-984-709A-38	Sequence 38, Appl
c 610	13	9.8	2032	4	US-09-045-284A-1	Sequence 1, Appli	13	683	13	9.8	2712	4	US-08-450-272-38	Sequence 38, Appl
c 611	13	9.8	2032	4	US-09-190-911-2	Sequence 2, Appli	13	684	13	9.8	2731	3	US-08-699-103B-11	Sequence 11, Appl

685	13	9.8	2731	4	US-09-229-059-11	Sequence 11, Appl	758	13	9.8	3546	3	US-08-459-595A-14	Sequence 14, Appl
686	13	9.8	2786	1	US-08-224-391-53	Sequence 53, Appl	759	13	9.8	3546	3	US-08-459-504B-10	Sequence 10, Appl
687	13	9.8	2786	1	US-08-484-304-53	Sequence 53, Appl	760	13	9.8	3546	3	US-08-459-504B-12	Sequence 12, Appl
688	13	9.8	2817	4	US-09-431-099-1	Sequence 1, Appl	761	13	9.8	3546	3	US-08-459-504B-14	Sequence 14, Appl
689	13	9.8	2844	4	US-09-257-703-2	Sequence 2, Appl	762	13	9.8	3546	3	US-08-459-444-10	Sequence 10, Appl
690	13	9.8	2897	2	US-08-927-394-1	Sequence 1, Appl	763	13	9.8	3546	3	US-08-459-444-12	Sequence 12, Appl
691	13	9.8	2903	4	US-08-928-941D-2	Sequence 2, Appl	764	13	9.8	3546	3	US-08-459-444-14	Sequence 14, Appl
692	13	9.8	2903	4	US-08-928-941D-3	Sequence 3, Appl	765	13	9.8	3546	3	US-09-547-422-10	Sequence 10, Appl
693	13	9.8	2903	4	US-09-280-590A-2	Sequence 2, Appl	766	13	9.8	3546	4	US-09-547-422-12	Sequence 12, Appl
694	13	9.8	2903	4	US-09-280-590A-3	Sequence 3, Appl	767	13	9.8	3546	4	US-09-547-422-14	Sequence 14, Appl
695	13	9.8	2938	4	US-09-072-917A-8	Sequence 8, Appl	768	13	9.8	3572	4	US-09-072-596-337	Sequence 337, App
696	13	9.8	2946	4	US-09-175-928-3	Sequence 3, Appl	769	13	9.8	3627	1	US-08-104-072B-6	Sequence 6, Appl
697	13	9.8	2852	4	US-09-134-001C-977	Sequence 977, App	770	13	9.8	3627	1	US-08-351-413-7	Sequence 7, Appl
698	13	9.8	2970	3	US-08-949-386-37	Sequence 37, Appl	771	13	9.8	3627	2	US-09-025-583-7	Sequence 7, Appl
699	13	9.8	2970	3	US-08-450-562-37	Sequence 37, Appl	772	13	9.8	3668	2	US-08-849-345-1	Sequence 1, Appl
700	13	9.8	2970	4	US-08-984-709A-37	Sequence 37, Appl	773	13	9.8	3931	2	US-08-144-121-1	Sequence 1, Appl
701	13	9.8	2970	4	US-08-450-272-37	Sequence 37, Appl	774	13	9.8	3931	2	US-08-735-893-1	Sequence 1, Appl
702	13	9.8	2973	4	US-09-133-962A-15	Sequence 15, Appl	775	13	9.8	3969	4	US-09-518-386B-4	Sequence 4, Appl
703	13	9.8	3120	1	US-08-222-616-22	Sequence 22, Appl	776	13	9.8	4016	5	PCT-US95-08354A-1	Sequence 1, Appl
704	13	9.8	3120	4	US-08-446-648-22	Sequence 22, Appl	777	13	9.8	4052	1	US-08-057-167-1	Sequence 1, Appl
705	13	9.8	3120	5	PCT-US95-04228-22	Sequence 869, App	778	13	9.8	4052	5	PCT-US93-05412-1	Sequence 1, Appl
706	13	9.8	3142	4	US-09-221-017B-869	Sequence 1, Appl	779	13	9.8	4069	4	US-09-302-812-3	Sequence 3, Appl
707	13	9.8	3156	2	US-08-887-518-1	Sequence 1, Appl	780	13	9.8	4069	4	US-09-511-477-3	Sequence 3, Appl
708	13	9.8	3156	2	US-09-023-321-1	Sequence 1, Appl	781	13	9.8	4069	4	US-09-511-507-3	Sequence 3, Appl
709	13	9.8	3156	2	US-09-032-475-1	Sequence 1, Appl	782	13	9.8	4141	4	US-09-245-281-42	Sequence 42, Appl
710	13	9.8	3257	5	PCT-US91-09784-1	Sequence 44, Appl	783	13	9.8	4141	4	US-09-207-359B-42	Sequence 42, Appl
711	13	9.8	3288	4	US-09-206-942-44	Sequence 44, Appl	784	13	9.8	4533	3	US-08-863-790-27	Sequence 27, Appl
712	13	9.8	3306	4	US-09-206-942-42	Sequence 42, Appl	785	13	9.8	4533	3	US-08-296-749-27	Sequence 27, Appl
713	13	9.8	3366	4	US-09-171-461-27	Sequence 27, Appl	786	13	9.8	4637	4	US-09-221-017B-818	Sequence 818, App
714	13	9.8	3375	4	US-09-309-572-1	Sequence 1, Appl	787	13	9.8	4698	1	US-07-807-043B-5	Sequence 5, Appl
715	13	9.8	3376	4	US-09-309-572-3	Sequence 3, Appl	788	13	9.8	4698	1	US-08-299-849B-5	Sequence 5, Appl
716	13	9.8	3403	4	US-08-448-489-2	Sequence 2, Appl	789	13	9.8	4698	2	US-08-142-368A-5	Sequence 5, Appl
717	13	9.8	3454	4	US-09-082-059-1	Sequence 1, Appl	790	13	9.8	4698	3	US-08-967-727-5	Sequence 5, Appl
718	13	9.8	3468	1	US-07-951-715A-2	Sequence 2, Appl	791	13	9.8	4698	4	US-08-037-230D-5	Sequence 5, Appl
719	13	9.8	3468	1	US-07-951-715A-4	Sequence 4, Appl	792	13	9.8	4698	4	US-09-439-261-34	Sequence 34, Appl
720	13	9.8	3468	2	US-08-459-448A-2	Sequence 2, Appl	793	13	9.8	4698	4	US-09-227-613-33	Sequence 33, Appl
721	13	9.8	3468	2	US-08-459-448A-4	Sequence 4, Appl	794	13	9.8	4700	4	US-09-150-460B-9	Sequence 9, Appl
722	13	9.8	3468	3	US-08-459-595A-2	Sequence 2, Appl	795	13	9.8	4712	4	US-09-221-017B-577	Sequence 577, App
723	13	9.8	3468	3	US-08-459-595A-4	Sequence 4, Appl	796	13	9.8	4868	5	PCT-US93-11310-12	Sequence 12, Appl
724	13	9.8	3468	3	US-08-459-504B-2	Sequence 2, Appl	797	13	9.8	4868	5	PCT-US93-11310-12	Sequence 12, Appl
725	13	9.8	3468	3	US-08-459-504B-4	Sequence 4, Appl	798	13	9.8	4895	4	US-09-436-568A-3	Sequence 3, Appl
726	13	9.8	3468	3	US-08-459-444-2	Sequence 2, Appl	799	13	9.8	4900	1	US-08-245-295-5	Sequence 5, Appl
727	13	9.8	3468	3	US-08-459-444-4	Sequence 4, Appl	800	13	9.8	4900	1	US-08-481-130-5	Sequence 5, Appl
728	13	9.8	3468	3	US-09-053-549-5	Sequence 5, Appl	801	13	9.8	4900	1	US-08-656-984A-5	Sequence 5, Appl
729	13	9.8	3468	3	US-09-053-549-5	Sequence 5, Appl	802	13	9.8	4900	2	US-08-485-604-5	Sequence 5, Appl
730	13	9.8	3468	4	US-09-547-422-2	Sequence 2, Appl	803	13	9.8	4900	2	US-08-487-595-5	Sequence 5, Appl
731	13	9.8	3471	4	US-09-002-285-73	Sequence 73, Appl	804	13	9.8	4900	3	US-08-863-790-26	Sequence 26, Appl
732	13	9.8	3471	5	PCT-US93-00227-2	Sequence 2, Appl	805	13	9.8	5011	1	US-08-296-749-26	Sequence 26, Appl
733	13	9.8	3475	1	US-08-222-299-3	Sequence 3, Appl	806	13	9.8	5011	1	US-08-141-893-1	Sequence 1, Appl
734	13	9.8	3475	2	US-08-434-878-3	Sequence 3, Appl	807	13	9.8	5011	1	US-08-463-092B-1	Sequence 1, Appl
735	13	9.8	3475	5	PCT-US95-03718-3	Sequence 3, Appl	808	13	9.8	5011	1	US-08-463-092B-3	Sequence 3, Appl
736	13	9.8	3476	1	US-08-183-211-1	Sequence 1, Appl	809	13	9.8	5011	2	US-08-462-109A-1	Sequence 1, Appl
737	13	9.8	3476	5	PCT-US95-00176A-1	Sequence 1, Appl	810	13	9.8	5011	2	US-08-462-109A-3	Sequence 3, Appl
738	13	9.8	3476	5	US-07-977-451-3	Sequence 3, Appl	811	13	9.8	5011	2	US-08-460-907B-1	Sequence 1, Appl
739	13	9.8	3501	1	US-08-252-517-3	Sequence 3, Appl	812	13	9.8	5011	2	US-08-460-907B-3	Sequence 3, Appl
740	13	9.8	3501	1	US-07-906-397A-3	Sequence 3, Appl	813	13	9.8	5011	3	US-08-463-179A-1	Sequence 1, Appl
741	13	9.8	3501	1	US-08-601-891-3	Sequence 3, Appl	814	13	9.8	5011	3	US-08-463-179A-3	Sequence 3, Appl
742	13	9.8	3501	2	PCT-US92-05401-3	Sequence 3, Appl	815	13	9.8	5011	3	US-08-461-384B-1	Sequence 1, Appl
743	13	9.8	3501	5	PCT-US92-09893-3	Sequence 3, Appl	816	13	9.8	5011	3	US-08-461-384B-3	Sequence 3, Appl
744	13	9.8	3501	5	US-08-315-468-3	Sequence 3, Appl	817	13	9.8	5011	3	US-08-407-207A-1	Sequence 1, Appl
745	13	9.8	3516	2	US-08-943-087-1	Sequence 1, Appl	818	13	9.8	5058	4	US-09-889-595-1	Sequence 1, Appl
746	13	9.8	3516	4	US-09-243-248B-59	Sequence 59, App	819	13	9.8	5077	1	US-08-481-130-8	Sequence 8, Appl
747	13	9.8	3539	1	US-08-086-634-1	Sequence 1, Appl	820	13	9.8	5077	1	US-08-485-604-8	Sequence 8, Appl
748	13	9.8	3546	1	US-07-951-715A-10	Sequence 10, Appl	821	13	9.8	5077	1	US-08-485-604-8	Sequence 8, Appl
749	13	9.8	3546	1	US-07-951-715A-12	Sequence 12, Appl	822	13	9.8	5077	1	US-08-485-604-8	Sequence 8, Appl
750	13	9.8	3546	1	US-07-951-715A-14	Sequence 14, Appl	823	13	9.8	5077	1	US-08-487-595-8	Sequence 8, Appl
751	13	9.8	3546	2	US-08-459-448A-10	Sequence 10, Appl	824	13	9.8	5089	6	5177197-31	Patent No. 5177197
752	13	9.8	3546	2	US-08-459-448A-12	Sequence 12, Appl	825	13	9.8	5134	2	US-08-635-121-1	Sequence 1, Appl
753	13	9.8	3546	2	US-08-459-448A-14	Sequence 14, Appl	826	13	9.8	5152	4	US-09-690-364-10	Sequence 10, Appl
754	13	9.8	3546	2	US-08-459-448A-12	Sequence 12, Appl	827	13	9.8	5240	4	US-09-171-337A-2	Sequence 2, Appl
755	13	9.8	3546	2	US-08-459-448A-14	Sequence 14, Appl	828	13	9.8	5261	1	US-08-045-806-3	Sequence 3, Appl
756	13	9.8	3546	2	US-08-459-595A-10	Sequence 10, Appl	829	13	9.8	5261	1	US-08-366-051B-3	Sequence 3, Appl
757	13	9.8	3546	3	US-08-459-595A-12	Sequence 12, Appl	830	13	9.8	5470	1	US-08-441-139-12	Sequence 12, Appl

831	13	9.8	5470	6	5196523-5	Patent No. 5196523	904	13	9.8	15894	1	US-08-348-891A-1	Sequence 1, Appli
c 832	13	9.8	5494	4	US-08-910-864-10	Sequence 10, Appl	905	13	9.8	15894	1	US-08-905-817-1	Sequence 1, Appli
c 833	13	9.8	5510	1	US-08-123-161A-7	Sequence 7, Appli	c 906	13	9.8	16389	4	US-09-741-154-3	Sequence 3, Appli
c 834	13	9.8	5510	1	US-08-483-278-7	Sequence 7, Appli	907	13	9.8	17341	4	US-09-415-946-1	Sequence 1, Appli
c 835	13	9.8	5578	1	US-08-081-610-2	Sequence 2, Appli	908	13	9.8	17606	4	US-08-943-731-4	Sequence 4, Appli
c 836	13	9.8	5690	2	US-08-447-464-2	Sequence 2, Appli	c 909	13	9.8	17606	4	US-08-943-731-4	Sequence 4, Appli
c 837	13	9.8	5690	2	US-08-716-679-2	Sequence 2, Appli	c 910	13	9.8	18436	4	US-08-961-527-87	Sequence 87, Appl
c 838	13	9.8	5737	1	US-08-259-264-1	Sequence 1, Appli	911	13	9.8	18627	4	US-08-961-527-113	Sequence 113, App
c 839	13	9.8	5838	3	US-08-578-096A-1	Sequence 1, Appli	c 912	13	9.8	19182	2	US-08-850-880-11	Sequence 11, Appl
c 840	13	9.8	5838	3	US-09-240-426-1	Sequence 1, Appli	c 913	13	9.8	19182	2	US-08-944-916-11	Sequence 11, Appl
c 841	13	9.8	5874	4	US-08-843-417-9	Sequence 9, Appli	c 914	13	9.8	19182	2	US-09-272-432A-11	Sequence 11, Appl
c 842	13	9.8	5893	1	US-08-592-126-54	Sequence 54, Appl	c 915	13	9.8	24979	3	US-08-147-777-3	Sequence 3, Appli
c 843	13	9.8	5893	2	US-08-687-080-44	Sequence 44, Appl	916	13	9.8	24979	3	US-08-452-872-3	Sequence 3, Appli
c 844	13	9.8	6002	1	US-08-698-551-15	Sequence 15, Appl	917	13	9.8	24979	5	PCT-US93-03985-3	Sequence 3, Appli
c 845	13	9.8	6002	2	US-08-602-228-15	Sequence 15, Appl	c 918	13	9.8	28001	4	US-09-819-993-3	Sequence 3, Appli
c 846	13	9.8	6002	2	US-08-839-032A-15	Sequence 15, Appl	c 919	13	9.8	28001	4	US-09-819-993-3	Sequence 3, Appli
c 847	13	9.8	6002	4	US-09-185-2580-15	Sequence 15, Appl	c 920	13	9.8	28720	4	US-09-341-587-7	Sequence 7, Appli
c 848	13	9.8	6122	1	US-08-403-545-1	Sequence 1, Appli	c 921	13	9.8	28720	4	US-09-341-587-7	Sequence 7, Appli
c 849	13	9.8	6122	4	US-08-404-381-1	Sequence 1, Appli	c 922	13	9.8	28882	4	US-08-961-527-140	Sequence 140, App
c 850	13	9.8	6315	2	US-08-808-793-2	Sequence 2, Appli	c 923	13	9.8	29598	4	US-09-341-587-6	Sequence 6, Appli
c 851	13	9.8	6315	3	US-08-772-512A-2	Sequence 2, Appli	c 924	13	9.8	29629	4	US-09-729-995-3	Sequence 3, Appli
c 852	13	9.8	6318	2	US-08-808-793-1	Sequence 2, Appli	c 925	13	9.8	31960	4	US-09-453-702B-11	Sequence 11, Appl
c 853	13	9.8	6318	3	US-08-772-512A-1	Sequence 1, Appli	c 926	13	9.8	36741	4	US-09-301-665-3	Sequence 3, Appli
c 854	13	9.8	6605	1	US-08-769-309A-4	Sequence 4, Appli	c 927	13	9.8	37948	4	US-09-251-645-11	Sequence 11, Appl
c 855	13	9.8	6605	3	US-08-594-570-4	Sequence 4, Appli	c 928	13	9.8	38564	4	US-09-724-673-3	Sequence 3, Appli
c 856	13	9.8	7082	4	US-09-362-831-1	Sequence 2, Appli	c 929	13	9.8	43804	4	US-09-171-461-1	Sequence 1, Appli
c 857	13	9.8	7152	4	US-09-167-681-29	Sequence 29, Appl	c 930	13	9.8	50000	4	US-09-146-053-4	Sequence 4, Appli
c 858	13	9.8	7163	4	US-08-961-527-67	Sequence 67, Appl	c 931	13	9.8	50341	1	US-08-247-901C-1	Sequence 1, Appli
c 859	13	9.8	7172	4	US-08-961-527-120	Sequence 120, App	c 932	13	9.8	50341	2	US-09-075-904-1	Sequence 1, Appli
c 860	13	9.8	7559	2	US-08-250-848-2	Sequence 2, Appli	c 933	13	9.8	51259	3	US-08-781-891-209	Sequence 209, App
c 861	13	9.8	7676	4	US-09-056-556-213	Sequence 213, App	c 934	13	9.8	52297	4	US-09-426-436-1	Sequence 1, Appli
c 862	13	9.8	7676	4	US-09-072-596-208	Sequence 208, App	c 935	13	9.8	52297	4	US-08-705-557-1	Sequence 1, Appli
c 863	13	9.8	7785	2	US-08-276-967-1	Sequence 2, Appli	c 936	13	9.8	84495	4	US-09-797-906-3	Sequence 3, Appli
c 864	13	9.8	7881	2	US-08-751-189-1	Sequence 1, Appli	c 937	13	9.8	87350	3	US-08-781-891-79	Sequence 79, Appl
c 865	13	9.8	7881	4	US-09-060-836-1	Sequence 1, Appli	c 938	13	9.8	87543	4	US-09-791-211-3	Sequence 3, Appli
c 866	13	9.8	7881	4	US-09-184-445-1	Sequence 1, Appli	c 939	13	9.8	90050	4	US-09-245-041-5	Sequence 5, Appli
c 867	13	9.8	8065	4	US-09-091-952A-6	Sequence 6, Appli	c 940	13	9.8	90050	4	US-09-245-041-5	Sequence 5, Appli
c 868	13	9.8	8703	4	US-08-961-527-177	Sequence 177, App	c 941	13	9.8	98844	4	US-09-791-211-10	Sequence 10, Appl
c 869	13	9.8	8789	1	US-08-328-254-5	Sequence 5, Appli	c 942	13	9.8	111282	4	US-09-754-250-3	Sequence 3, Appli
c 870	13	9.8	8791	5	PCT-US96-01735-5	Sequence 5, Appli	c 943	13	9.8	112132	4	US-09-741-150-3	Sequence 3, Appli
c 871	13	9.8	8854	3	US-09-053-549-1	Sequence 1, Appli	c 944	13	9.8	112132	3	US-09-741-150-3	Sequence 3, Appli
c 872	13	9.8	8916	4	US-09-579-181-11	Sequence 11, Appl	c 945	13	9.8	176373	3	US-09-128-155-17	Sequence 17, Appl
c 873	13	9.8	9354	4	US-09-579-181-10	Sequence 10, Appl	c 946	13	9.8	176373	3	US-09-128-155-17	Sequence 17, Appl
c 874	13	9.8	10136	1	US-08-353-700-2	Sequence 2, Appli	c 947	13	9.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 875	13	9.8	10136	5	PCT-US95-16210-2	Sequence 2, Appli	c 948	13	9.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 876	13	9.8	10357	1	US-08-961-527-191	Sequence 2, Appli	c 949	13	9.8	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 877	13	9.8	10409	3	US-08-772-440-33	Sequence 33, Appl	c 950	13	9.8	4403765	4	US-09-103-840A-2	Sequence 22, Appl
c 878	13	9.8	10642	4	US-09-934-551-3	Sequence 3, Appli	c 951	13	9.8	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c 879	13	9.8	10898	2	US-08-481-658B-5	Sequence 5, Appli	c 952	12	9.1	18	3	US-09-289-377-35	Sequence 35, Appl
c 880	13	9.8	10898	2	US-08-477-504A-5	Sequence 5, Appli	c 953	12	9.1	18	4	US-08-584-040-3067	Sequence 3067, Ap
c 881	13	9.8	10898	2	US-08-486-756A-5	Sequence 5, Appli	c 954	12	9.1	19	1	US-08-244-309-7	Sequence 7, Appli
c 882	13	9.8	10898	2	US-08-485-862B-5	Sequence 5, Appli	c 955	12	9.1	20	4	US-09-356-818A-3	Sequence 3, Appli
c 883	13	9.8	10898	3	US-08-787-739-5	Sequence 5, Appli	c 956	12	9.1	20	4	US-08-997-251-7	Sequence 7, Appli
c 884	13	9.8	10898	3	US-08-487-077A-5	Sequence 5, Appli	c 957	12	9.1	20	4	US-09-555-778-2	Sequence 2, Appli
c 885	13	9.8	10898	3	US-08-485-863A-5	Sequence 5, Appli	c 958	12	9.1	20	4	US-09-430-114-6	Sequence 6, Appli
c 886	13	9.8	10898	4	US-08-485-049D-5	Sequence 5, Appli	c 959	12	9.1	20	4	US-09-702-251-85	Sequence 85, Appl
c 887	13	9.8	10898	4	US-09-178-115-5	Sequence 5, Appli	c 960	12	9.1	21	1	US-09-517-467B-314	Sequence 314, App
c 888	13	9.8	10898	4	US-09-177-776-5	Sequence 5, Appli	c 961	12	9.1	21	1	US-08-151-574-36	Sequence 36, Appl
c 889	13	9.8	11298	1	US-07-869-933-31	Sequence 31, Appl	c 962	12	9.1	21	1	US-08-146-422-3	Sequence 3, Appli
c 890	13	9.8	11298	1	US-08-201-879A-2	Sequence 2, Appli	c 963	12	9.1	21	1	US-08-146-424-3	Sequence 3, Appli
c 891	13	9.8	11298	4	US-09-103-663-31	Sequence 31, Appl	c 964	12	9.1	21	1	US-08-626-554-19	Sequence 19, Appl
c 892	13	9.8	11464	4	US-08-591-840A-2	Sequence 2, Appli	c 965	12	9.1	21	1	US-08-693-709-17	Sequence 17, Appl
c 893	13	9.8	11873	2	US-08-970-269A-32	Sequence 32, Appl	c 966	12	9.1	21	1	US-08-638-448-3	Sequence 3, Appli
c 894	13	9.8	11873	4	US-09-407-562-32	Sequence 32, Appl	c 967	12	9.1	21	2	US-08-419-448-36	Sequence 36, Appl
c 895	13	9.8	11878	2	US-08-970-269A-31	Sequence 31, Appl	c 968	12	9.1	21	2	US-09-233-510-36	Sequence 36, Appl
c 896	13	9.8	11878	4	US-09-407-562-31	Sequence 31, Appl	c 969	12	9.1	22	4	US-08-505-617-10	Sequence 10, Appl
c 897	13	9.8	11883	2	US-08-970-269A-28	Sequence 28, Appl	c 970	12	9.1	22	3	US-09-018-170-10	Sequence 10, Appl
c 898	13	9.8	11883	4	US-09-407-562-28	Sequence 28, Appl	c 971	12	9.1	22	4	US-07-791-931-12	Sequence 12, Appl
c 899	13	9.8	12804	4	US-09-453-702B-149	Sequence 149, App	c 972	12	9.1	22	4	US-09-177-650-26	Sequence 26, Appl
c 900	13	9.8	13146	2	US-08-724-354D-3	Sequence 3, Appli	c 973	12	9.1	24	1	US-08-131-365B-46	Sequence 46, Appl
c 901	13	9.8	13146	3	US-09-270-984A-3	Sequence 3, Appli	c 974	12	9.1	24	1	US-08-302-537A-11	Sequence 11, Appl
c 902	13	9.8	13158	2	US-08-687-080-105	Sequence 105, App	c 975	12	9.1	24	1	US-08-579-667-10	Sequence 10, Appl
c 903	13	9.8	13965	4	US-09-453-702B-48	Sequence 48, Appl	c 976	12	9.1	24	1	US-08-566-037A-12	Sequence 12, Appl
												US-08-480-917-6	Sequence 6, Appli

c 977 12 9.1 24 2 US-08-568-123-46
c 978 12 9.1 24 2 US-08-987-466-10
c 979 12 9.1 24 2 US-08-360-546-4
c 980 12 9.1 24 2 US-08-974-565C-15
c 981 12 9.1 24 4 US-09-240-359-10
c 982 12 9.1 24 4 US-09-138-736-6
c 983 12 9.1 24 4 US-08-702-665A-14
c 984 12 9.1 24 4 US-09-436-068A-4
c 985 12 9.1 25 1 US-07-718-274A-38
c 986 12 9.1 25 1 US-08-149-106-38
c 987 12 9.1 25 2 US-08-298-021-38
c 988 12 9.1 25 2 US-08-596-319-18
c 989 12 9.1 27 3 US-08-997-803-9
c 990 12 9.1 27 3 US-09-005-165-9
c 991 12 9.1 27 4 US-08-584-040-5189
c 992 12 9.1 27 4 US-08-584-040-6419
c 993 12 9.1 28 1 US-08-336-526A-3
c 994 12 9.1 28 1 US-08-478-940-3
c 995 12 9.1 28 2 US-08-882-435-2
c 996 12 9.1 28 4 US-09-386-642-48
c 997 12 9.1 29 1 US-08-365-189-4
c 998 12 9.1 30 1 US-08-336-526A-4
c 999 12 9.1 30 1 US-08-478-940-4
c1000 12 9.1 30 1 US-08-450-945-34

ALIGNMENTS

RESULT 1
US-09-397-787-308/c
; Sequence 308, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-308

Query Match 12.9%; Score 17; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 ACCTGAAGGCCACAGAG 66
Db 401 AGCTGAAGGCCACAGAG 385

RESULT 2
US-09-484-970B-82/c
; Sequence 82, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PERL Program
; SEQ ID NO 82
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 199069.2CB1
US-09-484-970B-82

Query Match 12.9%; Score 17; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 ACCTGAAGGCCACAGAG 66
Db 691 AGCTGAAGGCCACAGAG 675

RESULT 3
US-08-445-520B-8
; Sequence 8, Application US/08445520B
; Patent No. 5866323
; GENERAL INFORMATION:
; APPLICANT: Markowitz, Sanford D.
; APPLICANT: Brattain, Michael G.
; APPLICANT: Willison, James K.V.
; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND
; TITLE OF INVENTION: THERAPY BASED ON MUTATION OF RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,520B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/417,867
; FILING DATE: 07-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 062361-0101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 336...2036
; OTHER INFORMATION:
US-08-445-520B-8

Query Match 12.9%; Score 17; DB 2; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

RESULT 4

US-08-451-946B-7
; Sequence 7, Application US/08451946B
; Patent No. 6001969
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,946B
; FILING DATE: 26-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09V
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-9540
; TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 336...2038

US-08-451-946B-7

Query Match 12.9%; Score 17; DB 3; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

RESULT 5

US-08-446-938B-7
; Sequence 7, Application US/08446938B
; Patent No. 6008011
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.

; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,938B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09FZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 336...2038

US-08-446-938B-7

Query Match 12.9%; Score 17; DB 3; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

RESULT 6

US-08-311-703A-7
; Sequence 7, Application US/08311703A
; Patent No. 6010872
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.

; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts

```
;; COUNTRY: U.S.A.
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/311.703A
;; FILING DATE: 23-SEP-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/786,063
;; FILING DATE: 31-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hogle, Doreen
;; REGISTRATION NUMBER: 36,361
;; REFERENCE/DOCKET NUMBER: WHI91-09F
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 781-861-6240
;; TELEFAX: 781-861-9540
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2090 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 336..2038
;; US-08-311-703A-7
```

```
Query Match 12.9%; Score 17; DB 3; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 41 ATAGGCCCAAGCTGAAG 57
Db 1111 ATAGGCCCAAGCTGAAG 1127
```

```
RESULT 7
US-08-446-939B-7
; Sequence 7, Application US/08446939B
; Patent No. 6046157
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,939B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-MAY-1995
```

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/786,063
;; FILING DATE: 23-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: WHI91-09FX
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2090 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 336..2038
;; US-08-446-939B-7
```

```
Query Match 12.9%; Score 17; DB 3; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 41 ATAGGCCCAAGCTGAAG 57
Db 1111 ATAGGCCCAAGCTGAAG 1127
```

```
RESULT 8
US-09-183-543-7
; Sequence 7, Application US/09183543A
; Patent No. 6086867
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Modulation of TGF-Beta by TGF-Beta Type III Receptor Polypept
; FILE REFERENCE: WHI91-09FXA
; CURRENT APPLICATION NUMBER: US/09/183,543A
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: US 08/446,939
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: US 08/311,703
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: US 07/786,063
; EARLIER FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (336)...(2038)
; US-09-183-543-7
```

```
Query Match 12.9%; Score 17; DB 3; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 41 ATAGGCCCAAGCTGAAG 57
Db 1111 ATAGGCCCAAGCTGAAG 1127
```

```
RESULT 9
US-08-446-936A-7
; Sequence 7, Application US/08446936A
```

Patent No. 6201108
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,936A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09FY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 336..2038
US-08-446-936A-7

Query Match 12.9%; Score 17; DB 4; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

RESULT 10
US-09-239-864A-10
; Sequence 10, Application US/09239864A
; Patent No. 6291237
; GENERAL INFORMATION:
; APPLICANT: Markowitz, Sanford D
; APPLICANT: Brattain, Michael G
; APPLICANT: Willson, James K.V.
; TITLE OF INVENTION: CANCER DIAGNOSIS, PROGNOSIS AND THERAPY BASED ON
; TITLE OF INVENTION: MUTATION OF RECEPTOR
; FILE REFERENCE: 062361.0108
; CURRENT APPLICATION NUMBER: US/09/239,864A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/417,867

; PRIOR FILING DATE: 1995-04-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 10
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (336)..(2036)
US-09-239-864A-10

Query Match 12.9%; Score 17; DB 4; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

RESULT 11
PCT-US92-09326-3
; Sequence 3, Application PC/TUS9209326
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; TITLE OF INVENTION: TGF-BETA TYPE RECEPTOR cDNAs ENCODED
; TITLE OF INVENTION: PRODUCTS AND USES THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09326
; FILING DATE: 19921030
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US92-09326-3

Query Match 12.9%; Score 17; DB 5; Length 2090;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 ATAAGGCCCAAGCTGAAG 57
|||||
Db 1111 ATAAGGCCCAAGCTGAAG 1127

```
RESULT 12
US-08-361-873A-1
; Sequence 1, Application US/08361873A
; Patent No. 5693607
; GENERAL INFORMATION:
; APPLICANT: SEGARINI, PATRICIA R.
; APPLICANT: DASCH, JAMES R.
; APPLICANT: OLSEN, DAVID R.
; APPLICANT: CARRILLO, PEDRO A.
; TITLE OF INVENTION: USES OF TGB-beta RECEPTOR FRAGMENT AS A
; TITLE OF INVENTION: THERAPEUTIC AGENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,873A
; FILING DATE: 22-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 22095-20261.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 341..2041
US-08-361-873A-1

Query Match 12.9%; Score 17; DB 1; Length 2095;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ATRAGGCCAAGCTGAAG 57
Db 1116 ATAAGGCCAAGCTGAAG 1132

RESULT 13
US-08-365-486A-12/c
; Sequence 12, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```

```
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bNOS cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349...4638
US-08-365-486A-12

Query Match 12.9%; Score 17; DB 2; Length 5057;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CCAGCTTGGATAAGGCC 48
Db 530 CCAGCTTGGATAAGGCC 514

RESULT 14
US-08-880-342-12/c
; Sequence 12, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
```

;; FILING DATE: 13-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/365,486
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 8255-0018.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5057 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: rat bNOS cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 349...4638
US-08-880-342-12

Query Match 12.9%; Score 17; DB 4; Length 5057;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CCAGCTTGGATAAGGCC 48
|||||
DB 530 CCAGCTTGGATAAGGCC 514

RESULT 15
US-07-642-002-1/c
; Sequence 1, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Bredt, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: One Thomas Circle, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,002
; FILING DATE: 19910118
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.033576
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 296-5500
; TELEFAX: (202) 296-7830
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 5108 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; ORIGINAL SOURCE:
;; ORGANISM: Rattus rattus
;; TISSUE TYPE: Brain
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 400...4686
;; OTHER INFORMATION:
US-07-642-002-1

Query Match 12.9%; Score 17; DB 1; Length 5108;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CCAGCTTGGATAAGGCC 48
|||||
DB 581 CCAGCTTGGATAAGGCC 565

RESULT 16
US-08-700-637-9/c
; Sequence 9, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAT03
; CLONE: 695983
US-08-700-637-9

Query Match 12.1%; Score 16; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGATGCAGAGAACAC 80
Db 112 AGATGCAGAGAACAC 97

RESULT 17
US-09-392-184-4
; Sequence 4, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1232)
; OTHER INFORMATION: sercarboxy (serine carboxypeptidase)
US-09-392-184-4

Query Match 12.1%; Score 16; DB 4; Length 1232;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AAGAAATGCCAGCTT 38
Db 790 AAGAAATGCCAGCTT 805

RESULT 18
US-08-704-711A-9
; Sequence 9, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; FILE REFERENCE: PatentIn Release #1.0, Version #1.30
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-9

Query Match 12.1%; Score 16; DB 3; Length 3437;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 CTGAAGGCCACAGAGA 67
Db 2701 CTGAAGGCCACAGAGA 2716

RESULT 19
US-09-521-220-9
; Sequence 9, Application US/09521220
; Patent No. 6395348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; FILE REFERENCE: PatentIn Release #1.0, Version #1.30
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear


```
; SEQUENCE DESCRIPTION: SEQ ID NO: 9;
US-09-521-220-9
Query Match      12.1%  Score 16;  DB 4;  Length 3437;
Best Local Similarity 100.0%;  Pred. No. 24;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  52 CTGAAGGCCACAGAGA 67
Db   2701 CTGAAGGCCACAGAGA 2735

RESULT 20
US-08-704-711A-8
; Sequence 8, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3456 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-704-711A-8
Query Match      12.1%  Score 16;  DB 3;  Length 3456;
Best Local Similarity 100.0%;  Pred. No. 24;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  52 CTGAAGGCCACAGAGA 67
Db   2720 CTGAAGGCCACAGAGA 2735

RESULT 21
US-07-582-945-1/c
; Sequence 1, Application US/07582945
; Patent No. 5369019
; GENERAL INFORMATION:
; APPLICANT: TARKER FOGED, Niels
; APPLICANT: PETERSON, Svend
; TITLE OF INVENTION: A PASTURELLA VACCINE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
```

STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/582.945
FILING DATE: 19901012
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/112 PLVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4380 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: Pasteurella multocida
FEATURE:
NAME/KEY: CDS
LOCATION: 219..4073
US-07-582-945-1

Query Match 12.1%; Score 16; DB 1; Length 4380;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CTGGAAGAAATTGCCA 34
Db 3459 CTGGAAGAAATTGCCA 3444

RESULT 23
US-08-453-141-1/c
Sequence 1, Application US/08453141
Patent No. 5885589
GENERAL INFORMATION:
APPLICANT: FOGED, Niels T.
TITLE OF INVENTION: PASTEURILLA VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453.141
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/293.314
FILING DATE: 22-AUG-1994
APPLICATION NUMBER: US 07/582.945
FILING DATE: 12-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/582.945
FILING DATE: 12-OCT-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DR89/00084
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1995/88
FILING DATE: 04-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40389/102/AKZO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4380 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 219..4076
US-08-453-141-1

Query Match 12.1%; Score 16; DB 2; Length 4380;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CTGGAAGAAATTGCCA 34
Db 3459 CTGGAAGAAATTGCCA 3444

RESULT 24
US-08-293-314-1/c
Sequence 1, Application US/08293314
Patent No. 6110470
GENERAL INFORMATION:
APPLICANT: FOGED, Niels T.
TITLE OF INVENTION: PASTEURILLA VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293.314
FILING DATE: 22-AUG-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/582.945
FILING DATE: 12-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DR89/00084
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1995/88
FILING DATE: 04-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40389/102/AKZO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 219..4076
US-08-293-314-1

Query Match 12.1%; Score 16; DB 3; Length 4380;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CTGGAAGAAATTGCCA 34
|||||
DB 3459 CTGGAAGAAATTGCCA 3444

RESULT 25
US-08-253-155A-9
; Sequence 9, Application US/08253155A
; Patent No 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: CDK4 Binding Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-028
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-253-155A-9

Query Match 12.1%; Score 16; DB 1; Length 8201;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CTGATGACCAAGAGA 97
|||||
DB 5803 CTGATGACCAAGAGA 5818

RESULT 26
US-09-453-702B-252/c

; Sequence 252, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12848
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-453-702B-252
Query Match 12.1%; Score 16; DB 4; Length 12848;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 CCACAGACGAGGAGAA 113
|||||
DB 3068 CCACAGACGAGGAGAA 3053
RESULT 27
US-09-245-041-3
; Sequence 3, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO 3
; LENGTH: 17056
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-245-041-3

Query Match      12.1%; Score 16; DB 4; Length 17056;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 CAGACGAGGAGAGTG 116
   |||||
Db 7892 CAGACGAGGAGAGTG 7907

RESULT 28
US-09-453-702B-79
; Sequence 79, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; NAME: Seay, Nicholas J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38155
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-09-453-702B-79

Query Match      12.1%; Score 16; DB 4; Length 38155;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCACAGACGAGGAGAA 113
   |||||
Db 32706 CCACAGACGAGGAGAA 32721

RESULT 29
US-09-453-702B-137/c
; Sequence 137, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; NAME: Seay, Nicholas J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48908
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:

US-09-453-702B-137

Query Match      12.1%; Score 16; DB 4; Length 48908;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCACAGACGAGGAGAA 113
   |||||
Db 14259 CCACAGACGAGGAGAA 14244

RESULT 30
US-08-153-799-9
; Sequence 9, Application US/08153799
; Patent No. 5766883
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J
; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..38
OTHER INFORMATION: /product= "encodes amino acids"
OTHER INFORMATION: 183-194 of HSA"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 39..53
OTHER INFORMATION: /function= "KEX2 spacer"
FEATURE:
NAME/KEY: CDS
LOCATION: 54..74
OTHER INFORMATION: /function= "encodes amino acids 1-7"
OTHER INFORMATION: of uPA"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..75
OTHER INFORMATION: /function= "LINKER 9"
US-08-153-799-9

Query Match 11.4%; Score 15; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TCCACGCTTGGATAA 44
Db 35 TCCACGCTTGGATAA 49

RESULT 31
US-09-040-984-83
Sequence 83, Application US/09040984
Patent No. 6210883
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-282-6031
TELEX:
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-984-83
Query Match 11.4%; Score 15; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GGAGTCAAAATTCCT 130
Db 180 GGAGTCAAAATTCCT 194

RESULT 32
US-09-123-912-83
Sequence 83, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 460
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (104)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (118)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (172)
OTHER INFORMATION: Where n is a, c, g or t

```
; NAME/KEY: modified_base
; LOCATION: (401)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (422)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (423)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (444)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (449)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-83
```

```
Query Match 11.4%; Score 15; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 116 GGAGTGAATTCCT 130
|||||
Db 180 GGAGTGAATTCCT 194
```

RESULT 33

```
US-09-643-597-83
; Sequence 83, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
```

```
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 460
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
```

```
; FEATURE:
```

```
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(460)
```

```
; OTHER INFORMATION: n = A,T,C or G
```

US-09-643-597-83

```
Query Match 11.4%; Score 15; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 116 GGAGTGAATTCCT 130
|||||
Db 180 GGAGTGAATTCCT 194
```

RESULT 34

```
US-08-671-525B-9/c
```

```
; Sequence 9, Application US/08671525B
; Patent No. 5703220
; GENERAL INFORMATION:
```

```
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
```

```
; STREET: P.O. Box 828
```

```
; CITY: Bloomfield Hills
```

```
; STATE: MI
```

```
; COUNTRY: US
```

```
; ZIP: 48303
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/671,525B
```

```
; FILING DATE: June 27, 1996
```

```
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Smith, DeAnn F.
```

```
; REGISTRATION NUMBER: 36683
```

```
; REFERENCE/DOCKET NUMBER: 2115-000853DVB
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (810)641-1600
```

```
; TELEFAX: (810)641-0270
```

```
; INFORMATION FOR SEQ ID NO: 9:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 975 base pairs
```

```
; TYPE: nucleic acid
```

```
; STRANDEDNESS: double
```

```
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA (genomic)
```

```
; HYPOTHETICAL: NO
```

```
; ANTI-SENSE: NO
```

```
; ORIGINAL SOURCE:
```

```
; ORGANISM: Mouse
```

```
; FEATURE:
```

```
; NAME/KEY: CDS
```

```
; LOCATION: 1..975
```

```
US-08-671-525B-9
```

```
Query Match 11.4%; Score 15; DB 1; Length 975;
```

```
Best Local Similarity 100.0%; Pred. No. 76;
```

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 59 CCACAGAGATGCAGA 73
```

```
|||||
```

```
Db 379 CCACAGAGATGCAGA 365
```

RESULT 35

```
US-08-672-109B-9/c
```

```
; Sequence 9, Application US/08672109B
```

```
; Patent No. 5710265
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Yamada, Tadataka
```

```
; APPLICANT: Gantz, Ira
```

```
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
```

```
; NUMBER OF SEQUENCES: 23
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
```

```
; STREET: P.O. Box 828
```

```
; CITY: Bloomfield Hills
```

```
; STATE: MI
```

```
; COUNTRY: US
```

```
; ZIP: 48303
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/672,109B
;; FILING DATE: June 27, 1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, Deann F.
;; REGISTRATION NUMBER: 36683
;; REFERENCE/DOCKET NUMBER: 2115-000853DVC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810)641-1600
;; TELEFAX: (810)641-0270
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 975 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mouse
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..975
US-08-672-109B-9

Query Match 11.4%; Score 15; DB 1; Length 975;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACAGAGATGCAGA 73
DB 379 CCACAGAGATGCAGA 365

RESULT 36
US-08-842-045-9/c
;; Sequence 9, Application US/08842045
;; Patent No. 5817787
;; GENERAL INFORMATION:
;; APPLICANT: Yamada, Tadataka
;; APPLICANT: Gantz, Ira
;; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
;; STREET: P.O. Box 828
;; CITY: Bloomfield Hills
;; STATE: MI
;; COUNTRY: US
;; ZIP: 48303
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/842,045
;; FILING DATE:
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, Deann F.
;; REGISTRATION NUMBER: 36683
;; REFERENCE/DOCKET NUMBER: 2115-000853DVE
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810)641-1600
;; TELEFAX: (810)641-0270
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 975 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double

;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mouse
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..975
US-08-842-045-9

Query Match 11.4%; Score 15; DB 1; Length 975;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACAGAGATGCAGA 73
DB 379 CCACAGAGATGCAGA 365

RESULT 37
US-08-842-238-9/c
;; Sequence 9, Application US/08842238
;; Patent No. 5869257
;; GENERAL INFORMATION:
;; APPLICANT: Yamada, Tadataka
;; APPLICANT: Gantz, Ira
;; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
;; STREET: P.O. Box 828
;; CITY: Bloomfield Hills
;; STATE: MI
;; COUNTRY: US
;; ZIP: 48303
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/842,238
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, Deann F.
;; REGISTRATION NUMBER: 36683
;; REFERENCE/DOCKET NUMBER: 2115-000853DVD
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810)641-1600
;; TELEFAX: (810)641-0270
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 975 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mouse
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..975
US-08-842-238-9

Query Match 11.4%; Score 15; DB 2; Length 975;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACAGAGATGCAGA 73

us-09-915-178-1.01110.rni

TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonists to Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS: McDonnell Boehrnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/706,281A

FILING DATE: 04-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION: Kevin E

NAME: NO. 6100048han, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 96,886

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX: 312-913-0002

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 978 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: CDS

NAME/KEY: 1..975

LOCATION: 1..975

US-08-706-281A-17

Query Match 11.4%; Score 15; DB 3; Length 978;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACAGAGATGCAGA 73

Db 379 CCACAGAGATGCAGA 365

GENERAL INFORMATION: Cone, Roger D

APPLICANT: Chen, Wenbiao

Low, Malcolm J

TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: McDonnell Boehrnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/097,231

FILING DATE: 12-Jun-1998

US-09-097-231-17/C

Sequence 17, Application US/09097231

Patent No. 6278038

GENERAL INFORMATION: Cone, Roger D

APPLICANT: Chen, Wenbiao

Low, Malcolm J

TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: McDonnell Boehrnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonists to Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS: McDonnell Boehrnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/706,281A

FILING DATE: 04-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION: Kevin E

NAME: NO. 6100048han, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 96,886

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX: 312-913-0002

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 978 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: CDS

NAME/KEY: 1..975

LOCATION: 1..975

US-08-706-281A-17

Query Match 11.4%; Score 15; DB 3; Length 975;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACAGAGATGCAGA 73

Db 379 CCACAGAGATGCAGA 365

GENERAL INFORMATION: Cone, Roger D

APPLICANT: Chen, Wenbiao

Low, Malcolm J

TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: McDonnell Boehrnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/097,231

FILING DATE: 12-Jun-1998

US-08-706-281A-17/C

Sequence 17, Application US/08706281A

Patent No. 6100048

GENERAL INFORMATION: Cone, Roger D

APPLICANT: Fan, Wei

APPLICANT: Boston, Bruce A

APPLICANT: Kesterton, Robert A

APPLICANT: Lu, Dongsi

APPLICANT: Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and

US-08-629-335B-9

Query Match 11.4%; Score 15; DB 3; Length 975;

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..975
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-097-231-17

Query Match 11.4%; Score 15; DB 4; Length 978;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 CCACAGATGCGAGA 73
Db 379 CCACAGATGCGAGA 365
|||||

RESULT 41
US-09-152-060-12
; Sequence 12, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-12

Query Match 11.4%; Score 15; DB 4; Length 1586;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 CAGGAGAAGTGGAGT 120
Db 11 CAGGAGAAGTGGAGT 25
|||||

RESULT 42
US-09-453-702B-105
; Sequence 105, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1711
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-453-702B-105

Query Match 11.4%; Score 15; DB 4; Length 1711;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ACCTGGAAGAAATTG 31
Db 1489 ACCTGGAAGAAATTG 1503
|||||

RESULT 43
US-08-615-170-18
; Sequence 18, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.

APPLICANT: LARKIN, Sarah B.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 23070-053120
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-615-170-18

Query Match 11.4%; Score 15; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 CCAAGCTGAAGGCCA 61
|||||
Db 672 CCAAGCTGAAGGCCA 686

RESULT 44
US-09-434-613-2/c
Sequence 2, Application US/09434613
Patent No. 6337187
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 18991, A No. 6337187el Human Lipase
FILE REFERENCE: 5800-63
CURRENT APPLICATION NUMBER: US/09/434,613
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)...(1174)
US-09-434-613-2

Query Match 11.4%; Score 15; DB 4; Length 1964;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GCTGAAGGCCACAGA 65
|||||
Db 261 GCTGAAGGCCACAGA 247

RESULT 45
US-09-149-476-132/c
Sequence 132, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 11.4%; Score 15; DB 4; Length 2012;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AGTGAATTTCTGA 132
DB 1688 AGTGAATTTCTGA 1674

RESULT 46
US-09-336-643A-17
; Sequence 17, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: NO. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)...(1705)
; OTHER INFORMATION: K:hnov11
US-09-336-643A-17

Query Match 11.4%; Score 15; DB 4; Length 3102;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAGCAGGAGAGTGG 117
|||||
DB 664 GAGCAGGAGAGTGG 678

RESULT 47
US-08-494-714-1
; Sequence 1, Application US/08494714
; Patent No. 5587290
; GENERAL INFORMATION:
; APPLICANT: Klionsky, Daniel.
; APPLICANT: Holzer, Helmut
; APPLICANT: Destruelle, Monica
; TITLE OF INVENTION: STRESS TOLERANT YEAST MUTANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,714
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-61036/DJB/RAO

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 210 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 579...3701
US-08-494-714-1

Query Match 11.4%; Score 15; DB 1; Length 3876;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TGGAGTGAATTTCC 129
|||||
DB 2229 TGGAGTGAATTTCC 2243

RESULT 48
PCT-US96-10782-1
; Sequence 1, Application PC/TUS9610782
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: STRESS TOLERANT YEAST MUTANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10782
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 579...3701
PCT-US96-10782-1

Query Match 11.4%; Score 15; DB 5; Length 3876;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TGGAGTGAATTC 129
|||||
Db 2229 TGGAGTGAATTC 2243

RESULT 49

US-09-295-593-37
; Sequence 37, Application US/09295593
; Patent No. 6417169
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Alping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: 032396-046
; CURRENT APPLICATION NUMBER: US/09/295,593
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 4350
; TYPE: DNA
; ORGANISM: Human
US-09-295-593-37

Query Match 11.4%; Score 15; DB 4; Length 4350;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCACAGACGAGGAGA 112
|||||
Db 3584 CCACAGACGAGGAGA 3598

RESULT 50

US-09-066-047-1/c
; Sequence 1, Application US/09066047A
; Patent No. 6306394
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Cheryl
; STOREY, James
; BELTZ, Gerald A.
; COUGHLIN, Richard T.
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
; USE OF GRANULOCYTIC ERHLLICHA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,047A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,869
; FILING DATE: 25-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 106.941.156

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-066-047-1

Query Match 11.4%; Score 15; DB 4; Length 4833;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 AGAAGACACTCTGA 85
|||||
Db 4006 AGAAGACACTCTGA 3992

Search completed: June 2, 2003, 16:39:48
Job time : 109 secs

THIS PAGE BLANK (3PT0)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 15:56:19 ; Search time 106 Seconds
(without alignments)
1679.096 Million cell updates/sec

Title: US-09-915-178-1
Perfect score: 132
Sequence: 1 atggcacacaaactagacct.....agtggagtgaattctcta 132

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 845702 seqs, 674182571 residues

Word size : 10

Total number of hits satisfying chosen parameters: 199495

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications, NA:*

- 1: /cgn2.6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2.6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2.6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2.6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2.6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2.6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2.6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2.6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2.6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2.6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2.6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	14.4	39776	9 US-10-160-293-3	Sequence 3, Appli
2	18	13.6	243	10 US-09-919-580-517	Sequence 517, App
3	18	13.6	353	10 US-09-919-580-224	Sequence 224, App
4	18	13.6	395	10 US-09-919-580-207	Sequence 207, App
5	18	13.6	404	10 US-09-960-352-10885	Sequence 10885, A
6	18	13.6	405	10 US-09-960-352-6906	Sequence 6906, Ap
7	18	13.6	408	10 US-09-960-352-12808	Sequence 12808, A
8	18	13.6	426	10 US-09-998-598-71	Sequence 71, Appl
9	18	13.6	428	10 US-09-919-580-503	Sequence 503, App
10	18	13.6	429	10 US-09-919-580-633	Sequence 633, App
11	18	13.6	434	10 US-09-919-580-627	Sequence 627, App
12	18	13.6	438	10 US-09-919-580-458	Sequence 458, App
13	18	13.6	438	10 US-09-919-580-583	Sequence 583, App
14	18	13.6	439	10 US-09-919-580-910	Sequence 910, App
15	18	13.6	443	10 US-09-919-580-659	Sequence 659, App
16	18	13.6	445	10 US-09-919-580-727	Sequence 727, App
17	18	13.6	446	10 US-09-919-580-891	Sequence 891, App
18	18	13.6	446	10 US-09-880-107-3158	Sequence 3158, Ap
19	18	13.6	449	9 US-09-918-995-15768	Sequence 15768, A

18	13.6	449	10	US-09-919-580-122	Sequence 122, App
20	18	451	10	US-09-919-580-190	Sequence 190, App
21	18	451	10	US-09-919-580-553	Sequence 553, App
22	18	452	10	US-09-919-580-348	Sequence 348, App
23	18	452	10	US-09-919-580-274	Sequence 274, App
24	18	453	10	US-09-880-107-3019	Sequence 3019, Ap
25	18	453	10	US-09-919-580-273	Sequence 273, App
26	18	455	10	US-09-919-580-219	Sequence 219, App
27	18	456	10	US-09-960-352-2605	Sequence 2605, Ap
28	18	461	10	US-09-919-580-56	Sequence 56, Appl
29	18	465	10	US-09-918-995-21161	Sequence 21161, A
30	18	468	9	US-09-918-995-24062	Sequence 24062, A
31	18	469	9	US-09-918-995-15273	Sequence 15273, A
32	18	473	9	US-09-918-995-22477	Sequence 22477, A
33	18	474	9	US-09-918-995-19906	Sequence 19906, A
34	18	483	9	US-09-918-995-24178	Sequence 24178, A
35	18	494	9	US-09-919-580-874	Sequence 874, App
36	18	517	10	US-09-919-580-159	Sequence 159, App
37	18	559	10	US-09-919-580-798	Sequence 798, App
38	18	693	10	US-09-918-995-1336	Sequence 1336, Ap
39	18	9953	9	US-09-764-847-1336	Sequence 1336, Ap
40	18	11189	9	US-10-092-154-1335	Sequence 1335, Ap
41	18	11189	9	US-09-764-847-1335	Sequence 1335, Ap
42	18	11189	9	US-09-918-995-6168	Sequence 6168, Ap
43	17	425	9	US-09-960-352-5941	Sequence 5941, Ap
44	17	428	10	US-09-918-995-4250	Sequence 4250, Ap
45	17	433	9	US-09-876-889-308	Sequence 308, App
46	17	439	10	US-09-918-995-22450	Sequence 22450, A
47	17	461	9	US-09-918-995-23067	Sequence 23067, A
48	17	465	9	US-10-102-806-146	Sequence 146, App
49	17	814	9	US-09-738-626-1039	Sequence 1039, Ap
50	17	1077	9	US-09-878-905-10	Sequence 10, Appl
51	17	2090	10	US-09-954-456-2001	Sequence 2001, Ap
52	17	5759	10	US-10-071-766-52	Sequence 52, Appl
53	17	5821	9	US-09-764-891-10217	Sequence 10217, A
54	17	13026	9	US-09-738-626-1	Sequence 1, Appli
55	17	3309400	9	US-09-925-299-674	Sequence 674, App
56	16	134	9	US-10-060-036-1389	Sequence 1389, Ap
57	16	12.1	134	10 US-09-983-965-1398	Sequence 1398, Ap
58	16	12.1	281	10 US-09-878-574-408	Sequence 408, App
59	16	12.1	336	10 US-10-092-154-466	Sequence 466, App
60	16	12.1	376	10 US-09-864-761-12	Sequence 12, Appl
61	16	12.1	434	10 US-09-918-995-35268	Sequence 35268, A
62	16	12.1	444	10 US-09-918-995-26427	Sequence 26427, A
63	16	12.1	444	10 US-10-103-313-122	Sequence 122, App
64	16	12.1	444	10 US-10-115-928-22	Sequence 22, Appl
65	16	12.1	65	10 US-09-815-242-6650	Sequence 6650, Ap
66	16	12.1	460	10 US-09-864-761-101	Sequence 101, App
67	16	12.1	475	10 US-09-867-550-1367	Sequence 1367, Ap
68	16	12.1	478	10 US-09-918-995-26427	Sequence 26427, A
69	16	12.1	532	10 US-10-103-313-636	Sequence 636, App
70	16	12.1	665	9 US-10-115-928-68	Sequence 68, Appl
71	16	12.1	665	9 US-09-381-6248-5	Sequence 5, Appli
72	16	12.1	665	10 US-09-745-763-99	Sequence 99, Appl
73	16	12.1	665	10 US-10-103-313-635	Sequence 635, App
74	16	12.1	665	10 US-10-103-313-637	Sequence 637, App
75	16	12.1	665	10 US-10-103-313-638	Sequence 638, App
76	16	12.1	665	10 US-10-115-928-67	Sequence 67, Appl
77	16	12.1	665	10 US-10-115-928-69	Sequence 69, Appl
78	16	12.1	665	10 US-10-115-928-70	Sequence 70, Appl
79	16	12.1	665	10 US-09-381-6248-4	Sequence 4, Appli
80	16	12.1	665	10 US-09-978-168-3	Sequence 3, Appli
81	16	12.1	665	10 US-09-919-497-34	Sequence 34, Appli

93	16	12.1	3437	10	US-09-954-456-1170	Sequence 1170, Ap	15	11.4	517	10	US-09-924-035A-541	Sequence 541, App
94	16	12.1	3705	12	US-10-044-090-307	Sequence 307, App	15	11.4	526	9	US-09-736-457-1473	Sequence 1473, Ap
95	16	12.1	4815	10	US-09-888-615-14	Sequence 14, Appl	15	11.4	526	9	US-09-902-941-1473	Sequence 1473, Ap
96	16	12.1	4863	10	US-09-815-242-4071	Sequence 4071, Ap	15	11.4	526	9	US-09-849-626-1473	Sequence 1473, Ap
97	16	12.1	5184	10	US-09-845-583-9	Sequence 9, Appl	15	11.4	526	10	US-10-017-754-1473	Sequence 1473, Ap
98	16	12.1	6093	9	US-09-764-891-8090	Sequence 8090, Ap	15	11.4	536	10	US-09-864-864-221	Sequence 221, App
99	16	12.1	6640	9	US-10-092-154-1077	Sequence 1077, Ap	15	11.4	674	10	US-09-833-790-141	Sequence 141, App
100	16	12.1	6640	10	US-09-764-847-1077	Sequence 1077, Ap	15	11.4	696	10	US-09-741-669-203	Sequence 203, App
101	16	12.1	6940	10	US-09-880-107-1724	Sequence 1724, Ap	15	11.4	696	10	US-09-815-242-6124	Sequence 6124, Ap
102	16	12.1	7878	10	US-09-962-436-562	Sequence 562, App	15	11.4	715	10	US-09-776-724A-12	Sequence 12, Appl
103	16	12.1	8408	9	US-10-098-841-51	Sequence 51, Appl	15	11.4	838	9	US-09-880-107-3491	Sequence 3491, Ap
104	16	12.1	8408	9	US-10-098-841-50	Sequence 50, Appl	15	11.4	838	9	US-09-989-920-11	Sequence 11, Appl
105	16	12.1	8495	9	US-10-108-605-356	Sequence 356, App	15	11.4	1032	10	US-09-764-891-2652	Sequence 2652, App
106	16	12.1	8974	9	US-10-092-154-1078	Sequence 1078, Ap	15	11.4	1032	10	US-09-770-445-190	Sequence 190, App
107	16	12.1	8974	10	US-09-764-847-1078	Sequence 1078, Ap	15	11.4	1033	10	US-09-989-920-12	Sequence 12, Appl
108	16	12.1	10923	10	US-10-092-154-1079	Sequence 1079, Ap	15	11.4	1093	10	US-09-759-468-1	Sequence 1, Appl
109	16	12.1	10923	10	US-09-764-847-1079	Sequence 1079, Ap	15	11.4	1132	9	US-10-103-313-67	Sequence 67, Appl
110	16	12.1	12848	9	US-09-893-238-3	Sequence 238, App	15	11.4	1158	9	US-09-938-842A-1737	Sequence 1737, Ap
111	16	12.1	17056	10	US-09-834-975-122	Sequence 975, Appl	15	11.4	1430	9	US-09-808-602-5	Sequence 5, Appl
112	16	12.1	23106	9	US-10-114-170-79	Sequence 1, Appl	15	11.4	1430	9	US-09-800-198-5	Sequence 5, Appl
113	16	12.1	38155	9	US-10-114-170-79	Sequence 79, Appl	15	11.4	1431	9	US-09-977-418-21	Sequence 21, Appl
114	16	12.1	48908	9	US-09-859-888-3	Sequence 137, App	15	11.4	1431	9	US-09-977-418-21	Sequence 21, Appl
115	16	12.1	65464	9	US-10-017-721-3	Sequence 3, Appl	15	11.4	1431	9	US-09-977-418-21	Sequence 21, Appl
116	16	12.1	175661	9	US-09-949-654-3	Sequence 3, Appl	15	11.4	1477	10	US-09-894-633A-90	Sequence 90, Appl
117	16	12.1	368004	10	US-10-066-543-2727	Sequence 2727, Ap	15	11.4	1526	9	US-09-852-797-12	Sequence 12, Appl
118	15	11.4	227	10	US-09-834-975-122	Sequence 975, Appl	15	11.4	1586	10	US-09-852-797-12	Sequence 12, Appl
119	15	11.4	231	10	US-10-066-543-1647	Sequence 1647, Ap	15	11.4	1586	10	US-09-852-797-12	Sequence 12, Appl
120	15	11.4	242	9	US-09-440-829-1	Sequence 1, Appl	15	11.4	1622	10	US-09-864-864-303	Sequence 303, App
121	15	11.4	293	10	US-09-834-975-107	Sequence 107, App	15	11.4	1653	9	US-09-938-842A-1054	Sequence 1054, Ap
122	15	11.4	293	10	US-10-066-543-1647	Sequence 1647, Ap	15	11.4	1674	9	US-09-764-891-8862	Sequence 8862, Ap
123	15	11.4	304	9	US-09-834-975-107	Sequence 107, App	15	11.4	1674	9	US-09-764-891-8865	Sequence 8865, Ap
124	15	11.4	304	10	US-09-833-263-501	Sequence 501, App	15	11.4	1711	9	US-10-114-170-105	Sequence 105, App
125	15	11.4	347	9	US-10-060-036-1888	Sequence 501, App	15	11.4	1859	9	US-10-132-744A-5	Sequence 5, Appl
126	15	11.4	347	9	US-10-060-036-2038	Sequence 1888, Ap	15	11.4	1864	10	US-09-963-908-2	Sequence 2, Appl
127	15	11.4	347	9	US-10-060-036-2038	Sequence 2038, Ap	15	11.4	1984	9	US-10-050-704-70	Sequence 70, Appl
128	15	11.4	347	9	US-09-764-891-7699	Sequence 3571, Ap	15	11.4	2004	9	US-09-987-576-217	Sequence 217, App
129	15	11.4	347	9	US-10-066-543-182	Sequence 182, App	15	11.4	2004	9	US-09-809-391-132	Sequence 132, App
130	15	11.4	347	9	US-10-066-543-2353	Sequence 2353, Ap	15	11.4	2031	10	US-09-764-853-342	Sequence 342, App
131	15	11.4	347	9	US-10-066-543-2682	Sequence 2682, Ap	15	11.4	2053	10	US-09-925-301-118	Sequence 118, App
132	15	11.4	347	9	US-09-764-891-7699	Sequence 7699, Ap	15	11.4	2190	9	US-10-138-927-75	Sequence 75, Appl
133	15	11.4	347	9	US-10-066-543-2353	Sequence 2353, Ap	15	11.4	2215	9	US-10-092-154-1595	Sequence 1595, Ap
134	15	11.4	347	9	US-10-066-543-3123	Sequence 3123, Ap	15	11.4	2215	9	US-10-092-154-1588	Sequence 1588, Ap
135	15	11.4	349	9	US-09-764-891-7699	Sequence 7699, Ap	15	11.4	2219	10	US-09-764-847-1588	Sequence 1588, Ap
136	15	11.4	351	9	US-10-060-036-3572	Sequence 3572, Ap	15	11.4	2220	9	US-10-092-154-1589	Sequence 1589, Ap
137	15	11.4	351	10	US-09-764-853-343	Sequence 343, App	15	11.4	2220	10	US-09-764-847-1589	Sequence 1589, Ap
138	15	11.4	366	10	US-09-834-975-498	Sequence 498, App	15	11.4	2250	10	US-09-925-297-62	Sequence 62, Appl
139	15	11.4	374	9	US-09-764-891-542	Sequence 542, App	15	11.4	2250	10	US-09-764-864-160	Sequence 160, App
140	15	11.4	386	9	US-09-918-995-35519	Sequence 35519, A	15	11.4	2760	10	US-10-121-746-17	Sequence 17, Appl
141	15	11.4	389	10	US-09-998-598-2550	Sequence 2550, Ap	15	11.4	3102	9	US-09-834-975-829	Sequence 829, App
142	15	11.4	396	9	US-09-970-966-148	Sequence 148, App	15	11.4	3507	10	US-09-834-975-838	Sequence 838, App
143	15	11.4	417	10	US-09-825-394-148	Sequence 148, App	15	11.4	3507	10	US-09-834-975-838	Sequence 838, App
144	15	11.4	420	10	US-09-960-352-12483	Sequence 12483, A	15	11.4	3894	9	US-09-764-891-5749	Sequence 5749, Ap
145	15	11.4	430	9	US-09-918-995-5960	Sequence 5960, Ap	15	11.4	3894	9	US-09-764-891-5749	Sequence 5749, Ap
146	15	11.4	431	10	US-09-960-352-933	Sequence 933, App	15	11.4	4333	9	US-10-028-072-233	Sequence 233, App
147	15	11.4	431	10	US-09-960-352-8748	Sequence 8748, Ap	15	11.4	4333	9	US-10-121-043-233	Sequence 233, App
148	15	11.4	443	10	US-09-800-729-159	Sequence 159, App	15	11.4	4333	9	US-10-123-904-233	Sequence 233, App
149	15	11.4	443	10	US-09-960-352-13726	Sequence 13726, A	15	11.4	4333	9	US-10-140-470-233	Sequence 233, App
150	15	11.4	445	10	US-09-960-352-13069	Sequence 13069, A	15	11.4	4333	9	US-10-175-746-233	Sequence 233, App
151	15	11.4	446	10	US-09-919-580-640	Sequence 580, App	15	11.4	4333	9	US-10-175-746-233	Sequence 233, App
152	15	11.4	447	9	US-09-933-797-510	Sequence 510, App	15	11.4	4333	9	US-10-176-918-233	Sequence 233, App
153	15	11.4	456	9	US-09-918-995-26903	Sequence 26903, A	15	11.4	4333	9	US-10-176-918-233	Sequence 233, App
154	15	11.4	460	10	US-09-735-705-83	Sequence 83, Appl	15	11.4	4333	9	US-10-137-865-233	Sequence 233, App
155	15	11.4	460	10	US-09-850-716A-83	Sequence 83, Appl	15	11.4	4333	9	US-10-140-474-233	Sequence 233, App
156	15	11.4	460	10	US-09-897-778-83	Sequence 83, Appl	15	11.4	4333	9	US-10-140-474-233	Sequence 233, App
157	15	11.4	461	10	US-09-864-761-6066	Sequence 6066, Ap	15	11.4	4333	9	US-10-143-114-233	Sequence 233, App
158	15	11.4	461	10	US-09-864-761-14441	Sequence 14441, A	15	11.4	4333	9	US-10-140-002-233	Sequence 233, App
159	15	11.4	462	9	US-09-918-995-13118	Sequence 13118, A	15	11.4	4333	9	US-10-142-419-233	Sequence 233, App
160	15	11.4	469	9	US-09-918-995-13890	Sequence 13890, A	15	11.4	4333	9	US-10-142-419-233	Sequence 233, App
161	15	11.4	491	9	US-09-918-995-15899	Sequence 15899, A	15	11.4	4333	9	US-10-142-419-233	Sequence 233, App
162	15	11.4	492	9	US-09-918-995-31964	Sequence 31964, A	15	11.4	4333	9	US-10-142-419-233	Sequence 233, App
163	15	11.4	496	9	US-09-918-995-25194	Sequence 25194, A	15	11.4	4333	9	US-10-141-755-233	Sequence 233, App
164	15	11.4	511	10	US-09-867-701-6033	Sequence 6033, Ap	15	11.4	4333	9	US-10-143-032-233	Sequence 233, App
165	15	11.4	513	9	US-09-918-995-32570	Sequence 32570, A	15	11.4	4333	9	US-10-123-108-233	Sequence 233, App

c 239	15	11.4	4333	9	US-10-123-236-233	Sequence 233, App	c 312	15	11.4	4333	9	US-10-137-868-233	Sequence 233, App
c 240	15	11.4	4333	9	US-10-123-261-233	Sequence 233, App	c 313	15	11.4	4333	9	US-10-146-729-233	Sequence 233, App
c 241	15	11.4	4333	9	US-10-140-921-233	Sequence 233, App	c 314	15	11.4	4333	9	US-10-146-791-233	Sequence 233, App
c 242	15	11.4	4333	9	US-10-140-928-233	Sequence 233, App	c 315	15	11.4	4333	9	US-10-147-484-233	Sequence 233, App
c 243	15	11.4	4333	9	US-10-121-045-233	Sequence 233, App	c 316	15	11.4	4333	9	US-10-147-492-233	Sequence 233, App
c 244	15	11.4	4333	9	US-10-123-292-233	Sequence 233, App	c 317	15	11.4	4333	9	US-10-147-508-233	Sequence 233, App
c 245	15	11.4	4333	9	US-10-123-903-233	Sequence 233, App	c 318	15	11.4	4333	9	US-10-147-512-233	Sequence 233, App
c 246	15	11.4	4333	9	US-10-124-813-233	Sequence 233, App	c 319	15	11.4	4333	9	US-10-158-782-233	Sequence 233, App
c 247	15	11.4	4333	9	US-10-124-813-233	Sequence 233, App	c 320	15	11.4	4333	9	US-10-175-735-233	Sequence 233, App
c 248	15	11.4	4333	9	US-10-140-925-233	Sequence 233, App	c 321	15	11.4	4333	9	US-10-123-905-233	Sequence 233, App
c 249	15	11.4	4333	9	US-10-160-498-233	Sequence 233, App	c 322	15	11.4	4333	9	US-10-123-907-233	Sequence 233, App
c 250	15	11.4	4333	9	US-10-121-041-233	Sequence 233, App	c 323	15	11.4	4333	9	US-10-124-815-233	Sequence 233, App
c 251	15	11.4	4333	9	US-10-121-043-233	Sequence 233, App	c 324	15	11.4	4333	9	US-10-125-921A-233	Sequence 233, App
c 252	15	11.4	4333	9	US-10-121-047-233	Sequence 233, App	c 325	15	11.4	4333	9	US-10-125-922A-233	Sequence 233, App
c 253	15	11.4	4333	9	US-10-123-215-233	Sequence 233, App	c 326	15	11.4	4333	9	US-10-127-821A-233	Sequence 233, App
c 254	15	11.4	4333	9	US-10-123-902-233	Sequence 233, App	c 327	15	11.4	4333	9	US-10-127-822A-233	Sequence 233, App
c 255	15	11.4	4333	9	US-10-123-908-233	Sequence 233, App	c 328	15	11.4	4333	9	US-10-127-824A-233	Sequence 233, App
c 256	15	11.4	4333	9	US-10-123-909-233	Sequence 233, App	c 329	15	11.4	4333	9	US-10-127-826A-233	Sequence 233, App
c 257	15	11.4	4333	9	US-10-123-910-233	Sequence 233, App	c 330	15	11.4	4333	9	US-10-127-827A-233	Sequence 233, App
c 258	15	11.4	4333	9	US-10-124-813-233	Sequence 233, App	c 331	15	11.4	4333	9	US-10-127-828A-233	Sequence 233, App
c 259	15	11.4	4333	9	US-10-124-817-233	Sequence 233, App	c 332	15	11.4	4333	9	US-10-127-830A-233	Sequence 233, App
c 260	15	11.4	4333	9	US-10-124-824-233	Sequence 233, App	c 333	15	11.4	4333	9	US-10-127-832A-233	Sequence 233, App
c 261	15	11.4	4333	9	US-10-125-922-233	Sequence 233, App	c 334	15	11.4	4333	9	US-10-127-833A-233	Sequence 233, App
c 262	15	11.4	4333	9	US-10-125-924-233	Sequence 233, App	c 335	15	11.4	4333	9	US-10-127-834A-233	Sequence 233, App
c 263	15	11.4	4333	9	US-10-127-828A-233	Sequence 233, App	c 336	15	11.4	4333	9	US-10-127-836A-233	Sequence 233, App
c 264	15	11.4	4333	9	US-10-127-835A-233	Sequence 233, App	c 337	15	11.4	4333	9	US-10-127-841A-233	Sequence 233, App
c 265	15	11.4	4333	9	US-10-127-835A-233	Sequence 233, App	c 338	15	11.4	4333	9	US-10-127-844A-233	Sequence 233, App
c 266	15	11.4	4333	9	US-10-127-839A-233	Sequence 233, App	c 339	15	11.4	4333	9	US-10-128-687A-233	Sequence 233, App
c 267	15	11.4	4333	9	US-10-127-901A-233	Sequence 233, App	c 340	15	11.4	4333	9	US-10-128-688A-233	Sequence 233, App
c 268	15	11.4	4333	9	US-10-128-693A-233	Sequence 233, App	c 341	15	11.4	4333	9	US-10-128-689A-233	Sequence 233, App
c 269	15	11.4	4333	9	US-10-131-818A-233	Sequence 233, App	c 342	15	11.4	4333	9	US-10-128-694A-233	Sequence 233, App
c 270	15	11.4	4333	9	US-10-131-822A-233	Sequence 233, App	c 343	15	11.4	4333	9	US-10-131-825A-233	Sequence 233, App
c 271	15	11.4	4333	9	US-10-131-822A-233	Sequence 233, App	c 344	15	11.4	4333	9	US-10-230-417-233	Sequence 233, App
c 272	15	11.4	4333	9	US-10-131-830A-233	Sequence 233, App	c 345	15	11.4	4333	9	US-10-121-051-233	Sequence 233, App
c 273	15	11.4	4333	9	US-10-131-830A-233	Sequence 233, App	c 346	15	11.4	4333	9	US-10-131-815A-233	Sequence 233, App
c 274	15	11.4	4333	9	US-10-131-837A-233	Sequence 233, App	c 347	15	11.4	4333	9	US-10-131-817A-233	Sequence 233, App
c 275	15	11.4	4333	9	US-10-137-872A-233	Sequence 233, App	c 348	15	11.4	4333	9	US-10-131-821A-233	Sequence 233, App
c 276	15	11.4	4333	9	US-10-140-860-233	Sequence 233, App	c 349	15	11.4	4333	9	US-10-131-822A-233	Sequence 233, App
c 277	15	11.4	4333	9	US-10-142-417-233	Sequence 233, App	c 350	15	11.4	4333	9	US-10-131-822A-233	Sequence 233, App
c 278	15	11.4	4333	9	US-10-147-500-233	Sequence 233, App	c 351	15	11.4	4333	9	US-10-131-835A-233	Sequence 233, App
c 279	15	11.4	4333	9	US-10-147-502-233	Sequence 233, App	c 352	15	11.4	4333	9	US-10-137-864A-233	Sequence 233, App
c 280	15	11.4	4333	9	US-10-147-515-233	Sequence 233, App	c 353	15	11.4	4333	9	US-10-137-869A-233	Sequence 233, App
c 281	15	11.4	4333	9	US-10-147-519-233	Sequence 233, App	c 354	15	11.4	4333	9	US-10-147-523-233	Sequence 233, App
c 282	15	11.4	4333	9	US-10-147-519-233	Sequence 233, App	c 355	15	11.4	4333	9	US-10-158-785-233	Sequence 233, App
c 283	15	11.4	4333	9	US-10-147-527-233	Sequence 233, App	c 356	15	11.4	4333	9	US-10-121-042-233	Sequence 233, App
c 284	15	11.4	4333	9	US-10-152-395-233	Sequence 233, App	c 357	15	11.4	4333	9	US-10-125-181-37	Sequence 37, Appl
c 285	15	11.4	4333	9	US-10-157-789-233	Sequence 233, App	c 358	15	11.4	4623	10	US-09-764-864-308	Sequence 308, App
c 286	15	11.4	4333	9	US-10-121-040-233	Sequence 233, App	c 359	15	11.4	4623	10	US-09-864-864-238	Sequence 288, App
c 287	15	11.4	4333	9	US-10-121-056-233	Sequence 233, App	c 360	15	11.4	5080	9	US-10-092-154-1197	Sequence 1197, Ap
c 288	15	11.4	4333	9	US-10-121-061-233	Sequence 233, App	c 361	15	11.4	5080	9	US-10-092-154-1197	Sequence 1197, Ap
c 289	15	11.4	4333	9	US-10-123-235-233	Sequence 233, App	c 362	15	11.4	5080	10	US-09-764-847-1197	Sequence 1197, Ap
c 290	15	11.4	4333	9	US-10-123-235-233	Sequence 233, App	c 363	15	11.4	5080	10	US-09-764-847-1198	Sequence 1198, Ap
c 291	15	11.4	4333	9	US-10-124-818-233	Sequence 233, App	c 364	15	11.4	5102	10	US-09-954-456-1870	Sequence 1870, Ap
c 292	15	11.4	4333	9	US-10-125-926A-233	Sequence 233, App	c 365	15	11.4	5289	9	US-10-044-807-1	Sequence 1, Appli
c 293	15	11.4	4333	9	US-10-125-930A-233	Sequence 233, App	c 366	15	11.4	5720	10	US-09-800-729-18	Sequence 18, Appl
c 294	15	11.4	4333	9	US-10-127-831A-233	Sequence 233, App	c 367	15	11.4	5769	10	US-09-764-851-134	Sequence 134, App
c 295	15	11.4	4333	9	US-10-127-837A-233	Sequence 233, App	c 368	15	11.4	7727	9	US-09-764-891-7685	Sequence 7685, Ap
c 296	15	11.4	4333	9	US-10-127-838B-233	Sequence 233, App	c 369	15	11.4	7831	9	US-10-043-487-182	Sequence 182, Ap
c 297	15	11.4	4333	9	US-10-127-842A-233	Sequence 233, App	c 370	15	11.4	8095	10	US-09-880-107-2228	Sequence 2228, Ap
c 298	15	11.4	4333	9	US-10-127-843A-233	Sequence 233, App	c 371	15	11.4	8689	9	US-09-808-602-78	Sequence 78, Appl
c 299	15	11.4	4333	9	US-10-127-843A-233	Sequence 233, App	c 372	15	11.4	8689	9	US-09-800-198-66	Sequence 66, Appl
c 300	15	11.4	4333	9	US-10-127-846A-233	Sequence 233, App	c 373	15	11.4	9729	9	US-09-808-602-12	Sequence 12, Appl
c 301	15	11.4	4333	9	US-10-127-848A-233	Sequence 233, App	c 374	15	11.4	9729	9	US-09-800-198-12	Sequence 12, Appl
c 302	15	11.4	4333	9	US-10-127-849A-233	Sequence 233, App	c 375	15	11.4	9826	9	US-09-808-602-7	Sequence 7, Appli
c 303	15	11.4	4333	9	US-10-127-850A-233	Sequence 233, App	c 376	15	11.4	9826	9	US-09-800-198-7	Sequence 7, Appli
c 304	15	11.4	4333	9	US-10-127-851A-233	Sequence 233, App	c 377	15	11.4	10319	9	US-09-764-868-1292	Sequence 1292, Ap
c 305	15	11.4	4333	9	US-10-128-686A-233	Sequence 233, App	c 378	15	11.4	15571	10	US-09-880-107-2387	Sequence 2387, Ap
c 306	15	11.4	4333	9	US-10-128-686A-233	Sequence 233, App	c 379	15	11.4	15849	10	US-09-880-107-2362	Sequence 2362, Ap
c 307	15	11.4	4333	9	US-10-128-690A-233	Sequence 233, App	c 380	15	11.4	16428	9	US-10-092-154-1613	Sequence 1613, Ap
c 308	15	11.4	4333	9	US-10-128-691A-233	Sequence 233, App	c 381	15	11.4	16428	10	US-09-764-847-1613	Sequence 1613, Ap
c 309	15	11.4	4333	9	US-10-131-819A-233	Sequence 233, App	c 382	15	11.4	19736	12	US-10-014-502-3	Sequence 3, Appli
c 310	15	11.4	4333	9	US-10-131-822A-233	Sequence 233, App	c 383	15	11.4	20029	9	US-10-092-154-1624	Sequence 1624, Ap
c 311	15	11.4	4333	9	US-10-131-836A-233	Sequence 233, App	c 384	15	11.4	20029	10	US-09-764-847-1624	Sequence 1624, Ap

C 385	15	11.4	31834	9	US-10-092-154-1612	Sequence 1612, Ap	c 458	14	10.6	380	10	US-09-960-352-6073	Sequence 6073, Ap
C 386	15	11.4	31834	10	US-09-764-847-1612	Sequence 1612, Ap	459	14	10.6	381	9	US-09-803-719-2081	Sequence 2081, Ap
C 387	15	11.4	32035	9	US-10-092-154-1611	Sequence 1611, Ap	c 460	14	10.6	385	10	US-09-960-352-328	Sequence 928, App
C 388	15	11.4	32035	10	US-09-764-847-1611	Sequence 1611, Ap	c 461	14	10.6	387	9	US-09-728-444-975	Sequence 975, App
C 389	15	11.4	170834	10	US-09-835-232-7	Sequence 7, Appl	c 462	14	10.6	394	9	US-09-918-995-5037	Sequence 5037, Ap
C 390	15	11.4	197496	9	US-09-877-177-10	Sequence 10, Appl	c 463	14	10.6	397	10	US-09-864-761-5116	Sequence 5116, Ap
C 391	15	11.4	225883	9	US-10-175-523-57	Sequence 57, Appl	c 464	14	10.6	398	10	US-09-960-253-117	Sequence 117, App
C 392	15	11.4	335913	9	US-09-754-853A-2	Sequence 2, Appl	c 465	14	10.6	400	7	US-08-781-986A-4291	Sequence 4291, Ap
C 393	15	11.4	335913	9	US-09-754-853A-3	Sequence 3, Appl	c 466	14	10.6	400	10	US-09-864-761-3628	Sequence 3628, Ap
C 394	15	11.4	659158	9	US-09-771-208-20	Sequence 20, Appl	c 467	14	10.6	400	10	US-09-880-407-1098	Sequence 1098, Ap
C 395	15	11.4	1691139	9	US-10-067-514-1	Sequence 1, Appl	c 468	14	10.6	401	9	US-09-946-807-715	Sequence 715, App
C 396	15	11.4	1691139	9	US-10-067-514-1	Sequence 1, Appl	469	14	10.6	401	9	US-09-946-807-715	Sequence 715, App
C 397	14	10.6	27	10	US-09-828-313-128	Sequence 128, App	470	14	10.6	401	10	US-09-795-668-715	Sequence 715, App
C 398	14	10.6	30	9	US-09-973-025-34	Sequence 34, Appl	471	14	10.6	401	10	US-09-795-668-715	Sequence 715, App
C 399	14	10.6	30	9	US-09-899-303-34	Sequence 34, Appl	472	14	10.6	401	10	US-09-795-668-715	Sequence 715, App
C 400	14	10.6	30	9	US-09-995-808-34	Sequence 34, Appl	473	14	10.6	401	10	US-09-795-668-715	Sequence 715, App
C 401	14	10.6	30	9	US-09-780-533A-3325	Sequence 3325, Ap	474	14	10.6	401	10	US-09-918-995-5508	Sequence 5508, Ap
C 402	14	10.6	38	9	US-09-864-761-21838	Sequence 1290, Ap	475	14	10.6	403	9	US-09-960-352-13218	Sequence 13218, A
C 403	14	10.6	81	10	US-09-864-761-21838	Sequence 21838, A	c 476	14	10.6	410	10	US-09-960-352-3698	Sequence 3698, Ap
C 404	14	10.6	122	10	US-09-864-761-21838	Sequence 21838, A	c 477	14	10.6	410	10	US-09-960-352-6586	Sequence 6586, Ap
C 405	14	10.6	137	10	US-09-864-761-21838	Sequence 21838, A	c 478	14	10.6	412	9	US-09-918-995-3096	Sequence 3096, Ap
C 406	14	10.6	140	10	US-09-864-761-21838	Sequence 21838, A	c 479	14	10.6	415	9	US-09-918-995-32996	Sequence 32996, A
C 407	14	10.6	151	10	US-09-864-761-21838	Sequence 21838, A	c 480	14	10.6	418	9	US-09-918-995-7120	Sequence 7120, A
C 408	14	10.6	151	10	US-09-864-761-21838	Sequence 21838, A	c 481	14	10.6	418	9	US-09-918-995-7120	Sequence 7120, A
C 409	14	10.6	158	10	US-09-923-876-3467	Sequence 3467, Ap	c 482	14	10.6	422	9	US-09-918-995-3954	Sequence 3954, Ap
C 410	14	10.6	172	9	US-10-060-036-2954	Sequence 2954, Ap	c 483	14	10.6	423	10	US-09-960-352-9386	Sequence 9386, Ap
C 411	14	10.6	175	10	US-09-867-701-1232	Sequence 1232, Ap	484	14	10.6	424	10	US-09-960-352-9386	Sequence 9386, Ap
C 412	14	10.6	191	10	US-09-864-761-26396	Sequence 26396, A	c 485	14	10.6	426	9	US-09-918-995-36190	Sequence 36190, A
C 413	14	10.6	193	10	US-09-864-761-26396	Sequence 26396, A	c 486	14	10.6	429	9	US-09-918-995-36190	Sequence 36190, A
C 414	14	10.6	198	10	US-09-864-761-21770	Sequence 21770, A	c 487	14	10.6	429	10	US-09-864-761-4259	Sequence 4259, A
C 415	14	10.6	198	10	US-09-864-761-25452	Sequence 25452, A	c 488	14	10.6	429	10	US-09-560-863-938	Sequence 938, App
C 416	14	10.6	211	10	US-09-864-761-30924	Sequence 30924, A	c 489	14	10.6	429	10	US-09-983-965-2539	Sequence 2539, App
C 417	14	10.6	211	10	US-09-864-761-30924	Sequence 30924, A	c 490	14	10.6	430	10	US-09-960-352-172	Sequence 172, App
C 418	14	10.6	213	8	US-08-796-570A-6	Sequence 6, Appl	c 491	14	10.6	432	9	US-09-918-995-36063	Sequence 36063, A
C 419	14	10.6	213	10	US-09-864-761-24166	Sequence 24166, A	c 492	14	10.6	432	9	US-09-918-995-36063	Sequence 36063, A
C 420	14	10.6	216	10	US-09-867-701-6943	Sequence 6943, Ap	c 493	14	10.6	445	9	US-09-918-995-26477	Sequence 26477, A
C 421	14	10.6	250	10	US-09-924-035A-491	Sequence 491, App	c 494	14	10.6	445	10	US-09-783-590-3731	Sequence 3731, Ap
C 422	14	10.6	251	9	US-09-535-459-1899	Sequence 1899, Ap	c 495	14	10.6	448	9	US-09-918-995-29023	Sequence 29023, A
C 423	14	10.6	265	10	US-09-878-574-10977	Sequence 10977, A	c 496	14	10.6	448	9	US-09-918-995-29023	Sequence 29023, A
C 424	14	10.6	270	9	US-10-066-543-2633	Sequence 2633, Ap	c 497	14	10.6	460	9	US-09-918-995-28383	Sequence 28383, A
C 425	14	10.6	280	10	US-09-878-574-14797	Sequence 14797, A	c 498	14	10.6	463	9	US-09-918-995-28383	Sequence 28383, A
C 426	14	10.6	282	9	US-09-938-842A-4480	Sequence 4480, Ap	c 499	14	10.6	464	9	US-09-918-995-27489	Sequence 27489, A
C 427	14	10.6	285	10	US-09-887-576-707	Sequence 707, App	c 500	14	10.6	466	9	US-09-918-995-11266	Sequence 11266, A
C 428	14	10.6	290	9	US-09-535-459-1931	Sequence 1931, Ap	c 501	14	10.6	468	10	US-09-864-761-619	Sequence 619, App
C 429	14	10.6	290	10	US-09-294-093B-3243	Sequence 3243, Ap	c 502	14	10.6	468	9	US-09-918-995-13248	Sequence 13248, A
C 430	14	10.6	293	10	US-09-878-574-14704	Sequence 14704, A	c 503	14	10.6	471	10	US-09-864-761-1293	Sequence 1293, Ap
C 431	14	10.6	295	10	US-09-294-093B-4928	Sequence 4928, Ap	c 504	14	10.6	472	10	US-09-918-995-11303	Sequence 11303, A
C 432	14	10.6	298	10	US-09-783-590-1846	Sequence 1846, Ap	c 505	14	10.6	472	10	US-09-864-761-2616	Sequence 2616, Ap
C 433	14	10.6	311	10	US-09-864-761-19338	Sequence 19338, A	c 506	14	10.6	473	9	US-10-152-661-355	Sequence 355, App
C 434	14	10.6	321	9	US-09-738-626-3336	Sequence 3336, Ap	c 507	14	10.6	473	9	US-09-866-050A-355	Sequence 355, App
C 435	14	10.6	331	9	US-10-070-676-15	Sequence 15, Appl	c 508	14	10.6	474	10	US-09-918-995-27832	Sequence 27832, A
C 436	14	10.6	339	9	US-09-535-459-1263	Sequence 1263, Ap	c 509	14	10.6	475	10	US-09-867-701-5248	Sequence 5248, Ap
C 437	14	10.6	343	10	US-09-294-093B-107	Sequence 107, App	c 510	14	10.6	476	10	US-09-918-995-32592	Sequence 32592, A
C 438	14	10.6	347	10	US-09-834-975-296	Sequence 296, App	c 511	14	10.6	477	10	US-09-864-761-5167	Sequence 5167, Ap
C 439	14	10.6	352	10	US-09-878-574-5303	Sequence 5303, Ap	c 512	14	10.6	477	10	US-09-918-995-27851	Sequence 27851, Ap
C 440	14	10.6	356	9	US-10-046-935-1053	Sequence 1053, Ap	c 513	14	10.6	479	9	US-09-918-995-1242	Sequence 1242, Ap
C 441	14	10.6	356	9	US-10-046-935-1244	Sequence 1244, Ap	c 514	14	10.6	486	9	US-09-918-995-9663	Sequence 9663, Ap
C 442	14	10.6	356	9	US-10-046-935-1480	Sequence 1480, Ap	c 515	14	10.6	486	10	US-09-918-995-27300	Sequence 27300, A
C 443	14	10.6	356	9	US-10-042-125A-13	Sequence 13, Appl	c 516	14	10.6	488	9	US-09-864-761-1360	Sequence 1360, Ap
C 444	14	10.6	356	9	US-09-878-178-1053	Sequence 1053, Ap	c 517	14	10.6	490	9	US-09-918-995-29138	Sequence 29138, A
C 445	14	10.6	356	9	US-09-878-178-1244	Sequence 1244, Ap	c 518	14	10.6	491	9	US-09-918-995-1650	Sequence 1650, Ap
C 446	14	10.6	356	9	US-09-878-178-1480	Sequence 1480, Ap	c 519	14	10.6	494	9	US-09-918-995-6573	Sequence 6573, Ap
C 447	14	10.6	356	9	US-10-146-502-1053	Sequence 1053, Ap	c 520	14	10.6	496	10	US-09-833-381-1545	Sequence 1545, Ap
C 448	14	10.6	356	9	US-10-146-502-1244	Sequence 1244, Ap	c 521	14	10.6	497	10	US-09-878-574-4839	Sequence 4839, Ap
C 449	14	10.6	356	9	US-10-146-502-1480	Sequence 1480, Ap	c 522	14	10.6	499	9	US-09-918-995-38029	Sequence 38029, Ap
C 450	14	10.6	356	9	US-10-146-502-1480	Sequence 1480, Ap	c 523	14	10.6	500	10	US-09-991-936-1762	Sequence 1762, Ap
C 451	14	10.6	357	10	US-09-867-701-4366	Sequence 4366, Ap	c 524	14	10.6	500	10	US-09-864-761-7753	Sequence 7753, Ap
C 452	14	10.6	359	10	US-09-878-574-3339	Sequence 3339, Ap	c 525	14	10.6	501	9	US-09-918-995-1764	Sequence 1764, Ap
C 453	14	10.6	370	9	US-09-918-995-37583	Sequence 37583, A	c 526	14	10.6	505	9	US-09-918-995-20056	Sequence 20056, A
C 454	14	10.6	372	9	US-10-152-661-60	Sequence 60, Appl	c 527	14	10.6	506	9	US-09-918-995-31662	Sequence 31662, A
C 455	14	10.6	372	9	US-09-866-050A-60	Sequence 60, Appl	c 528	14	10.6	510	9	US-09-918-995-11644	Sequence 11644, A
C 456	14	10.6	373	9	US-09-918-995-37603	Sequence 37603, A	c 529	14	10.6	512	10	US-09-878-574-1324	Sequence 1324, Ap
C 457	14	10.6	379	10	US-09-960-352-164	Sequence 164, App	c 530	14	10.6	516	9	US-09-978-295A-484	Sequence 484, App

c 531	14	10.6	9	US-09-978-697-484	Sequence 484, App	c 604	14	10.6	10	US-09-960-253-106	Sequence 106, App
c 532	14	10.6	9	US-09-978-192A-484	Sequence 484, App	605	14	10.6	10	US-09-833-381-1457	Sequence 1457, App
c 533	14	10.6	9	US-09-999-832A-484	Sequence 484, App	606	14	10.6	10	US-09-773-774A-3	Sequence 3, Appli
c 534	14	10.6	9	US-09-978-189-484	Sequence 484, App	607	14	10.6	10	US-09-771-961-3	Sequence 3, Appli
c 535	14	10.6	9	US-09-978-608A-484	Sequence 484, App	608	14	10.6	10	US-09-815-242-9391	Sequence 9391, Ap
c 536	14	10.6	9	US-09-978-191A-484	Sequence 484, App	609	14	10.6	10	US-09-815-242-9515	Sequence 9515, Ap
c 537	14	10.6	9	US-09-978-403A-484	Sequence 484, App	c 610	14	10.6	9	US-09-738-626-2788	Sequence 2788, Ap
c 538	14	10.6	9	US-09-978-564A-484	Sequence 484, App	611	14	10.6	10	US-09-815-242-6918	Sequence 6918, Ap
c 539	14	10.6	9	US-09-978-585A-484	Sequence 484, App	c 612	14	10.6	10	US-09-746-491-55	Sequence 55, Appl
c 540	14	10.6	9	US-10-017-081A-484	Sequence 484, App	613	14	10.6	876	US-09-815-242-9175	Sequence 9175, Ap
c 541	14	10.6	9	US-09-978-824-484	Sequence 484, App	c 614	14	10.6	884	US-09-770-445-516	Sequence 516, App
c 542	14	10.6	9	US-09-981-915A-484	Sequence 484, App	c 615	14	10.6	886	US-09-938-842A-3702	Sequence 3702, Ap
c 543	14	10.6	9	US-09-999-833A-484	Sequence 484, App	616	14	10.6	918	US-09-974-300-4772	Sequence 4772, Ap
c 544	14	10.6	9	US-10-167-749-484	Sequence 484, App	617	14	10.6	919	US-09-925-297-14	Sequence 14, Appl
c 545	14	10.6	9	US-09-918-585A-484	Sequence 484, App	618	14	10.6	924	US-09-816-714-3	Sequence 3, Appli
c 546	14	10.6	9	US-09-978-423A-484	Sequence 484, App	619	14	10.6	948	US-09-815-242-7678	Sequence 7678, Ap
c 547	14	10.6	9	US-10-013-921A-484	Sequence 484, App	620	14	10.6	954	US-09-738-396-3	Sequence 3, Appli
c 548	14	10.6	9	US-09-978-193A-484	Sequence 484, App	621	14	10.6	984	US-09-773-774A-1	Sequence 1, Appli
c 549	14	10.6	9	US-10-013-929A-484	Sequence 484, App	622	14	10.6	984	US-09-771-961-1	Sequence 1, Appli
c 550	14	10.6	9	US-10-016-177A-484	Sequence 484, App	c 623	14	10.6	1033	US-10-228-794-73	Sequence 73, Appl
c 551	14	10.6	9	US-09-999-830A-484	Sequence 484, App	c 624	14	10.6	1089	US-10-139-483-1	Sequence 1, Appli
c 552	14	10.6	9	US-09-978-757A-484	Sequence 484, App	625	14	10.6	1098	US-09-741-669-160	Sequence 160, App
c 553	14	10.6	9	US-09-978-187B-484	Sequence 484, App	626	14	10.6	1099	US-09-263-959-245	Sequence 245, App
c 554	14	10.6	9	US-09-907-969-138	Sequence 484, App	c 627	14	10.6	1113	US-09-796-965-1	Sequence 1, Appli
c 555	14	10.6	10	US-09-864-761-15327	Sequence 15327, A	628	14	10.6	1142	US-09-263-959-248	Sequence 248, App
c 556	14	10.6	10	US-09-864-761-12828	Sequence 12828, A	629	14	10.6	1151	US-09-974-879-105	Sequence 105, App
c 557	14	10.6	9	US-09-833-790-349	Sequence 349, App	c 630	14	10.6	1151	US-09-305-736-105	Sequence 105, App
c 558	14	10.6	9	US-09-854-133-642	Sequence 642, App	c 631	14	10.6	1160	US-09-764-891-5481	Sequence 5481, Ap
c 559	14	10.6	9	US-09-833-790-312	Sequence 312, App	c 632	14	10.6	1161	US-09-770-445-64	Sequence 64, Appl
c 560	14	10.6	9	US-09-998-598-1386	Sequence 1386, Ap	633	14	10.6	1179	US-09-738-396-1	Sequence 1, Appli
c 561	14	10.6	9	US-09-907-969-138	Sequence 138, App	634	14	10.6	1285	US-09-938-842A-2520	Sequence 2520, Ap
c 562	14	10.6	10	US-09-864-761-7394	Sequence 7394, App	635	14	10.6	1285	US-09-925-302-10	Sequence 10, Appl
c 563	14	10.6	10	US-09-884-441-138	Sequence 138, App	c 636	14	10.6	1216	US-09-746-491-21	Sequence 21, Appl
c 564	14	10.6	9	US-09-918-995-30660	Sequence 30660, A	637	14	10.6	1228	US-09-263-959-246	Sequence 246, App
c 565	14	10.6	9	US-09-918-995-27673	Sequence 27673, A	c 638	14	10.6	1272	US-08-796-570A-2	Sequence 2, Appli
c 566	14	10.6	9	US-09-864-761-16140	Sequence 16140, A	639	14	10.6	1272	US-10-067-477-2	Sequence 2, Appli
c 567	14	10.6	9	US-10-092-154-1940	Sequence 1940, Ap	640	14	10.6	1279	US-09-974-879-68	Sequence 68, Appl
c 568	14	10.6	9	US-09-764-847-1940	Sequence 1940, Ap	641	14	10.6	1279	US-09-305-736-68	Sequence 68, Appl
c 569	14	10.6	9	US-09-764-847-471	Sequence 471, App	c 642	14	10.6	1286	US-09-746-491-56	Sequence 56, Appl
c 570	14	10.6	9	US-09-764-868-531	Sequence 531, App	c 643	14	10.6	1286	US-09-746-491-57	Sequence 57, Appl
c 571	14	10.6	9	US-09-535-459-1930	Sequence 1930, Ap	c 644	14	10.6	1293	US-09-945-527-36	Sequence 36, Appl
c 572	14	10.6	9	US-09-918-995-29374	Sequence 29374, A	645	14	10.6	1300	US-09-263-959-251	Sequence 251, App
c 573	14	10.6	10	US-09-864-761-12772	Sequence 12772, A	646	14	10.6	1311	US-09-738-626-3441	Sequence 3441, Ap
c 574	14	10.6	9	US-09-864-761-761	Sequence 7761, App	647	14	10.6	1321	US-10-174-520-371	Sequence 371, App
c 575	14	10.6	9	US-09-535-459-1928	Sequence 1928, Ap	648	14	10.6	1321	US-10-176-758-371	Sequence 371, App
c 576	14	10.6	9	US-10-178-782-1	Sequence 1, Appli	649	14	10.6	1321	US-10-175-737-371	Sequence 371, App
c 577	14	10.6	10	US-09-864-761-9702	Sequence 9702, Ap	650	14	10.6	1321	US-10-173-706-371	Sequence 371, App
c 578	14	10.6	9	US-09-834-975-421	Sequence 421, App	651	14	10.6	1321	US-10-175-738-371	Sequence 371, App
c 579	14	10.6	9	US-10-056-543-2782	Sequence 2782, Ap	652	14	10.6	1321	US-10-175-752-371	Sequence 371, App
c 580	14	10.6	10	US-09-864-761-8150	Sequence 8150, Ap	653	14	10.6	1321	US-10-176-482-371	Sequence 371, App
c 581	14	10.6	9	US-09-535-459-1929	Sequence 1929, Ap	654	14	10.6	1321	US-10-176-757-371	Sequence 371, App
c 582	14	10.6	9	US-09-864-761-6845	Sequence 6845, Ap	655	14	10.6	1321	US-10-176-913-371	Sequence 371, App
c 583	14	10.6	9	US-09-907-969-106	Sequence 106, App	656	14	10.6	1321	US-10-180-552-371	Sequence 371, App
c 584	14	10.6	9	US-09-884-441-106	Sequence 106, App	657	14	10.6	1321	US-10-180-557-371	Sequence 371, App
c 585	14	10.6	10	US-09-864-761-8793	Sequence 8793, Ap	658	14	10.6	1321	US-10-173-700-371	Sequence 371, App
c 586	14	10.6	10	US-09-864-761-9068	Sequence 9068, Ap	659	14	10.6	1321	US-10-174-572-371	Sequence 371, App
c 587	14	10.6	10	US-09-864-761-9075	Sequence 9075, Ap	660	14	10.6	1321	US-10-174-582-371	Sequence 371, App
c 588	14	10.6	9	US-09-864-761-12817	Sequence 12817, A	661	14	10.6	1321	US-10-174-582-371	Sequence 371, App
c 589	14	10.6	9	US-09-764-891-1170	Sequence 1170, Ap	662	14	10.6	1321	US-10-174-588-371	Sequence 371, App
c 590	14	10.6	9	US-09-925-301-439	Sequence 439, App	663	14	10.6	1321	US-10-175-739-371	Sequence 371, App
c 591	14	10.6	10	US-09-834-975-597	Sequence 597, App	664	14	10.6	1321	US-10-175-740-371	Sequence 371, App
c 592	14	10.6	10	US-09-770-149-966	Sequence 966, App	665	14	10.6	1321	US-10-175-743-371	Sequence 371, App
c 593	14	10.6	603	US-09-917-800A-252	Sequence 252, App	666	14	10.6	1321	US-10-176-488-371	Sequence 371, App
c 594	14	10.6	617	US-09-998-598-463	Sequence 463, Appl	667	14	10.6	1321	US-10-176-492-371	Sequence 371, App
c 595	14	10.6	625	US-09-910-664-23	Sequence 23, Appl	668	14	10.6	1321	US-10-176-747-371	Sequence 371, App
c 596	14	10.6	625	US-09-917-800A-1280	Sequence 1280, Ap	669	14	10.6	1321	US-10-176-750-371	Sequence 371, App
c 597	14	10.6	9	US-09-764-891-1349	Sequence 1349, Ap	670	14	10.6	1321	US-10-176-985-371	Sequence 371, App
c 598	14	10.6	633	US-09-834-975-357	Sequence 357, App	671	14	10.6	1321	US-10-176-987-371	Sequence 371, App
c 599	14	10.6	649	US-09-747-155-115	Sequence 115, App	672	14	10.6	1321	US-10-176-991-371	Sequence 371, App
c 600	14	10.6	665	US-09-960-253-107	Sequence 107, App	673	14	10.6	1321	US-10-176-992-371	Sequence 371, App
c 601	14	10.6	665	US-09-764-877-2132	Sequence 2132, Ap	674	14	10.6	1321	US-10-176-993-371	Sequence 371, App
c 602	14	10.6	696	US-09-925-300-330	Sequence 330, App	675	14	10.6	1321	US-10-184-658-371	Sequence 371, App
c 603	14	10.6	716	US-10-033-528-1830	Sequence 1830, App	676	14	10.6	1321	US-10-173-695-371	Sequence 371, App

823	14	10.6	1321	9	US-10-195-890-371	Sequence 371, App	Sequence 371, App	896	14	10.6	1321	9	US-10-200-617-371	Sequence 371, App
824	14	10.6	1321	9	US-10-195-899-371	Sequence 371, App	Sequence 371, App	897	14	10.6	1321	9	US-10-205-893-371	Sequence 371, App
825	14	10.6	1321	9	US-10-196-748-371	Sequence 371, App	Sequence 371, App	898	14	10.6	1321	9	US-10-205-897-371	Sequence 371, App
826	14	10.6	1321	9	US-10-196-750-371	Sequence 371, App	Sequence 371, App	899	14	10.6	1321	9	US-10-015-393A-365	Sequence 365, App
827	14	10.6	1321	9	US-10-197-699-371	Sequence 371, App	Sequence 371, App	900	14	10.6	1321	9	US-10-174-571-371	Sequence 371, App
828	14	10.6	1321	9	US-10-197-700-371	Sequence 371, App	Sequence 371, App	901	14	10.6	1321	9	US-10-176-746-371	Sequence 371, App
829	14	10.6	1321	9	US-10-197-708-371	Sequence 371, App	Sequence 371, App	902	14	10.6	1321	9	US-10-176-923-371	Sequence 371, App
830	14	10.6	1321	9	US-10-197-708-371	Sequence 371, App	Sequence 371, App	903	14	10.6	1321	9	US-10-183-011-371	Sequence 371, App
831	14	10.6	1321	9	US-10-198-764-371	Sequence 371, App	Sequence 371, App	904	14	10.6	1321	9	US-10-183-011-371	Sequence 371, App
832	14	10.6	1321	9	US-10-198-765-371	Sequence 371, App	Sequence 371, App	905	14	10.6	1321	9	US-10-184-633-371	Sequence 371, App
833	14	10.6	1321	9	US-10-198-768-371	Sequence 371, App	Sequence 371, App	906	14	10.6	1321	9	US-10-184-639-371	Sequence 371, App
834	14	10.6	1321	9	US-10-198-769-371	Sequence 371, App	Sequence 371, App	907	14	10.6	1321	9	US-10-187-742-371	Sequence 371, App
835	14	10.6	1321	9	US-10-199-305-371	Sequence 371, App	Sequence 371, App	908	14	10.6	1321	9	US-10-187-748-371	Sequence 371, App
836	14	10.6	1321	9	US-10-199-306-371	Sequence 371, App	Sequence 371, App	909	14	10.6	1321	9	US-10-188-766-371	Sequence 371, App
837	14	10.6	1321	9	US-10-199-310-371	Sequence 371, App	Sequence 371, App	910	14	10.6	1321	9	US-10-188-771-371	Sequence 371, App
838	14	10.6	1321	9	US-10-199-311-371	Sequence 371, App	Sequence 371, App	911	14	10.6	1321	9	US-10-192-006-371	Sequence 371, App
839	14	10.6	1321	9	US-10-199-314-371	Sequence 371, App	Sequence 371, App	912	14	10.6	1321	9	US-10-192-008-371	Sequence 371, App
840	14	10.6	1321	9	US-10-199-317-371	Sequence 371, App	Sequence 371, App	913	14	10.6	1321	9	US-10-192-009-371	Sequence 371, App
841	14	10.6	1321	9	US-10-199-665-371	Sequence 371, App	Sequence 371, App	914	14	10.6	1321	9	US-10-192-012-371	Sequence 371, App
842	14	10.6	1321	9	US-10-199-666-371	Sequence 371, App	Sequence 371, App	915	14	10.6	1321	9	US-10-192-014-371	Sequence 371, App
843	14	10.6	1321	9	US-10-199-669-371	Sequence 371, App	Sequence 371, App	916	14	10.6	1321	9	US-10-192-016-371	Sequence 371, App
844	14	10.6	1321	9	US-10-201-534-371	Sequence 371, App	Sequence 371, App	917	14	10.6	1321	9	US-10-194-362-371	Sequence 371, App
845	14	10.6	1321	9	US-10-201-534-371	Sequence 371, App	Sequence 371, App	918	14	10.6	1321	9	US-10-194-364-371	Sequence 371, App
846	14	10.6	1321	9	US-10-201-770-371	Sequence 371, App	Sequence 371, App	919	14	10.6	1321	9	US-10-194-395-371	Sequence 371, App
847	14	10.6	1321	9	US-10-201-855-371	Sequence 371, App	Sequence 371, App	920	14	10.6	1321	9	US-10-194-424-371	Sequence 371, App
848	14	10.6	1321	9	US-10-201-856-371	Sequence 371, App	Sequence 371, App	921						

969 14 10.6 1321 9 US-10-205-898-371 Sequence 371, App
 970 14 10.6 1321 9 US-10-205-901-371 Sequence 371, App
 971 14 10.6 1321 9 US-10-205-903-371 Sequence 371, App
 972 14 10.6 1321 9 US-10-206-909-371 Sequence 371, App
 973 14 10.6 1321 9 US-10-206-910-371 Sequence 371, App
 974 14 10.6 1321 9 US-10-206-911-371 Sequence 371, App
 975 14 10.6 1321 9 US-10-206-912-371 Sequence 371, App
 976 14 10.6 1321 9 US-10-206-913-371 Sequence 371, App
 977 14 10.6 1321 9 US-10-206-914-371 Sequence 371, App
 978 14 10.6 1321 9 US-10-206-920-371 Sequence 371, App
 979 14 10.6 1321 9 US-10-206-921-371 Sequence 371, App
 980 14 10.6 1321 9 US-10-206-923-371 Sequence 371, App
 981 14 10.6 1321 9 US-10-206-925-371 Sequence 371, App
 982 14 10.6 1321 9 US-10-206-926-371 Sequence 371, App
 983 14 10.6 1321 9 US-10-207-916-371 Sequence 371, App
 984 14 10.6 1321 9 US-10-207-917-371 Sequence 371, App
 985 14 10.6 1321 9 US-10-207-918-371 Sequence 371, App
 986 14 10.6 1321 9 US-10-207-919-371 Sequence 371, App
 987 14 10.6 1321 9 US-10-207-920-371 Sequence 371, App
 988 14 10.6 1321 9 US-10-207-921-371 Sequence 371, App
 989 14 10.6 1321 9 US-10-208-021-371 Sequence 371, App
 990 14 10.6 1321 9 US-10-208-022-371 Sequence 371, App
 991 14 10.6 1321 9 US-10-208-023-371 Sequence 371, App
 992 14 10.6 1321 9 US-10-208-026-371 Sequence 371, App
 993 14 10.6 1321 9 US-10-208-029-371 Sequence 371, App
 994 14 10.6 1321 9 US-10-208-030-371 Sequence 371, App
 995 14 10.6 1321 9 US-10-232-232-371 Sequence 371, App
 996 14 10.6 1321 9 US-09-946-374-365 Sequence 365, App
 997 14 10.6 1321 9 US-10-012-121A-365 Sequence 365, App
 998 14 10.6 1321 9 US-10-015-869A-365 Sequence 365, App
 999 14 10.6 1321 12 US-10-052-586-371 Sequence 371, App
 1000 14 10.6 1321 12 US-10-052-586-371 Sequence 371, App

ALIGNMENTS

RESULT 1
 US-10-160-293-3
 ; Sequence 3, Application US/10160293
 ; Publication No. US20030022208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LINQUIST, Erika et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL001241-PROV
 ; CURRENT APPLICATION NUMBER: US/10/160,293
 ; CURRENT FILING DATE: 2002-06-04
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 39776
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-160-293-3

Query Match 14.4%; Score 19; DB 9; Length 39776;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GGCCACAGAGATGCGAAG 75
 Db 18251 GGCCACAGAGATGCGAAG 18269
 |||||

RESULT 2
 US-09-919-580-517
 ; Sequence 517, Application US/09919580
 ; Patent No. US20020110832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Xu, Jiangchun

; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.552
 ; CURRENT APPLICATION NUMBER: US/09/919,580
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 517
 ; LENGTH: 243
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 243
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-919-580-517

Query Match 13.6%; Score 18; DB 10; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
 Db 102 GATAAGGCCCAAGCTGAAG 119
 |||||

RESULT 3
 US-09-919-580-224
 ; Sequence 224, Application US/09919580
 ; Patent No. US20020110832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 210121.552
 ; CURRENT APPLICATION NUMBER: US/09/919,580
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 224
 ; LENGTH: 353
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-919-580-224

Query Match 13.6%; Score 18; DB 10; Length 353;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
 Db 76 GATAAGGCCCAAGCTGAAG 93
 |||||

RESULT 4
 US-09-919-580-207
 ; Sequence 207, Application US/09919580
 ; Patent No. US20020110832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 210121.552
 ; CURRENT APPLICATION NUMBER: US/09/919,580
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 207

; LENGTH: 395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-207

Query Match 13.6%; Score 18; DB 10; Length 395;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAGGCCAAGCTGAAG 57
|||||

Db 111 GATAGGCCAAGCTGAAG 128
|||||

RESULT 5

US-09-960-352-10885
; Sequence 10885, Application US/09960352
; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 10885

; LENGTH: 404

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 47-LIB188-013-Q1-E1-D4

US-09-960-352-10885

Query Match 13.6%; Score 18; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAGGCCAAGCTGAAG 57
|||||

Db 153 GATAGGCCAAGCTGAAG 170
|||||

RESULT 6

US-09-960-352-6906
; Sequence 6906, Application US/09960352
; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 6906

; LENGTH: 405

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 30-LIB188-021-Q1-E1-H5

US-09-960-352-6906

Query Match 13.6%; Score 18; DB 10; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAGGCCAAGCTGAAG 57
|||||

Db 153 GATAGGCCAAGCTGAAG 170
|||||

RESULT 7

US-09-960-352-12808
; Sequence 12808, Application US/09960352
; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 12808

; LENGTH: 408

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 55-LIB188-007-Q1-E1-F12

US-09-960-352-12808

Query Match 13.6%; Score 18; DB 10; Length 408;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAGGCCAAGCTGAAG 57
|||||

Db 164 GATAGGCCAAGCTGAAG 181
|||||

RESULT 8

US-09-998-598-71
; Sequence 71, Application US/09998598
; Patent No. US20020150922A1

; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.

; APPLICANT: Chenault, Ruth A.

; APPLICANT: Meagher, Madelein Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.561

; CURRENT APPLICATION NUMBER: US/09/998,598

; CURRENT FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 2606

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 71

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-998-598-71

Query Match 13.6%; Score 18; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GATAGGCCAAGCTGAAG 57
|||||

Db 87 GATAGGCCAAGCTGAAG 104
|||||

RESULT 9

US-09-919-580-503
; Sequence 503, Application US/09919580
; Patent No. US20020110832A1

; GENERAL INFORMATION:

; APPLICANT: Pyle, Ruth

; APPLICANT: Xu, Jiangchun

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 503
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-503

Query Match 13.6%; Score 18; DB 10; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 89 GATAAGGCCCAAGCTGAAG 106

RESULT 10
US-09-919-580-633
; Sequence 633, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-633

Query Match 13.6%; Score 18; DB 10; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 90 GATAAGGCCCAAGCTGAAG 107

RESULT 11
US-09-919-580-627
; Sequence 627, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-627

Query Match 13.6%; Score 18; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 99 GATAAGGCCCAAGCTGAAG 116

RESULT 12
US-09-919-580-458
; Sequence 458, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-458

Query Match 13.6%; Score 18; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 99 GATAAGGCCCAAGCTGAAG 116

RESULT 13
US-09-919-580-583
; Sequence 583, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 583
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-583

Query Match 13.6%; Score 18; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 99 GATAAGGCCCAAGCTGAAG 116

RESULT 14
US-09-919-580-910
; Sequence 910, Application US/09919580
; Patent No. US20020110832A1

; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 910
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 438, 439
; OTHER INFORMATION: n = A,T,C or G

US-09-919-580-910

Query Match 13.6%; Score 18; DB 10; Length 439;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 94 GATAAGGCCAAGCTGAAG 111

RESULT 15

US-09-919-580-659
; Sequence 659, Application US/09919580
; Patent No. US20020110832A1

; GENERAL INFORMATION:

; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 659
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-919-580-659

Query Match 13.6%; Score 18; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 104 GATAAGGCCAAGCTGAAG 121

RESULT 16

US-09-919-580-727
; Sequence 727, Application US/09919580
; Patent No. US20020110832A1

; GENERAL INFORMATION:

; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30

; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 727
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-727

Query Match 13.6%; Score 18; DB 10; Length 445;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 99 GATAAGGCCAAGCTGAAG 116

RESULT 17

US-09-919-580-891
; Sequence 891, Application US/09919580
; Patent No. US20020110832A1

; GENERAL INFORMATION:

; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 891
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 427, 444
; OTHER INFORMATION: n = A,T,C or G

US-09-919-580-891

Query Match 13.6%; Score 18; DB 10; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 83 GATAAGGCCAAGCTGAAG 100

RESULT 18

US-09-880-107-3158/C
; Sequence 3158, Application US/09880107
; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3158
; LENGTH: 446
; TYPE: DNA

```

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T59161
; NAME/KEY: unsure
; LOCATION: (1)...(446)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3158

Query Match      13.6%; Score 18; DB 10; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 GATAAGGCCCAAGCTGAAG 57
      |||||||
Db      336 GATAAGGCCCAAGCTGAAG 319

RESULT 19
US-09-918-995-15768
; Sequence 13768, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15768
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-15768

Query Match      13.6%; Score 18; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 GATAAGGCCCAAGCTGAAG 57
      |||||||
Db      146 GATAAGGCCCAAGCTGAAG 163

RESULT 20
US-09-919-580-122
; Sequence 122, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-122

Query Match      13.6%; Score 18; DB 10; Length 449;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 GATAAGGCCCAAGCTGAAG 57

```

```

      |||||||
Db      112 GATAAGGCCCAAGCTGAAG 129

RESULT 21
US-09-919-580-190
; Sequence 190, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-190

Query Match      13.6%; Score 18; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 GATAAGGCCCAAGCTGAAG 57
      |||||||
Db      112 GATAAGGCCCAAGCTGAAG 129

RESULT 22
US-09-919-580-553
; Sequence 553, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-553

Query Match      13.6%; Score 18; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 GATAAGGCCCAAGCTGAAG 57
      |||||||
Db      112 GATAAGGCCCAAGCTGAAG 129

RESULT 23
US-09-919-580-348
; Sequence 348, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-348

Query Match 13.6%; Score 18; DB 10; Length 452;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 113 GATAAGGCCCAAGCTGAAG 130

RESULT 24
US-09-919-580-274
; Sequence 274, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-274

Query Match 13.6%; Score 18; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 114 GATAAGGCCCAAGCTGAAG 131

RESULT 25
US-09-880-107-3019
; Sequence 3019, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 3950
; SEQ ID NO 3019
; LENGTH: 453
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 S54005
US-09-880-107-3019

Query Match 13.6%; Score 18; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 105 GATAAGGCCCAAGCTGAAG 122

RESULT 26
US-09-919-580-273
; Sequence 273, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 273
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-273

Query Match 13.6%; Score 18; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 112 GATAAGGCCCAAGCTGAAG 129

RESULT 27
US-09-919-580-219
; Sequence 219, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-219

Query Match 13.6%; Score 18; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 117 GATAAGGCCCAAGCTGAAG 134

RESULT 28

US-09-960-352-2605/c
; Sequence 2605, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warten, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2605
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (278)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 12-LIB188-023-Q1-El-C7
US-09-960-352-2605

Query Match 13.6%; Score 18; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 403 GATAAGGCCCAAGCTGAAG 386

RESULT 29

US-09-919-580-56
; Sequence 56, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919.580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 404..446, 459
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-56

Query Match 13.6%; Score 18; DB 10; Length 465;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 101 GATAAGGCCCAAGCTGAAG 118

RESULT 30

US-09-918-995-21161
; Sequence 21161, Application US/09918995

; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918.995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21161
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(468)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-21161

Query Match 13.6%; Score 18; DB 9; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 118 GATAAGGCCCAAGCTGAAG 135

RESULT 31

US-09-918-995-24062
; Sequence 24062, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918.995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235.076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24062
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24062

Query Match 13.6%; Score 18; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
|||||
Db 108 GATAAGGCCCAAGCTGAAG 125

RESULT 32

US-09-918-995-15273
; Sequence 15273, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918.995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235.076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15273
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15273

FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15273
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: (1)...(473)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15273

Query Match 13.6%; Score 18; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
|||||
DB 142 GATAGGCCCAAGCTGAAG 159

RESULT 33

US-09-918-995-22477
Sequence 22477, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22477
LENGTH: 474
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: (1)...(474)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22477

Query Match 13.6%; Score 18; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
|||||
DB 68 GATAGGCCCAAGCTGAAG 85

RESULT 34

US-09-918-995-19906
Sequence 19906, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19906
LENGTH: 483
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: (1)...(483)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19906

Query Match 13.6%; Score 18; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
|||||
DB 130 GATAGGCCCAAGCTGAAG 147

RESULT 35

US-09-918-995-24178/c
Sequence 24178, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24178
LENGTH: 494
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: (1)...(494)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24178

Query Match 13.6%; Score 18; DB 9; Length 494;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
|||||
DB 384 GATAGGCCCAAGCTGAAG 367

RESULT 36

US-09-919-580-874
Sequence 874, Application US/09919580
Patent No. US20020110832A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 874
LENGTH: 517
TYPE: DNA

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 446, 503, 505
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-874

Query Match      13.6%; Score 18; DB 10; Length 517;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
   |||||||
Db 103 GATAAGGCCAAGCTGAAG 120

RESULT 37
US-09-919-580-159
; Sequence 159, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: SECRET, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 414, 556
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-159

Query Match      13.6%; Score 18; DB 10; Length 559;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
   |||||||
Db 90 GATAAGGCCAAGCTGAAG 107

RESULT 38
US-09-919-580-798
; Sequence 798, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: SECRET, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 428, 429, 431, 481, 487, 490, 492, 494, 497, 505, 511, 516,
; LOCATION: 539, 554, 562, 575, 597, 641, 664, 682

; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-798

Query Match      13.6%; Score 18; DB 10; Length 693;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
   |||||||
Db 80 GATAAGGCCAAGCTGAAG 97

RESULT 39
US-10-092-154-1336
; Sequence 1336, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1336
; LENGTH: 9953
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-092-154-1336

Query Match      13.6%; Score 18; DB 9; Length 9953;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCC 60
   |||||||
Db 1721 AAGGCCAAGCTGAAGGCC 1738

RESULT 40
US-09-764-847-1336
; Sequence 1336, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1336
; LENGTH: 9953
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-847-1336

Query Match      13.6%; Score 18; DB 10; Length 9953;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AAGGCCAAGCTGAAGGCC 60
   |||||||
Db 1721 AAGGCCAAGCTGAAGGCC 1738

RESULT 41
US-10-092-154-1335
; Sequence 1335, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1335
; LENGTH: 11189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1335

Query Match      13.6%; Score 18; DB 9; Length 11189;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 AAGGCCAAGCTGAAGGCC 60
      |||
Db      2957 AAGGCCAAGCTGAAGGCC 2974

RESULT 42
US-09-764-847-1335
; Sequence 1335, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1335
; LENGTH: 11189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1335

Query Match      13.6%; Score 18; DB 10; Length 11189;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 AAGGCCAAGCTGAAGGCC 60
      |||
Db      2957 AAGGCCAAGCTGAAGGCC 2974

RESULT 43
US-09-918-995-6168/c
; Sequence 6168, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6168
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-6168

Query Match      12.9%; Score 17; DB 9; Length 425;
```

```
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      50 AGCTGAAGGCCACAGAG 66
      |||
Db      104 AGCTGAAGGCCACAGAG 88

RESULT 44
US-09-960-352-5941/c
; Sequence 5941, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5941
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 26-BOVMS1-020-Q1-El-G5
US-09-960-352-5941

Query Match      12.9%; Score 17; DB 10; Length 428;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      75 GAACACTCTGATGACCA 91
      |||
Db      51 GAACACTCTGATGACCA 35

RESULT 45
US-09-918-995-4250/c
; Sequence 4250, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4250
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(433)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4250

Query Match      12.9%; Score 17; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      50 AGCTGAAGGCCACAGAG 66
      |||
Db      104 AGCTGAAGGCCACAGAG 88
```

RESULT 46

US-09-876-889-308/c
; Sequence 308, Application US/09876889
; Patent No. US20020076715A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C3
; CURRENT APPLICATION NUMBER: US/09/876,889
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-889-308

Query Match 12.9%; Score 17; DB 10; Length 439;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 AGCTGAAGGCCACAGAG 66
|||||
Db 401 AGCTGAAGGCCACAGAG 385

RESULT 47

US-09-918-995-22450
; Sequence 22450, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22450
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22450

Query Match 12.9%; Score 17; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAA 56
|||||
Db 131 GATAAGGCCAAGCTGAA 147

RESULT 48

US-09-918-995-23067
; Sequence 23067, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23067
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23067

Query Match 12.9%; Score 17; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAA 56
|||||
Db 162 GATAAGGCCAAGCTGAA 178

RESULT 49

US-10-102-806-146/c
; Sequence 146, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-806-146

Query Match 12.9%; Score 17; DB 9; Length 814;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 AGCTGAAGGCCACAGAG 66
|||||
Db 688 AGCTGAAGGCCACAGAG 672

RESULT 50

US-09-738-626-1039
; Sequence 1039, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOHI, AKIHIRO
; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1039
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1039

Query Match 12.98; Score 17; DB 9; Length 1077;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CACAGATGCAGAGAAC 78
|||||
Db 690 CACAGATGCAGAGAAC 706

Search completed: June 2, 2003, 17:18:33
Job time : 135 secs

THIS PAGE BLANK (1/3/79)

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.
Source version 3.1.0

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 14:37:52 ; Search time 214 Seconds
(without alignments)

(without alignments)
1389.083·Million cel

1389.083· Million cell updates/sec

Title: US-09-915-178-1

perfect score:

Sequence: 1 atggcacacaactagacct.....agtqgaqtgaaatttcctga 132

Scoring table:

scoring cable. OIRGO_NOC
Gapop 60.6

[illegible]

Searched: 2185239 seqs, 1125999159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 258815

Minimum DB seq length: 0

Minimum	DB seq	length:	0
Maximum	DB seq	length:	2000000000

Post-processing: Listing first 1000 summaries

Database : N Geneseq 101002:*

1:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1980..DAT:*
2:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1981..DAT:*
3:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1982..DAT:*
4:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1983..DAT:*
5:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1984..DAT:*
6:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1985..DAT:*
7:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1986..DAT:*
8:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1987..DAT:*
9:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1988..DAT:*
10:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1989..DAT:*
11:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1990..DAT:*
12:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1991..DAT:*
13:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1992..DAT:*
14:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1993..DAT:*
15:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1994..DAT:*
16:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1995..DAT:*
17:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1996..DAT:*
18:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1997..DAT:*
19:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1998..DAT:*
20:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA1999..DAT:*
21:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA2000..DAT:*
22:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA2001A..DAT:*
23:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA2001B..DAT:*
24:	/SID\$2/cgcgdata/geneseq/geneseqn-emb1/NA2002..DAT:*

```

database : n_geneseq_101002 :
1: /SID52/qcadata/geneseq/geneseq-emb1/NA1980.DAT:*

```

```
1: /SIDS2/ycyaca/geneseq/geneseqn-embol/NA1980.DAT:*
2: /SIDS2/qcdata/geneseq/geneseqn-embol/NA1981.DAT:*
```

3: /SIDS2/qcadata/geneseq/geneseqn-emb1/NA1982.DAT: *

4: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:

11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:

12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:

13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:

14: /SIBS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:
15: /SIBS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:

15: /SIBS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:
16: /SIBS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:

```

I6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
I7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:

```

```

I/: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:

```

```

18: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1997.DAT:
19: /SIDS2/tcdata/geneseq/geneseq-emb1/NA1998.DAT:

```

```
19: /STDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:
20: /STDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:
```

```

20: /SIDSZ/qcguata/geneseq/geneseq1-emb1/NA1999.DAT:
21: /SIDSZ/qcguata/geneseq/geneseq1-emb1/NA2000.DAT:

```

```

zi: /SIDS2/yccgata/geneseq/geneseq-emb1/NA2000.DAT
22: /SIDS2/qcqdta/geneseq/geneseq-emb1/NA2001A.DAT

```

```

22: /SIPD2/ycydata/geneseq/geneseqn emb1/NA2001A.DAT
23: /SIPD2/qcadata/geneseq/geneseqn -emb1/NA2001B.DAT

```

23: /SIPDS2/qc9qdata/geneseq/geneseqn emb1/NA2001B.DAT
24: /SIPDS2/qc9qdata/geneseq/geneseqn -emb1/NA2002.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Length	DB	ID	Description
		Match	Query				
1	132	100.0		147	24	ABA92649	Human NOV2a encodi
2	132	100.0		147	24	ABA92650	Human NOV2b encodi
3	132	100.0		147	24	ABA92651	Human NOV2c encodi
4	18	13.6		65	24	ABN29874	Rat spliced transc
5	18	13.6		203	23	ABV08667	Human prostate exp
6	18	13.6		243	24	ABK55047	Human colon cancer
7	18	13.6		283	21	AAC00909	Human secreted pro
8	18	13.6		353	24	ABK54754	Human colon cancer
9	18	13.6		395	24	ABK54737	Human colon cancer

83	17	12.9	2090	22	AAH27095	Human transforming	156	16	12.1	1232	24	ABN86297	Human protease cDN
84	17	12.9	2095	15	ABN86290	Type II TGF-beta re	157	16	12.1	1239	22	AAK51749	Human polynucleoti
85	17	12.9	2090	14	AAQ64830	TGF-beta receptor	c 158	16	12.1	1257	23	AAK51581	DNA encoding novel
86	17	12.9	2715	18	ABN79809	Fungal ZPC gene se	159	16	12.1	1312	21	AAK59439	Nucleotide sequenc
87	17	12.9	4590	18	AAAT94612	Rat penile neurona	160	16	12.1	1320	23	AAK58533	DNA encoding novel
88	17	12.9	5108	14	AAQ53403	Sequence encoding	161	16	12.1	1320	23	AAK58221	DNA encoding novel
89	17	12.9	5759	24	ABQ88231	Human osteoblast d	162	16	12.1	1385	22	AAH16077	Human cDNA sequenc
90	17	12.9	5759	24	ABK83678	Human cDNA differe	163	16	12.1	1406	16	AAQ97295	Marek's disease vi
91	17	12.9	5759	24	ABL66691	Lung cancer relate	164	16	12.1	1416	22	AAI160976	Human polynucleoti
92	17	12.9	5760	23	AAK76568	DNA encoding novel	165	16	12.1	1453	22	AAK85078	Atherosclerosis-as
93	17	12.9	13026	22	ABA15222	Human nervous syst	166	16	12.1	1464	24	ABA93723	Human amygdala der
94	17	12.9	13026	22	AAK07529	Human reproductive	167	16	12.1	1492	22	ABA93723	Human breast cell
95	17	12.9	14970	22	AAK42037	Genomic sequence #	168	16	12.1	1492	22	ABA93723	Probe #2209 for ge
96	17	12.9	14976	22	AAK42038	Genomic sequence #	169	16	12.1	1492	22	AAK02262	Human brain expres
97	17	12.9	34980	22	AAH68527	C glutamicum codin	170	16	12.1	1492	22	AAK27709	Human bone marrow
98	16	12.1	60	24	ABN36497	Human spliced tran	171	16	12.1	1492	22	AAI12288	Probe #2221 for ge
99	16	12.1	134	21	ABN36497	Human colon cancer	172	16	12.1	1492	22	AAI133645	Probe #2331 used t
100	16	12.1	281	22	AAK98664	Human breast cancer	173	16	12.1	1492	22	AAI02204	Probe #2195 used t
101	16	12.1	294	22	AAK16566	Human breast cancer	174	16	12.1	1492	22	AAI02204	Human genome-deriv
102	16	12.1	307	22	AAH72404	Human cervical can	175	16	12.1	1584	22	AAI02204	Human novel protei
103	16	12.1	311	22	AAH70853	Human cervical can	176	16	12.1	1584	22	AAK16566	DNA #58 encoding h
104	16	12.1	329	22	AAH07663	Human breast cancer	177	16	12.1	1931	24	AAK30581	Human protease, PR
105	16	12.1	331	22	AAH69518	Human cervical can	c 178	16	12.1	2109	22	AAK94222	Human full-length
106	16	12.1	347	22	AAK23252	Human breast cancer	179	16	12.1	2135	23	AAK78501	DNA encoding novel
107	16	12.1	397	22	AAK16301	Human breast cancer	c 180	16	12.1	2199	19	AAK15431	Coding region of D
108	16	12.1	426	22	AAH72979	Human breast cancer	181	16	12.1	2352	21	AAK59695	Human secreted pro
109	16	12.1	429	24	ABL62160	Human cervical can	182	16	12.1	2355	19	AAK63188	cDNA from clone bl
110	16	12.1	434	23	ABK43038	Colon adenocarcino	183	16	12.1	2355	24	ABQ92038	Human polynucleoti
111	16	12.1	444	23	ABK43038	Genomic sequence #	184	16	12.1	2527	22	AAH16264	Human cDNA sequenc
112	16	12.1	444	24	ABL64166	Gene #131 used to	185	16	12.1	2545	22	AAH17775	Human cDNA sequenc
113	16	12.1	460	23	ABK42068	Stomach cancer rel	186	16	12.1	2693	22	AAI16565	Human novel protei
114	16	12.1	475	22	ABA51709	cDNA encoding nove	187	16	12.1	2693	22	AAI16565	Human novel protei
115	16	12.1	475	22	ABA51806	Human foetal liver	188	16	12.1	2693	22	AAI16568	Human novel protei
116	16	12.1	475	22	ABA21546	Human foetal liver	c 189	16	12.1	2693	22	AAK35107	DNA #57 encoding h
117	16	12.1	475	22	ABA21635	Probe #12 for gene	c 190	16	12.1	2693	22	AAK35109	DNA #59 encoding h
118	16	12.1	475	22	AAK00021	Probe #101 for gen	c 191	16	12.1	2693	22	AAK35110	DNA #60 encoding h
119	16	12.1	475	22	AAK00113	Human brain expres	c 192	16	12.1	2805	23	ABL05310	Drosophila melanog
120	16	12.1	475	22	AAK25456	Human bone marrow	c 193	16	12.1	2817	19	AAK15430	DNA encoding treha
121	16	12.1	475	22	AAK25550	Human bone marrow	194	16	12.1	2863	22	AAH48299	Human phosphoenol
122	16	12.1	475	22	AAI10079	Probe #12 for gene	195	16	12.1	3149	24	ABD39131	Rat obesity-specif
123	16	12.1	475	22	AAI10173	Probe #106 for gen	196	16	12.1	3270	19	AAV73472	Human UBP cDNA #2
124	16	12.1	475	22	AAI131327	Probe #13 used to	197	16	12.1	3270	23	AAK87519	DNA encoding novel
125	16	12.1	475	22	AAI131423	Probe #109 used to	c 198	16	12.1	3327	23	ABL11284	Drosophila melanog
126	16	12.1	475	22	AAI00022	Probe #13 used to	199	16	12.1	3437	16	AAK03437	Human matrix metal
127	16	12.1	475	22	AAI000116	Probe #107 used to	200	16	12.1	3437	24	ABL65860	Lung cancer relate
128	16	12.1	475	24	ABS00021	Human genome-deriv	201	16	12.1	3437	24	ABK35514	Human endometrial
129	16	12.1	475	24	ABS00119	Human genome-deriv	202	16	12.1	3456	16	AAK03436	Human matrix metal
130	16	12.1	527	22	AAK23305	Human breast cancer	203	16	12.1	3540	24	AAI70820	Mouse laminin-15 g
131	16	12.1	528	24	ABN60577	Human breast cancer	204	16	12.1	4010	22	AAI26509	Human breast cancer
132	16	12.1	534	22	AAK25144	Human cancer relat	205	16	12.1	4023	24	ABK14799	cDNA encoding huma
133	16	12.1	567	22	AAK14443	Human breast cancer	c 206	16	12.1	4173	23	ABL05334	Drosophila melanog
134	16	12.1	649	24	ABQ59067	Human colon cancer	c 207	16	12.1	4380	10	AAK91839	Pasteurella multoc
135	16	12.1	665	22	AAK16538	Human novel protei	c 208	16	12.1	4381	12	AAQ10519	Pasteurella multoc
136	16	12.1	665	22	AAK34878	cDNA encoding nove	209	16	12.1	4672	23	AAK37372	DNA encoding novel
137	16	12.1	685	22	AAH05932	Human cDNA clone (210	16	12.1	4815	24	ABK31757	DNA encoding novel
138	16	12.1	712	21	AAK34195	Arabidopsis thalia	211	16	12.1	4863	23	AAK51489	Pseudomonas aerugi
139	16	12.1	733	22	AAH06563	Human cDNA clone (212	16	12.1	4890	20	AAK59765	cDNA encoding huma
140	16	12.1	741	23	ABL05311	Drosophila melanog	213	16	12.1	4946	24	ABK3922	Human cDNA differe
141	16	12.1	779	20	AAK16506	Human gene expres	c 214	16	12.1	4998	22	AAK65573	Human ORF ORF681
142	16	12.1	802	24	ABQ89923	Human prostate exp	215	16	12.1	5300	21	AAK75126	Human ORF ORF681
143	16	12.1	870	23	AAK53013	Enterococcus faeca	216	16	12.1	6093	22	ABL05402	Human reproductive
144	16	12.1	977	24	ABQ73799	Human colon specif	217	16	12.1	6093	23	ABL98264	Human testicular a
145	16	12.1	1020	24	ABL90381	Human polynucleoti	218	16	12.1	6273	23	ABL15731	Drosophila melanog
146	16	12.1	1093	22	ABA48654	Human breast cell	c 219	16	12.1	6315	22	AAK15744	Drosophila melanog
147	16	12.1	1093	22	ABA33630	Probe #12096 for g	c 220	16	12.1	6390	22	AAK81370	Quorum sensing con
148	16	12.1	1093	22	AAK14990	Human brain expres	c 221	16	12.1	6640	23	ABK42190	Genomic sequence #
149	16	12.1	1093	22	AAK40723	Human bone marrow	c 222	16	12.1	6940	24	ABN95226	Gene #1724 used to
150	16	12.1	1093	22	AAI21485	Probe #11418 for g	223	16	12.1	7856	23	AAK85531	DNA encoding novel
151	16	12.1	1093	22	AAI46777	Probe #15463 used	224	16	12.1	7856	23	AAK8213	DNA encoding novel
152	16	12.1	1093	22	AAI07183	Probe #7174 used t	225	16	12.1	7878	24	ABL84684	Stomach cancer rel
153	16	12.1	1093	22	AAK14683	Human genome-deriv	c 226	16	12.1	8134	23	ABL03228	Drosophila melanog
154	16	12.1	1179	22	AAK52733	Human polynucleoti	227	16	12.1	8180	23	AAK8212	DNA encoding novel
155	16	12.1	1211	21	AAA62055	Hydrophobic domain	228	16	12.1	8201	17	AAI12170	pJG4-5-CDK-BP CDNA

229	16	12.1	8284	23	AAS85535	Human genome-deriv	15	11.4	461	24	ABS07273	Human genome-deriv
230	16	12.1	8309	22	AAI59190	Human polynucleoti	15	11.4	463	22	AAL19114	Human breast cance
231	16	12.1	8408	22	AAI57848	Human polynucleoti	15	11.4	471	21	AAC00538	Human secreted pro
232	16	12.1	8420	22	AAI57847	Human polynucleoti	15	11.4	472	23	ABV45615	Human prostate exp
233	16	12.1	8435	22	AAI59633	Human polynucleoti	15	11.4	480	22	AAH06068	Human CDNA clone (
234	16	12.1	8435	22	AAI59634	Human polynucleoti	15	11.4	485	22	AAH08949	Human CDNA clone (
235	16	12.1	8974	23	ABK42191	Genomic sequence #	15	11.4	487	23	AAC79710	DNA encoding novel
236	16	12.1	10855	23	ABK15730	Drosophila melanog	15	11.4	499	21	AAC40972	zea mays DNA fragm
237	16	12.1	10923	23	ABK42192	Genomic sequence #	15	11.4	505	22	AAH29674	Drosophila melanog
238	16	12.1	14822	20	AAK20543	Polynucleotide seq	15	11.4	508	22	AAL13213	Human breast cance
239	16	12.1	16956	21	AAZ91923	Wild type (C57BL/6	15	11.4	511	24	ABL83055	Human ovarian cance
240	16	12.1	22680	22	AAK66308	Human immune/haema	15	11.4	518	22	AAL31184	Human diagnostic a
241	16	12.1	22680	22	AAK73334	Human immune/haema	15	11.4	520	22	AAL22083	Human breast cance
242	16	12.1	22680	22	AAK73344	Human immune/haema	15	11.4	522	24	ABN66905	Streptococcus poly
243	16	12.1	22680	22	AAK73625	Human immune/haema	15	11.4	526	24	ABK39435	DNA encoding lung
244	16	12.1	22680	22	AAK73847	Human immune/haema	15	11.4	533	22	AAH13579	Human CDNA clone (
245	16	12.1	22680	22	AAK73934	Human immune/haema	15	11.4	536	24	ABK09684	Human ovarian tumo
246	16	12.1	22680	22	AAK78350	Human immune/haema	15	11.4	547	22	AAH05727	Human CDNA clone (
247	16	12.1	37116	23	AAS59553	Propionibacterium	15	11.4	554	22	AAL21812	Human breast cance
248	16	12.1	46765	24	AAS99306	DNA encoding Aldeh	15	11.4	555	22	AAL21487	Human breast cance
249	16	12.1	112190	22	AAH44801	Human GPCR protein	15	11.4	557	22	AAH12614	Human breast cance
250	16	12.1	368004	24	ABL57909	Human transporters	15	11.4	563	23	ABV06749	Human prostate exp
251	15	11.4	27	22	AAS04265	Saccharomyces cere	15	11.4	566	23	ABV34753	Human prostate exp
252	15	11.4	27	24	ABK53065	S. Cerevisiae HMG	15	11.4	574	24	ABN65854	Human cancer relat
253	15	11.4	45	22	AAI17288	Human thymosin bet	15	11.4	580	23	ABV06926	Human prostate exp
254	15	11.4	213	16	AAT20156	Human gene signatu	15	11.4	581	22	AAH09232	Human CDNA clone (
255	15	11.4	231	22	AAS60121	Human cancer agent	15	11.4	584	22	AAH05114	Human CDNA clone (
256	15	11.4	257	21	AAK43117	Human secreted exp	15	11.4	595	22	AAK69867	Human immune/haema
257	15	11.4	267	21	AAK00908	Human secreted pro	15	11.4	597	24	ABN65484	Human cancer relat
258	15	11.4	273	16	AAT24694	Human gene signatu	15	11.4	615	23	ABV34822	Human prostate exp
259	15	11.4	277	20	AAS13372	Human gene express	15	11.4	617	21	AAF09329	Fusarium venenatum
260	15	11.4	293	22	AAS60106	Human cancer agent	15	11.4	647	22	AAL12941	Human breast cance
261	15	11.4	293	22	AAH77501	Human DNA repair p	15	11.4	653	23	ABV36695	Human prostate exp
262	15	11.4	304	22	AAI28952	Colon tumour relat	15	11.4	654	23	ABV36870	Human prostate exp
263	15	11.4	338	21	AAC53477	Arabidopsis thalia	15	11.4	670	23	AAH76415	DNA encoding novel
264	15	11.4	347	22	AAH05011	Human reproductive	15	11.4	674	24	AAS61600	Lung small cell ca
265	15	11.4	347	23	ABL97904	Human testicular a	15	11.4	681	22	AAI17184	Human zinculne fr
266	15	11.4	349	22	AAH01333	Human reproductive	15	11.4	684	22	AAH05689	Human CDNA clone (
267	15	11.4	349	23	ABL96787	Human testicular a	15	11.4	696	21	AAH95469	E. coli essential
268	15	11.4	351	22	ABA06677	Human CDNA SEQ ID	15	11.4	696	21	AAH88696	E. coli FUN essent
269	15	11.4	366	22	AAS60497	Human cancer agent	15	11.4	696	22	AAH81404	Escherichia coli p
270	15	11.4	366	24	ABQ58932	Human colon cancer	15	11.4	696	23	AAS52487	E. coli DNA for ce
271	15	11.4	369	14	AAQ61270	Human brain expres	15	11.4	714	23	AAS87333	DNA encoding novel
272	15	11.4	374	22	AAQ00541	Human reproductive	15	11.4	714	23	AAS92676	DNA encoding novel
273	15	11.4	388	24	ABN60045	Human cancer relat	15	11.4	715	20	AAH22212	Human secreted pro
274	15	11.4	390	22	AAI29498	Human polynucleoti	15	11.4	724	22	AAH05993	Human CDNA clone (
275	15	11.4	396	22	AAH94957	Human ovarian cnc	15	11.4	724	24	AAS62054	Porcine muscular s
276	15	11.4	396	24	ABT03224	Human ovarian carc	15	11.4	781	22	AAH196499	Human neuroblastom
277	15	11.4	396	24	ABL48907	Ovarian carcinoma	15	11.4	782	24	ABN96994	Gene #3492 used to
278	15	11.4	399	21	AAH30571	Human colon cancer	15	11.4	786	20	AAZ16704	Human gene express
279	15	11.4	399	22	AAH12265	Human CDNA clone (15	11.4	817	22	AAH04312	Human CDNA clone (
280	15	11.4	406	23	ABV14058	Human prostate exp	15	11.4	837	22	AAH80410	Nucleotide sequenc
281	15	11.4	419	23	AAH2468	DNA encoding novel	15	11.4	837	24	AAK85175	Arabidopsis thalia
282	15	11.4	422	14	AAQ59867	Human brain expres	15	11.4	843	21	AAC37750	Arabidopsis thalia
283	15	11.4	425	22	AAH12338	Human CDNA clone (15	11.4	849	23	AAS88546	DNA encoding novel
284	15	11.4	441	23	ABV04889	Human prostate exp	15	11.4	867	24	ABN67373	Streptococcus poly
285	15	11.4	442	22	AAH79798	Human secreted pro	15	11.4	888	23	AAH09165	Drosophila melanog
286	15	11.4	443	23	ABV35163	Human prostate exp	15	11.4	888	18	AAH75097	Arabidopsis flower
287	15	11.4	443	23	ABV44005	Human prostate exp	15	11.4	908	22	AAL02651	Human reproductive
288	15	11.4	446	24	ABK55170	Human colon cancer	15	11.4	908	22	AAH297318	Human testicular a
289	15	11.4	448	22	AAH33334	Human colon cancer	15	11.4	913	20	AAZ28273	Rat neuronal immed
290	15	11.4	459	23	ABV15813	Human prostate exp	15	11.4	913	22	AAH05068	Human CDNA clone (
291	15	11.4	460	20	AAZ24583	Human lung tumor a	15	11.4	918	23	ABL03121	Drosophila melanog
292	15	11.4	460	21	AAH65822	Human lung cancer-	15	11.4	930	22	AAS30994	Human diagnostic a
293	15	11.4	460	24	ABL49041	Human lung tumour	15	11.4	936	23	ABV22483	Human prostate exp
294	15	11.4	461	22	ABA58579	Human foetal liver	15	11.4	936	23	ABV23104	Human prostate exp
295	15	11.4	461	22	ABA27600	Probe #6066 for ge	15	11.4	936	23	ABV28298	Human prostate exp
296	15	11.4	461	22	AAK06701	Human brain expres	15	11.4	936	23	ABV28942	Human prostate exp
297	15	11.4	461	22	AAK32400	Human bone marrow	15	11.4	975	18	AAH68791	Melanocortin-5 rec
298	15	11.4	461	22	AAK32488	Human bone marrow	15	11.4	975	19	AAV62353	Melanocortin-5 rec
299	15	11.4	461	22	AAH16060	Human bone marrow	15	11.4	975	19	AAV03916	Mouse melanocortin
300	15	11.4	461	22	AAI38243	Probe #5993 for ge	15	11.4	975	19	AAV06405	Mouse melanocortin
301	15	11.4	461	24	ABS07184	Probe #6929 used t	15	11.4	975	20	AAH01965	Mouse MC5 DNA. Mu

c 375	15	11.4	975	21	AAV15830	DNA encoding a hum	448	15	11.4	2490	22	AAH17721	Human cDNA sequenc
c 376	15	11.4	978	19	AAV19143	Mouse melanocortin	449	15	11.4	2506	22	AA544993	Human encoding nove
c 377	15	11.4	978	20	AAV63708	Mouse melanocortin	450	15	11.4	2509	16	AAQ92776	Human thymopoietin
c 378	15	11.4	979	23	ABV22327	Human prostate exp	451	15	11.4	2512	22	AAH17639	Human cDNA sequenc
c 379	15	11.4	979	23	ABV22327	Human prostate exp	452	15	11.4	2512	22	AAH17639	Human polynucleoti
c 380	15	11.4	1014	22	AA544571	Human prostate exp	453	15	11.4	2571	22	AA161213	Human polynucleoti
c 381	15	11.4	1014	22	AA544571	Human prostate exp	454	15	11.4	2593	21	AA161213	Human pancreatic c
c 382	15	11.4	1032	24	AA592052	DNA encoding novel	455	15	11.4	2615	22	AAQ02597	Human Electron Tra
c 383	15	11.4	1032	24	AA592052	DNA encoding novel	456	15	11.4	2621	22	AAH15693	Human cDNA sequenc
c 384	15	11.4	1036	22	AA592056	Arabidopsis thalia	457	15	11.4	2638	24	ABN59719	Novel human coding
c 385	15	11.4	1093	21	AA56537	Human cDNA encodin	458	15	11.4	2676	23	AA567421	DNA encoding novel
c 386	15	11.4	1128	22	AA56537	Human cytokine fam	459	15	11.4	2694	22	AA567421	Human hydrophobic
c 387	15	11.4	1132	22	AA56537	DNA encoding nove	460	15	11.4	2760	22	AA567421	Human cDNA encodin
c 388	15	11.4	1161	21	AA56537	Human secreted pro	461	15	11.4	2826	23	AA56537	Human prostate exp
c 389	15	11.4	1378	22	AAH15719	Human cDNA sequenc	462	15	11.4	2826	23	AA56537	Human prostate exp
c 390	15	11.4	1430	22	AA514084	Human FcR3a DNA s	463	15	11.4	2877	23	ABL02791	Drosophila melanog
c 391	15	11.4	1431	22	AA514084	Human FcR3a DNA s	464	15	11.4	2877	23	ABL02791	DNA encoding novel
c 392	15	11.4	1434	22	AA514084	Human polynucleoti	465	15	11.4	2928	23	AA573816	Drosophila melanog
c 393	15	11.4	1477	24	AA514084	Human polynucleoti	466	15	11.4	3005	23	AA573816	DNA encoding novel
c 394	15	11.4	1482	23	AA514084	Human polynucleoti	467	15	11.4	3011	23	AA573816	DNA encoding novel
c 395	15	11.4	1499	22	AA514084	Human polynucleoti	468	15	11.4	3012	23	AA573816	Human potassum ch
c 396	15	11.4	1526	22	AA514084	Human polynucleoti	469	15	11.4	3027	24	AA51516	Human polynucleoti
c 397	15	11.4	1562	22	AA514084	Human polynucleoti	470	15	11.4	3102	22	AA51516	Saccharomyces cere
c 398	15	11.4	1586	19	AA514084	Human polynucleoti	471	15	11.4	3116	22	AA51516	S. cerevisiae acid
c 399	15	11.4	1587	22	AA514084	Human polynucleoti	472	15	11.4	3126	20	AA51516	Human zinculing co
c 400	15	11.4	1592	22	AA514084	Human polynucleoti	473	15	11.4	3201	22	AA51516	Human zinculing co
c 401	15	11.4	1622	24	AA514084	Human polynucleoti	474	15	11.4	3201	22	AA51516	Human zinculing co
c 402	15	11.4	1626	20	AA514084	Human polynucleoti	475	15	11.4	3276	22	AA51516	Human zinculing co
c 403	15	11.4	1640	22	AA514084	Human polynucleoti	476	15	11.4	3302	23	AA51516	Human zinculing co
c 404	15	11.4	1656	22	AA514084	Human polynucleoti	477	15	11.4	3367	23	AA51516	Human zinculing co
c 405	15	11.4	1674	22	AA514084	Human polynucleoti	478	15	11.4	3465	22	AA51516	Human zinculing co
c 406	15	11.4	1674	22	AA514084	Human polynucleoti	479	15	11.4	3507	22	AA51516	Human zinculing co
c 407	15	11.4	1674	22	AA514084	Human polynucleoti	480	15	11.4	3510	22	AA51516	Human zinculing co
c 408	15	11.4	1674	22	AA514084	Human polynucleoti	481	15	11.4	3510	22	AA51516	Human zinculing co
c 409	15	11.4	1674	22	AA514084	Human polynucleoti	482	15	11.4	3510	22	AA51516	Human zinculing co
c 410	15	11.4	1674	22	AA514084	Human polynucleoti	483	15	11.4	3510	22	AA51516	Human zinculing co
c 411	15	11.4	1674	22	AA514084	Human polynucleoti	484	15	11.4	3510	22	AA51516	Human zinculing co
c 412	15	11.4	1674	22	AA514084	Human polynucleoti	485	15	11.4	3510	22	AA51516	Human zinculing co
c 413	15	11.4	1674	22	AA514084	Human polynucleoti	486	15	11.4	3510	22	AA51516	Human zinculing co
c 414	15	11.4	1674	22	AA514084	Human polynucleoti	487	15	11.4	3510	22	AA51516	Human zinculing co
c 415	15	11.4	1674	22	AA514084	Human polynucleoti	488	15	11.4	3510	22	AA51516	Human zinculing co
c 416	15	11.4	1674	22	AA514084	Human polynucleoti	489	15	11.4	3510	22	AA51516	Human zinculing co
c 417	15	11.4	1674	22	AA514084	Human polynucleoti	490	15	11.4	3510	22	AA51516	Human zinculing co
c 418	15	11.4	1674	22	AA514084	Human polynucleoti	491	15	11.4	3510	22	AA51516	Human zinculing co
c 419	15	11.4	1674	22	AA514084	Human polynucleoti	492	15	11.4	3510	22	AA51516	Human zinculing co
c 420	15	11.4	1674	22	AA514084	Human polynucleoti	493	15	11.4	3510	22	AA51516	Human zinculing co
c 421	15	11.4	1674	22	AA514084	Human polynucleoti	494	15	11.4	3510	22	AA51516	Human zinculing co
c 422	15	11.4	1674	22	AA514084	Human polynucleoti	495	15	11.4	3510	22	AA51516	Human zinculing co
c 423	15	11.4	1674	22	AA514084	Human polynucleoti	496	15	11.4	3510	22	AA51516	Human zinculing co
c 424	15	11.4	1674	22	AA514084	Human polynucleoti	497	15	11.4	3510	22	AA51516	Human zinculing co
c 425	15	11.4	1674	22	AA514084	Human polynucleoti	498	15	11.4	3510	22	AA51516	Human zinculing co
c 426	15	11.4	1674	22	AA514084	Human polynucleoti	499	15	11.4	3510	22	AA51516	Human zinculing co
c 427	15	11.4	1674	22	AA514084	Human polynucleoti	500	15	11.4	3510	22	AA51516	Human zinculing co
c 428	15	11.4	1674	22	AA514084	Human polynucleoti	501	15	11.4	3510	22	AA51516	Human zinculing co
c 429	15	11.4	1674	22	AA514084	Human polynucleoti	502	15	11.4	3510	22	AA51516	Human zinculing co
c 430	15	11.4	1674	22	AA514084	Human polynucleoti	503	15	11.4	3510	22	AA51516	Human zinculing co
c 431	15	11.4	1674	22	AA514084	Human polynucleoti	504	15	11.4	3510	22	AA51516	Human zinculing co
c 432	15	11.4	1674	22	AA514084	Human polynucleoti	505	15	11.4	3510	22	AA51516	Human zinculing co
c 433	15	11.4	1674	22	AA514084	Human polynucleoti	506	15	11.4	3510	22	AA51516	Human zinculing co
c 434	15	11.4	1674	22	AA514084	Human polynucleoti	507	15	11.4	3510	22	AA51516	Human zinculing co
c 435	15	11.4	1674	22	AA514084	Human polynucleoti	508	15	11.4	3510	22	AA51516	Human zinculing co
c 436	15	11.4	1674	22	AA514084	Human polynucleoti	509	15	11.4	3510	22	AA51516	Human zinculing co
c 437	15	11.4	1674	22	AA514084	Human polynucleoti	510	15	11.4	3510	22	AA51516	Human zinculing co
c 438	15	11.4	1674	22	AA514084	Human polynucleoti	511	15	11.4	3510	22	AA51516	Human zinculing co
c 439	15	11.4	1674	22	AA514084	Human polynucleoti	512	15	11.4	3510	22	AA51516	Human zinculing co
c 440	15	11.4	1674	22	AA514084	Human polynucleoti	513	15	11.4	3510	22	AA51516	Human zinculing co
c 441	15	11.4	1674	22	AA514084	Human polynucleoti	514	15	11.4	3510	22	AA51516	Human zinculing co
c 442	15	11.4	1674	22	AA514084	Human polynucleoti	515	15	11.4	3510	22	AA51516	Human zinculing co
c 443	15	11.4	1674	22	AA514084	Human polynucleoti	516	15	11.4	3510	22	AA51516	Human zinculing co
c 444	15	11.4	1674	22	AA514084	Human polynucleoti	517	15	11.4	3510	22	AA51516	Human zinculing co
c 445	15	11.4	1674	22	AA514084	Human polynucleoti	518	15	11.4	3510	22	AA51516	Human zinculing co
c 446	15	11.4	1674	22	AA514084	Human polynucleoti	519	15	11.4	3510	22	AA51516	Human zinculing co
c 447	15	11.4	1674	22	AA514084	Human polynucleoti	520	15	11.4	3510	22	AA51516	Human zinculing co

c 521	15	11.4	7120	23	ABL04480	Drosophila melanog	c 594	14	10.6	51	15	AAQ69677	Human hepatic lipa
c 522	15	11.4	7676	19	AAV62906	Human galactokinas	c 595	14	10.6	51	18	AAT64139	Human hepatic lipa
c 523	15	11.4	7727	22	AAAL04997	Human reproductiv	c 596	14	10.6	51	20	AAK17427	Test sequence from
c 524	15	11.4	7727	23	ABL97890	Human testicular a	c 597	14	10.6	51	24	ABK62918	DNA binding molecu
c 525	15	11.4	7997	23	ABL28198	Drosophila melanog	c 598	14	10.6	60	24	ABN32701	Human spliced tran
c 526	15	11.4	8095	24	ABN95730	Gene #2228 used to	c 599	14	10.6	60	24	ABN33731	Human spliced tran
c 527	15	11.4	8280	23	AA574108	DNA encoding novel	c 600	14	10.6	60	24	ABN45615	Human spliced tran
c 528	15	11.4	8367	18	AA737321	Human filamin cDNA	c 601	14	10.6	65	24	ABN53425	Mouse spliced tran
c 529	15	11.4	8367	20	AA206508	Carboxyl terminal	c 602	14	10.6	81	22	ABA36518	Probe #14984 for g
c 530	15	11.4	8368	22	AAH81766	Human differential	c 603	14	10.6	99	18	AAT48762	Polyclonal anti-fe
c 531	15	11.4	8368	24	ABL62478	Colon adenocarcino	c 604	14	10.6	122	22	ABA72504	Human foetal liver
c 532	15	11.4	8806	17	AAT093549	Rat IP3 receptor g	c 605	14	10.6	122	22	ABA38258	Probe #16724 for g
c 533	15	11.4	9729	22	AA514089	Human FCTR3f DNA s	c 606	14	10.6	122	22	AAK20927	Human brain expres
c 534	15	11.4	9826	22	AA514085	Human FCTR3b DNA s	c 607	14	10.6	122	22	AAK47080	Human bone marrow
c 535	15	11.4	10319	22	AA527632	DNA encoding novel	c 608	14	10.6	122	22	AAK152916	Probe #21602 used
c 536	15	11.4	10438	23	AA574106	DNA encoding novel	c 609	14	10.6	122	24	ABS21314	Human genome-deriv
c 537	15	11.4	10479	23	ABL15220	Drosophila melanog	c 610	14	10.6	137	22	ABA50761	Human breast cell
c 538	15	11.4	10718	14	AAQ51476	DEN1-S275/90 (ECAC	c 611	14	10.6	137	22	ABA68729	Human foetal liver
c 539	15	11.4	12081	23	ABL09560	Drosophila melanog	c 612	14	10.6	137	22	ABA35692	Probe #14158 for g
c 540	15	11.4	12666	19	AAV52270	Streptococcus pneu	c 613	14	10.6	137	22	AAK17072	Human brain expres
c 541	15	11.4	15571	24	ABN95889	Gene #2387 used to	c 614	14	10.6	137	22	AAK42855	Human bone marrow
c 542	15	11.4	15571	24	ABL68256	Kidney cancer rela	c 615	14	10.6	137	22	AAI23619	Probe #13552 for g
c 543	15	11.4	15571	24	ABL68528	Kidney cancer rela	c 616	14	10.6	137	22	RAI48930	Probe #17616 used
c 544	15	11.4	15848	20	AAZ32190	Human heparin cofa	c 617	14	10.6	137	22	AAI09234	Probe #9225 used t
c 545	15	11.4	15849	24	ABN95864	Gene #2362 used to	c 618	14	10.6	137	24	ABSI6909	Human genome-deriv
c 546	15	11.4	16428	22	AAK81010	Human immune/haema	c 619	14	10.6	138	23	ABV04928	Human prostate exp
c 547	15	11.4	16428	23	ABK42726	Genomic sequence #	c 620	14	10.6	140	16	AAT20692	Human genome-deriv
c 548	15	11.4	18909	23	ABL07204	Drosophila melanog	c 621	14	10.6	140	22	AAI00065	Human reproductiv
c 549	15	11.4	19736	24	ABN89474	Human protease gen	c 622	14	10.6	151	22	ABA72978	Human foetal liver
c 550	15	11.4	19736	24	ABA92158	Human protease gen	c 623	14	10.6	151	22	AAK21410	Human brain expres
c 551	15	11.4	20029	23	ABK42737	Genomic sequence #	c 624	14	10.6	151	22	AAK47570	Human bone marrow
c 552	15	11.4	23241	22	AAK84291	Human immune/haema	c 625	14	10.6	151	22	AAI53402	Probe #22088 used
c 553	15	11.4	23241	22	AAK87225	Human immune/haema	c 626	14	10.6	157	22	ABA74875	Human foetal liver
c 554	15	11.4	28720	23	ABL07302	Drosophila melanog	c 627	14	10.6	157	22	ABA39572	Probe #18038 for g
c 555	15	11.4	31834	22	AAK81009	Human immune/haema	c 628	14	10.6	157	22	AAK23368	Human brain expres
c 556	15	11.4	31834	22	ABK42725	Genomic sequence #	c 629	14	10.6	157	22	AAK49523	Human bone marrow
c 557	15	11.4	32035	22	AAK81008	Human immune/haema	c 630	14	10.6	157	22	AAI26635	Probe #16568 for g
c 558	15	11.4	32035	22	ABK42724	Genomic sequence #	c 631	14	10.6	157	22	AAI55400	Probe #24086 used
c 559	15	11.4	32220	22	ABA20618	Human nervous syst	c 632	14	10.6	157	22	ABS23007	Human genome-deriv
c 560	15	11.4	41488	22	AAK87512	Human immune/haema	c 633	14	10.6	166	21	AAC29995	Human secreted pro
c 561	15	11.4	49634	24	ABL68647	Kidney cancer rela	c 634	14	10.6	175	24	ABL78254	Human ovarian canc
c 562	15	11.4	50575	23	ABL29244	Drosophila melanog	c 635	14	10.6	181	22	AAK72231	Human immune/haema
c 563	15	11.4	66788	24	ABQ88140	Human osteoblast d	c 636	14	10.6	191	22	ABA76564	Human foetal liver
c 564	15	11.4	67894	23	AA595915	Propionibacterium	c 637	14	10.6	191	22	ABA41076	Probe #19542 for g
c 565	15	11.4	74574	23	ABL03438	Drosophila melanog	c 638	14	10.6	191	22	AAK52505	Human brain expres
c 566	15	11.4	96518	21	AAF22285	BAC containing rep	c 639	14	10.6	191	22	AAK51208	Human bone marrow
c 567	15	11.4	96583	21	AAF22297	BAC containing rep	c 640	14	10.6	191	22	AAI28220	Probe #18153 for g
c 568	15	11.4	99660	21	AAZ50905	Human TBC-1 partia	c 641	14	10.6	191	22	AAI57262	Probe #25948 used
c 569	15	11.4	101786	21	AAF22293	BAC containing rep	c 642	14	10.6	191	22	ABS24743	Human genome-deriv
c 570	15	11.4	160755	23	AAH88704	Human DNA sequence	c 643	14	10.6	193	22	ABA51494	Human breast cell
c 571	15	11.4	160771	24	ABQ88179	Human osteoblast d	c 644	14	10.6	193	22	ABA36450	Probe #14916 for g
c 572	15	11.4	197496	24	ABN85584	Human EGFR SEQ ID	c 645	14	10.6	193	22	AAK17771	Human brain expres
c 573	15	11.4	215980	24	ABL38337	Complementary stra	c 646	14	10.6	193	22	AAK43599	Human bone marrow
c 574	15	11.4	305107	22	AAH62689	Shrimp white spot	c 647	14	10.6	193	22	AAI24382	Probe #14315 for g
c 575	15	11.4	335913	22	AAI61371	Soybean 240017 reg	c 648	14	10.6	193	22	AAI09920	Probe #9911 used t
c 576	15	11.4	335913	22	AAI61372	Soybean 240017 reg	c 649	14	10.6	193	22	ABS17764	Human genome-deriv
c 577	15	11.4	910715	20	AAZ20248	Borrelia burgdorfe	c 650	14	10.6	195	24	ABK97946	Botulinum toxin ge
c 578	15	11.4	1038602	20	AAZ01425	Complete genome se	c 651	14	10.6	198	22	AAI56087	Probe #24773 used
c 579	15	11.4	2365589	24	ABA90521	Genomic sequence o	c 652	14	10.6	198	22	ABA40132	Drosophila melanog
c 580	15	11.4	2365589	24	ABA90521	Genomic sequence o	c 653	14	10.6	198	22	AAK24085	Human genome-deriv
c 581	15	11.4	2944528	24	ABA03041	Listeria monocytog	c 654	14	10.6	198	22	AAK50147	Human bone marrow
c 582	15	11.4	4403765	22	AAI99683	Mycobacterium tube	c 655	14	10.6	198	22	AAI27230	Probe #17163 for g
c 583	15	11.4	4411529	22	AAI99682	Mycobacterium tube	c 656	14	10.6	198	22	AAI27230	Probe #24773 used
c 584	14	10.6	27	24	ABK97949	Botulin toxin gene	c 657	14	10.6	198	23	ABL27031	Drosophila melanog
c 585	14	10.6	27	24	ABA91170	Physcomitrella pat	c 658	14	10.6	198	24	ABS19180	Human genome-deriv
c 586	14	10.6	28	24	AAD28745	Human ion channel	c 659	14	10.6	198	24	ABS23624	Human genome-deriv
c 587	14	10.6	34	21	AAAS4350	Mutagenic primer E	c 660	14	10.6	198	24	ABN22386	Human OREX polynuc
c 588	14	10.6	38	23	AAK04417	Human NOGO Hammerh	c 661	14	10.6	201	24	AAD28727	Human ion channel
c 589	14	10.6	38	23	ABK07955	Human CD20 Hammerh	c 662	14	10.6	213	17	AAT13902	Human amygdaloid G
c 590	14	10.6	50	15	AAQ69676	Human hepatic lipa	c 663	14	10.6	213	18	AAT98798	3' fragment of G p
c 591	14	10.6	50	18	AAT64138	Human hepatic lipa	c 664	14	10.6	215	22	ABA73589	Human foetal liver
c 592	14	10.6	50	20	AAI17426	Test sequence from	c 665	14	10.6	215	22	ABA38846	Probe #17312 for g
c 593	14	10.6	50	24	ABK82917	DNA binding molecu	c 666	14	10.6	215	22	AAK22035	Human brain expres

us-09-915-178-1-olilo.rng

Wed Jun 4 11:04:53 2003

c 667	14	10.6	215	22	AAK48198	Human bone marrow
c 668	14	10.6	215	22	AAI54028	Probe #22714 used
c 669	14	10.6	215	24	ABN52089	Human genome-deriv
c 670	14	10.6	215	24	ABN52089	Human ORFX polynuc
c 671	14	10.6	224	16	AAT20613	Human gene signatu
c 672	14	10.6	226	21	AAC12797	Human secreted pro
c 673	14	10.6	233	21	AAZ58761	Human huntingtin-1
c 674	14	10.6	236	24	ABL83965	Human ovarian canc
c 675	14	10.6	249	19	ABL10948	Human biallelic po
c 676	14	10.6	256	21	AAZ22202	Single nucleotide
c 677	14	10.6	260	21	AAZ72193	Eucalyptus grandis
c 678	14	10.6	262	21	AAA67400	Drosophila melanog
c 679	14	10.6	262	22	AAH29389	Human ovarian tumo
c 680	14	10.6	263	20	AAZ77510	Human secreted pro
c 681	14	10.6	275	21	AAZ30596	Human ORFX polynuc
c 682	14	10.6	279	24	ABN18171	Human brain Expres
c 683	14	10.6	281	14	AAQ60426	Human prostate exp
c 684	14	10.6	284	23	ABL73869	Human prostate exp
c 685	14	10.6	290	24	ABL75554	Corn tassal-deriv
c 686	14	10.6	295	24	ABL75554	Corn tassal-deriv
c 687	14	10.6	298	21	AAZ07474	Human secreted pro
c 688	14	10.6	301	21	AAZ05655	Human secreted pro
c 689	14	10.6	304	14	AAQ59447	Human breast cell
c 690	14	10.6	311	22	ABN49017	Human breast cell
c 691	14	10.6	311	22	ABN49017	Human breast cell
c 692	14	10.6	311	22	AAK15377	Human brain expres
c 693	14	10.6	311	22	AAK15377	Human brain expres
c 694	14	10.6	311	22	AAK15377	Human brain expres
c 695	14	10.6	311	22	AAK15377	Human brain expres
c 696	14	10.6	311	22	AAK15377	Human brain expres
c 697	14	10.6	311	22	AAK15377	Human brain expres
c 698	14	10.6	311	22	AAK15377	Human brain expres
c 699	14	10.6	311	22	AAK15377	Human brain expres
c 700	14	10.6	311	22	AAK15377	Human brain expres
c 701	14	10.6	311	22	AAK15377	Human brain expres
c 702	14	10.6	311	22	AAK15377	Human brain expres
c 703	14	10.6	311	22	AAK15377	Human brain expres
c 704	14	10.6	311	22	AAK15377	Human brain expres
c 705	14	10.6	311	22	AAK15377	Human brain expres
c 706	14	10.6	311	22	AAK15377	Human brain expres
c 707	14	10.6	311	22	AAK15377	Human brain expres
c 708	14	10.6	311	22	AAK15377	Human brain expres
c 709	14	10.6	311	22	AAK15377	Human brain expres
c 710	14	10.6	311	22	AAK15377	Human brain expres
c 711	14	10.6	311	22	AAK15377	Human brain expres
c 712	14	10.6	311	22	AAK15377	Human brain expres
c 713	14	10.6	311	22	AAK15377	Human brain expres
c 714	14	10.6	311	22	AAK15377	Human brain expres
c 715	14	10.6	311	22	AAK15377	Human brain expres
c 716	14	10.6	311	22	AAK15377	Human brain expres
c 717	14	10.6	311	22	AAK15377	Human brain expres
c 718	14	10.6	311	22	AAK15377	Human brain expres
c 719	14	10.6	311	22	AAK15377	Human brain expres
c 720	14	10.6	311	22	AAK15377	Human brain expres
c 721	14	10.6	311	22	AAK15377	Human brain expres
c 722	14	10.6	311	22	AAK15377	Human brain expres
c 723	14	10.6	311	22	AAK15377	Human brain expres
c 724	14	10.6	311	22	AAK15377	Human brain expres
c 725	14	10.6	311	22	AAK15377	Human brain expres
c 726	14	10.6	311	22	AAK15377	Human brain expres
c 727	14	10.6	311	22	AAK15377	Human brain expres
c 728	14	10.6	311	22	AAK15377	Human brain expres
c 729	14	10.6	311	22	AAK15377	Human brain expres
c 730	14	10.6	311	22	AAK15377	Human brain expres
c 731	14	10.6	311	22	AAK15377	Human brain expres
c 732	14	10.6	311	22	AAK15377	Human brain expres
c 733	14	10.6	311	22	AAK15377	Human brain expres
c 734	14	10.6	311	22	AAK15377	Human brain expres
c 735	14	10.6	311	22	AAK15377	Human brain expres
c 736	14	10.6	311	22	AAK15377	Human brain expres
c 737	14	10.6	311	22	AAK15377	Human brain expres
c 738	14	10.6	311	22	AAK15377	Human brain expres
c 739	14	10.6	311	22	AAK15377	Human brain expres

Nucleotide sequenc
Human prostate exp
Probe #5116 for ge
Human lung cancer
Novel human polynu
Staphylococcus aur
Human breast cell
Human foetal liver
Probe #3628 for ge
Human brain expres
Human bone marrow
Probe #3662 for ge
Probe #3773 used t
Probe #3798 used t
Gene #1098 used to
Human genome-deriv
Human cancer relat
Human neuroregulin g
Human neuroregulin g
Human neuroregulin g
Human neuroregulin g
Human immune/haema
Human prostate exp
Human prostate exp
Human secreted exp
Human ORFX polynuc
Human brain Expres
CDNA encoding nove
Human colon cancer
Human immune/haema
Colon adenocarcino
Human immune/haema
Human contig polyn
Human contig polyn
Human contig polyn
DNA encoding novel
Human polynucleoti
Human prostate exp
Colon adenocarcino
y lipolytica EST-d
DNA encoding novel
DNA encoding novel
DNA encoding novel
Human prostate exp
Human cervical can
Human breast cell
Human foetal liver
Probe #4259 for ge
Human brain expres
Human bone marrow
Probe #4350 for ge
Probe #4476 used t
Probe #4231 used t
Human genome-deriv
Human CDNA clone (
Human cancer relat
Human kidney relat
Human kidney relat
Human secreted pro
Human tumour assoc
Human prostate exp
Chromosome 6q27 va
Human polynucleoti
Human chromosome 6
Human nervous syst
Human breast cance
DNA encoding novel
Pinus radiata tran
Human foetal liver
Probe #619 for gen
Human brain expres
Human bone marrow

813	14	10.6	466	22	AA110708	Probe #641 for gen	886	14	10.6	533	22	AAH70263	Human cervical can
814	14	10.6	466	22	AAI19166	Probe #652 used to	887	14	10.6	533	24	ABN73668	Bovine embryonic g
815	14	10.6	466	22	AAI00638	Probe #629 used to	888	14	10.6	534	22	AAH13527	Human cDNA clone (
816	14	10.6	466	24	ABS00663	Human genome-deriv	c 889	14	10.6	535	21	AAA41276	Human secreted exp
c 817	14	10.6	471	22	ABA42624	Human breast cell	c 890	14	10.6	535	24	ABN61678	Human prostate relat
c 818	14	10.6	471	22	ABA53053	Human foetal liver	c 891	14	10.6	536	23	ABV55416	Human prostate exp
c 819	14	10.6	471	22	ABA22827	Probe #1293 for ge	c 892	14	10.6	541	22	AAK36437	Human bone marrow
c 820	14	10.6	471	22	AAI32657	Probe #1343 used t	893	14	10.6	542	22	AAK86449	Human immune/haema
c 821	14	10.6	471	22	ABN69058	Streptococcus poly	894	14	10.6	542	23	ABK43053	Genomic sequence #
c 822	14	10.6	472	22	ABN43918	Human breast cell	895	14	10.6	543	23	ABK42073	CDNA encoding nove
c 823	14	10.6	472	22	ABA44150	Probe #2616 for ge	896	14	10.6	543	23	ABV60205	Human prostate exp
c 824	14	10.6	472	22	AAK02667	Human brain expres	c 897	14	10.6	544	23	ABV60205	Human prostate exp
c 825	14	10.6	472	22	AAK28104	Human bone marrow	c 898	14	10.6	545	22	AAK29492	Human cDNA 3'-end
c 826	14	10.6	472	22	AAI12680	Probe #2613 for ge	c 899	14	10.6	546	22	AAK29492	CDNA encoding nove
c 827	14	10.6	472	22	AAI34032	Probe #2718 used t	c 900	14	10.6	554	22	ABA60439	Human foetal liver
c 828	14	10.6	472	22	AAI02589	Probe #2580 used t	c 901	14	10.6	554	22	ABA60439	Human foetal liver
c 829	14	10.6	472	22	ABS02597	Human genome-deriv	c 902	14	10.6	554	22	AAK34604	Human bone marrow
c 830	14	10.6	473	21	AAZ61808	CDNA encoding muri	c 903	14	10.6	554	22	AAI40323	Probe #9009 used t
c 831	14	10.6	473	22	AAC99741	Skin cell cDNA, SE	c 904	14	10.6	555	24	ABK53445	Human eosinophil-m
c 832	14	10.6	473	24	ABL34893	Murine cDNA isolat	c 905	14	10.6	559	22	AAH97867	Murine 7-transmemb
c 833	14	10.6	474	24	ABL82270	Human ovarian can	c 906	14	10.6	560	22	ABA61635	Human foetal liver
c 834	14	10.6	475	23	ABV35199	Human prostate exp	c 907	14	10.6	560	22	ABA29295	Probe #7761 for ge
c 835	14	10.6	476	22	ABA26701	Probe #5167 for ge	c 908	14	10.6	560	22	AAK09935	Human brain expres
c 836	14	10.6	476	22	AAH71693	Human cervical can	c 909	14	10.6	560	22	AAK35830	Human bone marrow
c 837	14	10.6	476	22	AAH72522	Human cervical can	c 910	14	10.6	560	22	AAI41547	Probe #10233 used
c 838	14	10.6	476	22	AAS31050	Human diagnostic a	c 911	14	10.6	562	22	ABK97866	Murine 7-transmemb
c 839	14	10.6	477	24	ABK63335	Rat sequence diffe	c 912	14	10.6	562	22	ABA31236	Probe #9702 for ge
c 840	14	10.6	477	23	ABV03982	Human prostate exp	c 913	14	10.6	564	22	AAI19068	Probe #9001 for ge
c 841	14	10.6	480	22	ABA42697	Human breast cell	c 914	14	10.6	564	22	AAI44217	Probe #12903 used
c 842	14	10.6	486	22	ABA53120	Human foetal liver	c 915	14	10.6	564	22	ABS12321	Human genome-deriv
c 843	14	10.6	486	22	ABA22894	Probe #1360 for ge	c 916	14	10.6	566	22	AAS60420	Human cancer relat
c 844	14	10.6	486	22	AAK01370	Human brain expres	c 917	14	10.6	567	22	ABA60925	Human cancer relat
c 845	14	10.6	486	22	AAK26825	Human bone marrow	c 918	14	10.6	568	22	ABA62343	Human foetal liver
c 846	14	10.6	486	22	AAI11456	Probe #1389 for ge	c 919	14	10.6	568	22	ABA29684	Probe #8150 for ge
c 847	14	10.6	486	22	AAI32727	Probe #1413 used t	c 920	14	10.6	568	22	AAI10186	Human breast cance
c 848	14	10.6	486	22	AAI01372	Probe #1363 used t	c 921	14	10.6	568	22	AAK10677	Human brain expres
c 849	14	10.6	486	24	ABS01423	Human genome-deriv	c 922	14	10.6	568	22	AAK36563	Human bone marrow
c 850	14	10.6	497	17	AAC33959	Chromosome 6q27 va	c 923	14	10.6	568	22	AAI17419	Probe #7352 for ge
c 851	14	10.6	497	21	AAC75204	Human ORF ORF759	c 924	14	10.6	568	22	AAI42321	Probe #11007 used
c 852	14	10.6	500	21	AAC95267	Cat flea head and	c 925	14	10.6	568	24	ABS10560	Human genome-deriv
c 853	14	10.6	500	21	AAC95267	Mouse EST AA619904	c 926	14	10.6	568	24	ABS10560	Human foetal liver
c 854	14	10.6	500	22	ABA61624	Human foetal liver	c 927	14	10.6	569	22	ABA28379	Probe #6845 for ge
c 855	14	10.6	500	22	ABA29287	Probe #7753 for ge	c 928	14	10.6	569	22	AAK08223	Human brain expres
c 856	14	10.6	500	22	AAK09924	Human brain expres	c 929	14	10.6	569	22	AAK34112	Human bone marrow
c 857	14	10.6	500	22	AAK35819	Human bone marrow	c 930	14	10.6	569	22	AAI39835	Probe #8521 used t
c 858	14	10.6	500	22	AAI17145	Probe #7078 for ge	c 931	14	10.6	569	24	ABS08880	Human genome-deriv
c 859	14	10.6	500	22	AAI41536	Probe #10222 used	c 932	14	10.6	570	22	ABS31073	Human diagnostic a
c 860	14	10.6	500	22	ABS10054	Human genome-deriv	c 933	14	10.6	570	23	ABV02703	Human prostate exp
c 861	14	10.6	501	22	ABA12010	Human nervous syst	c 934	14	10.6	571	21	ABV02703	Human ovarian carc
c 862	14	10.6	503	23	AAS66282	DNA encoding novel	c 935	14	10.6	571	24	ABN72690	Ovarian carcinoma
c 863	14	10.6	506	21	AAC37038	Arabidopsis thalia	c 936	14	10.6	578	22	AAH07261	Human cDNA clone (
c 864	14	10.6	516	20	AAZ34293	Human EST DNA24256	c 937	14	10.6	580	24	ABN65651	Human cancer relat
c 865	14	10.6	516	21	AAC78581	Human EST DNA24256	c 938	14	10.6	582	23	ABV02707	Human prostate exp
c 866	14	10.6	518	22	ABA62830	Human foetal liver	c 939	14	10.6	585	22	ABA63060	Human foetal liver
c 867	14	10.6	518	22	ABS11031	Human genome-deriv	c 940	14	10.6	585	22	ABA30317	Probe #8783 for ge
c 868	14	10.6	520	22	ABA61592	Human foetal liver	c 941	14	10.6	585	22	AAK11484	Human brain expres
c 869	14	10.6	520	22	AAK09895	Human brain expres	c 942	14	10.6	585	22	AAK37264	Human bone marrow
c 870	14	10.6	521	24	AAS61798	Lung small cell ca	c 943	14	10.6	585	22	AAI18093	Probe #8026 for ge
c 871	14	10.6	524	24	ABA61761	Lung small cell ca	c 944	14	10.6	585	22	AAI43027	Probe #11783 used
c 872	14	10.6	525	23	ABA11497	Human nervous syst	c 945	14	10.6	585	22	ABS11258	Human genome-deriv
c 873	14	10.6	527	23	ABV55621	Human prostate exp	c 946	14	10.6	586	22	ABA63402	Human foetal liver
c 874	14	10.6	528	21	AAI14445	Aspergillus oryzae	c 947	14	10.6	586	22	ABA30602	Probe #9068 for ge
c 875	14	10.6	529	23	ABV58861	Human prostate exp	c 948	14	10.6	586	22	AAK11936	Human brain expres
c 876	14	10.6	529	23	AAS76160	DNA encoding novel	c 949	14	10.6	586	22	AAK37642	Human bone marrow
c 877	14	10.6	531	21	AAAG9828	Human ovarian carc	c 950	14	10.6	586	22	AAI18397	Probe #8330 for ge
c 878	14	10.6	531	22	ABA60989	Human foetal liver	c 951	14	10.6	586	22	AAI43513	Probe #12199 used
c 879	14	10.6	531	22	ABA28928	Probe #7394 for ge	c 952	14	10.6	586	24	ABS11628	Human genome-deriv
c 880	14	10.6	531	22	AAK09281	Human brain expres	c 953	14	10.6	586	24	ABQ58834	Human colon cancer
c 881	14	10.6	531	22	AAK35170	Human bone marrow	c 954	14	10.6	588	22	AAK63292	Human immune/haema
c 882	14	10.6	531	22	AAI40886	Probe #9572 used t	c 955	14	10.6	589	22	AAK61566	Human foetal liver
c 883	14	10.6	531	24	ABS09609	Human genome-deriv	c 956	14	10.6	589	22	ABA63408	Human foetal liver
c 884	14	10.6	531	24	ABN72722	Ovarian carcinoma	c 957	14	10.6	589	22	ABA30609	Probe #9075 for ge
c 885	14	10.6	532	22	AAI18972	Human breast cance	c 958	14	10.6	589	22	AAK09870	Human brain expres

XX	Key	Location/Qualifiers
XX	FT	6..137
XX	FT	/*tag= a
XX	FT	/product= "NOV2a"
XX	PN	WO200190155-A2.
XX	PD	29-NOV-2001.
XX	PD	24-MAY-2001; 2001WO-US17073.
XX	PR	24-MAY-2000; 2000US-206679P.
XX	PR	24-MAY-2000; 2000US-206688P.
XX	PR	24-MAY-2000; 2000US-206829P.
XX	PR	24-MAY-2000; 2000US-207748P.
XX	PR	30-MAY-2000; 2000US-207798P.
XX	PR	31-MAY-2000; 2000US-208263P.
XX	PR	02-JUN-2000; 2000US-208831P.
XX	PR	05-JUN-2000; 2000US-209451P.
XX	PR	07-JUN-2000; 2000US-210060P.
XX	PR	20-JUL-2000; 2000US-219507P.
XX	PR	26-JUL-2000; 2000US-221337P.
XX	PR	31-JUL-2000; 2000US-221927P.
XX	PR	19-JAN-2001; 2001US-263135P.
XX	PR	24-JAN-2001; 2001US-263688P.
XX	PR	24-JAN-2001; 2001US-263694P.
XX	PR	23-MAY-2001; 2001US-0863776.
XX	XX	(CURA-) CURAGEN CORP.
XX	XX	Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
XX	XX	Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
XX	XX	WPI; 2002-106174/14..
XX	XX	P-PSDB; ABB05034.
XX	XX	Novel polypeptide, useful for treating pain, cancer, urinary retention,
XX	XX	osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
XX	XX	asthma, ulcer, allergy and Huntington's disease, comprises isolated
XX	XX	polypeptide NOVX
XX	XX	Claim 8; page 20; 266pp; English.
XX	XX	The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
XX	XX	proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
XX	XX	fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
XX	XX	antiasthmatic, hypotensive, osteopathic, antiinflammatory, antitumor,
XX	XX	neuroprotective, cardiant, antiallergic, antidepressant, neurotropic,
XX	XX	anticonvulsant and neuroleptic activities. (I) and polynucleotides (II)
XX	XX	can be used in gene therapy and vaccine production. (I) and (II) can be
XX	XX	used for treating or preventing a NOVX-associated disorder such as
XX	XX	cardiomyopathy, atherosclerosis and diabetes in a human, where the
XX	XX	disorder is related to cell signal processing and metabolic path way
XX	XX	modulation, in a subject, preferably human. (I) and (II) can be used for
XX	XX	diagnosing, preventing or treating developmental diseases, immune
XX	XX	diseases, taste and scent detectability disorder, Burkitt's lymphoma,
XX	XX	signal transduction pathway disorders, retinal diseases including those,
XX	XX	involving photoreception, cell growth rate disorders, feeding disorders,
XX	XX	noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
XX	XX	Parkinson's disease, acute heart failure, hypotension, hypertension,
XX	XX	urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
XX	XX	Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
XX	XX	infarction, allergies, benign prostatic hypertrophy, manic depression,
XX	XX	dementia, severe mental retardation and dyskinesias, such as
XX	XX	Huntington's disease or Gilles de la Tourette syndrome. The present
XX	XX	sequence encodes human NOV2a, which is isolated to chromosome 9.
XX	XX	Sequence 147 BP; 56 A; 30 C; 41 G; 20 T; 0 other;
XX	XX	Query Match: 100.0%; Score 132; DB 24; Length 147;
XX	XX	Best Local Similarity 100.0%; Pred. No. 2.9e-56;
XX	XX	Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC sequence encodes human NOV2c, from the present invention.
XX
SQ Sequence 147 BP; 56 A; 30 C; 41 G; 20 T; 0 other;
Query Match 100.0%; Score 132; DB 24; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGCACAACTAGACCTGGAGAAATTCGCCAGCTTGGGATAAGGCCAAGCTGAAGGCC 60
DB 6 ATGCGCACAACTAGACCTGGAGAAATTCGCCAGCTTGGGATAAGGCCAAGCTGAAGGCC 65
QY 61 ACAGAGATGCGAGAGAACACTCTGATGACCAAGAGACCAAGAGAGAGAGAGAGAGAGAG 120
DB 66 ACAGAGATGCGAGAGAACACTCTGATGACCAAGAGACCAAGAGAGAGAGAGAGAGAGAG 125
QY 121 GAAATTTCTTGA 132
DB 126 GAAATTTCTTGA 137
RESULT 4
ABN29874
ID ABN29874 standard; DNA; 65 BP.
AC ABN29874;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2622.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
PS Example 1; SEQ ID 2622; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes

XX
KW hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
KW multiple sclerosis; angina pectoris; myocardial infarction; delirium;
KW benign prostatic hypertrophy; manic depression; dementia; dyskinesia;
KW severe metal retardation; Huntington's disease; gene;
XX Gilles de la Tourette syndrome; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 6..137
XX /*tag= a "NOV2c"
XX /product= "NOV2c"
XX
XX WO200190155-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17073.
XX
XX 24-MAY-2000; 2000US-206679P.
XX 24-MAY-2000; 2000US-206688P.
XX 24-MAY-2000; 2000US-206829P.
XX 30-MAY-2000; 2000US-207748P.
XX 30-MAY-2000; 2000US-207798P.
XX 31-MAY-2000; 2000US-208263P.
XX 02-JUN-2000; 2000US-208831P.
XX 05-JUN-2000; 2000US-209451P.
XX 07-JUN-2000; 2000US-210060P.
XX 20-JUL-2000; 2000US-219507P.
XX 26-JUL-2000; 2000US-221337P.
XX 31-JUL-2000; 2000US-221927P.
XX 19-JAN-2001; 2001US-263135P.
XX 24-JAN-2001; 2001US-263688P.
XX 24-JAN-2001; 2001US-263694P.
XX 23-MAY-2001; 2001US-0863776.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigar M;
XX Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
XX
XX WPI; 2002-106174/14.
XX P-PSDB; ABB05036.
XX
XX Novel polypeptide, useful for treating pain, cancer, urinary retention,
XX osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
XX asthma, ulcer, allergy and Huntington's disease, comprises isolated
XX polypeptide NOVX -
XX
XX Claim 8; page 23; 266pp; English.
XX
XX The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
XX proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
XX fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
XX antiasthmatic, hypotensive, osteopathic, antiinflammatory, antitumor,
XX neuroprotective, cardiac, antiallergic, antidepressant, nootropic,
XX anticonvulsant and neuroleptic activities. (I) and polynucleotides (II)
XX can be used in gene therapy and vaccine production. (I) and (II) can be
XX used for treating or preventing a NOVX-associated disorder such as
XX cardiomyopathy, atherosclerosis and diabetes in a human, where the
XX disorder is related to cell signal processing and metabolic path way
XX modulation, in a subject, preferably human. (I) and (II) can be used for
XX diagnosing, preventing or treating developmental diseases, immune
XX diseases, taste and scent detectability disorder, Burkitt's lymphoma,
XX transesophageal pathway disorders, retinal diseases including those
XX involving photoreception, cell growth rate disorders, feeding disorders,
XX noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
XX Parkinson's disease, acute heart failure, hypotension, hypertension,
XX urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
XX Albrit Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
XX infarction, allergies, benign prostatic hypertrophy, manic depression,
XX delirium, dementia, severe metal retardation and dyskinesias, such as
XX Huntington's disease or Gilles de la Tourette syndrome. The present

CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the amplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 24 A; 13 C; 20 G; 8 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 65;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
DB 47 GATAGGCCCAAGCTGAAG 64
|||||
RESULT 5
ABV08667/c
ID ABV08667 standard; cDNA; 203 BP.
XX
XX
AC ABV08667;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 8658.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
OS
XX WO200160860-A2.
PN
XX 23-AUG-2001.
PD
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 1368; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 203 BP; 30 A; 65 C; 50 G; 58 T; 0 other;

Query Match 13.6%; Score 18; DB 23; Length 203;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
DB 73 GATAGGCCCAAGCTGAAG 56
|||||
RESULT 6
ABK55047
ID ABK55047 standard; cDNA; 243 BP.
XX
XX AC ABK55047;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human colon cancer-associated cDNA, SEQ ID No 517.
XX
KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX Homo sapiens.
OS
XX WO200212280-A2.
PN
XX 14-FEB-2002.
PD
XX
PF 30-JUL-2001; 2001WO-US23826.
XX
PR 03-AUG-2000; 2000US-223265P.
PR 02-OCT-2000; 2000US-237406P.
PR 20-MAR-2001; 2001US-277495P.
PR 03-JUL-2001; 2001US-302702P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Pyle RA, Xu J, Secríst H;
XX WPI; 2002-257462/30.
DR
XX
PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers.
XX
PS Claim 1; Page 297; 425pp; English.
XX
CC The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.
XX
SQ Sequence 243 BP; 73 A; 64 C; 68 G; 37 T; 1 other;

Query Match 13.6%; Score 18; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57
|||||

Wed Jun 4 11:04:53 2003

us-09-915-178-1.olil0.rng

Db 102 GATAGGCCAAGCTGAAG 119

RESULT 7
AAC00909
ID AAC00909 standard; cDNA; 283 BP.
XX AC AAC00909;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 907.
XX DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX KW Homo sapiens.
XX OS EP1033401-A2.
XX PN 06-SEP-2000.
XX PD 21-FEB-2000; 2000EP-0200610.
XX PF 26-FEB-1999; 99US-0122487.
XX PR (GEST) GENSET.
XX PA Dumas Milne Edwards J, Duclert A, Giordano J;
XX PI WPI: 2000-500381/45.
XX DR P-PSDB; AAG00903.
XX DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PT Claim 1; SEQ ID 907; 71pp + CD-ROM; English.
XX PS The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. An ORF has been identified within the
XX CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX CC derived from 30 different tissues. EST sequences usually correspond
XX CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX CC well suited for isolating cDNA sequences derived from the 5' ends of
XX CC mRNAs and even in those cases where longer cDNA sequences have been
XX CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX CC mRNAs with intact 5' ends and can therefore be used to obtain full length
XX CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX CC gene therapy and chromosome mapping procedures. They are used to obtain
XX CC upstream regulatory sequences and to design expression and secretion
XX CC vectors.
XX SQ Sequence 283 BP; 71 A; 87 C; 78 G; 47 T; 0 other;
Query Match 13.6%; Score 18; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 40 GATAGGCCAAGCTGAAG 57
|||||
Db 147 GATAGGCCAAGCTGAAG 164

RESULT 8
ABK54754
ID ABK54754 standard; cDNA; 353 BP.
XX AC ABK54754;
XX DT 18-JUN-2002 (first entry)
XX PF 30-JUL-2001; 2001WO-US23826.
XX SQ

Human colon cancer-associated cDNA, SEQ ID No 224.
Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
Homo sapiens.
WO200212280-A2.
14-FEB-2002.
30-JUL-2001; 2001WO-US23826.
03-AUG-2000; 2000US-223265P.
02-OCT-2000; 2000US-237406P.
20-MAR-2001; 2001US-277495P.
03-JUL-2001; 2001US-302702P.
(CORI-) CORIXA CORP.
Pyle RA, Xu J, Secrlist H;
WPI: 2002-257462/30.
Novel polynucleotide encoding colon tumour polypeptides, useful as
vaccines for treating colon cancers
Claim 1; Page 214; 425pp; English.
The invention relates to isolated polynucleotides (I) encoding colon
tumour polypeptides (II). (I) is useful for stimulating an immune
response in a patient and treating colon cancer in a patient.
Oligonucleotides derived from (I) are useful for determining the presence
of cancer in a patient. (I) and (II) are useful in pharmaceutical
compositions, e.g. vaccines, and other compositions for the diagnosis
and treatment of colon cancer. A composition comprising a first component
selected from physiologically acceptable carriers and immunostimulants,
and an antigen-presenting cell expressing (II) is useful for inhibiting
development of cancer in a patient. (I) is useful in the design and
preparation of ribozyme molecules for inhibiting expression of tumour
polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
sequences of the invention.
Sequence 353 BP; 97 A; 103 C; 98 G; 55 T; 0 other;
Query Match 13.6%; Score 18; DB 24; Length 353;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 40 GATAGGCCAAGCTGAAG 57
|||||
Db 76 GATAGGCCAAGCTGAAG 93

RESULT 9
ABK54737
ID ABK54737 standard; cDNA; 395 BP.
XX AC ABK54737;
XX DT 18-JUN-2002 (first entry)
XX DE Human colon cancer-associated cDNA, SEQ ID No 207.
XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200212280-A2.
XX PD 14-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US23826.
XX SQ

PR 03-AUG-2000; 2000US-223265P.
PR 02-OCT-2000; 2000US-237406P.
PR 20-MAR-2001; 2001US-277495P.
PR 03-JUL-2001; 2001US-302702P.
XX (CORI-) CORIXA CORP.
PA
XX
XX
PI Pyle RA, Xu J, Secrlist H;
XX
XX
XX WPI; 2002-257462/30.
DR
XX
XX Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers -
XX
XX
PS Claim 1; Page 209; 425pp; English.
XX
XX The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.
XX
XX
SQ Sequence 395 BP; 105 A; 113 C; 115 G; 62 T; 0 other;
Query Match 13.6%; Score 18; DB 24; Length 395;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 111 GATAAGGCCAAGCTGAAG 128
RESULT 10
ABV38568/c
ID ABV38568 standard; cDNA; 399 BP.
XX
XX AC ABV38568;
XX
XX DT 16-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 38559.
XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PI Schlegel R, Endege WO, Monahan JE;
XX

DR WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX PS Claim 1; Page 7850; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX SQ Sequence 399 BP; 70 A; 116 C; 100 G; 113 T; 0 other;
Query Match 13.6%; Score 18; DB 23; Length 399;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 78 GATAAGGCCAAGCTGAAG 61
RESULT 11
ABK55033
ID ABK55033 standard; cDNA; 428 BP.
XX
XX AC ABK55033;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Human colon cancer-associated cDNA, SEQ ID No 503.
XX
XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200212280-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 30-JUL-2001; 2001WO-US23826.
XX
XX PR 03-AUG-2000; 2000US-223265P.
XX PR 02-OCT-2000; 2000US-237406P.
XX PR 20-MAR-2001; 2001US-277495P.
XX PR 03-JUL-2001; 2001US-302702P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Pyle RA, Xu J, Secrlist H;
XX
XX XX WPI; 2002-257462/30.
XX
XX XX Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers -
XX
XX PS Claim 1; Page 294; 425pp; English.
XX
XX CC The invention relates to isolated polynucleotides (I) encoding colon
XX tumour polypeptides (II). (I) is useful for stimulating an immune

CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

XX SQ Sequence 428 BP; 124 A; 114 C; 115 G; 75 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 428;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
 |||||
 Db 89 GATAAGGCCCAAGCTGAAG 106

RESULT 12
 ABK55163
 ID ABK55163 standard; cDNA; 429 BP.

XX AC ABK55163;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human colon cancer-associated cDNA, SEQ ID No 633.
 XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
 XX OS Homo sapiens.

XX PN WO200212280-A2.
 XX PD 14-FEB-2002.
 XX PF 30-JUL-2001; 2001WO-US23826.
 XX PR 03-AUG-2000; 2000US-223265P.
 XX PR 02-OCT-2000; 2000US-237406P.
 XX PR 20-MAR-2001; 2001US-277495P.
 XX PR 03-JUL-2001; 2001US-302702P.

XX PA (CORI-) CORIXA CORP.
 XX PI Pyle RA, Xu J, Secretist H;
 XX PT WPI; 2002-257462/30.
 XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX vaccines for treating colon cancers

XX PS Claim 1; Page 329; 425pp; English.
 XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

XX

SQ Sequence 429 BP; 124 A; 115 C; 115 G; 75 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 429;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
 |||||
 Db 90 GATAAGGCCCAAGCTGAAG 107

RESULT 13
 ABK55157
 ID ABK55157 standard; cDNA; 434 BP.

XX AC ABK55157;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human colon cancer-associated cDNA, SEQ ID No 627.
 XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
 XX OS Homo sapiens.

XX PN WO200212280-A2.
 XX PD 14-FEB-2002.
 XX PF 30-JUL-2001; 2001WO-US23826.
 XX PR 03-AUG-2000; 2000US-223265P.
 XX PR 02-OCT-2000; 2000US-237406P.
 XX PR 20-MAR-2001; 2001US-277495P.
 XX PR 03-JUL-2001; 2001US-302702P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Pyle RA, Xu J, Secretist H;
 XX PT WPI; 2002-257462/30.
 XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX vaccines for treating colon cancers

XX PS Claim 1; Page 328; 425pp; English.
 XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

XX SQ Sequence 434 BP; 124 A; 116 C; 117 G; 77 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 434;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57
 |||||
 Db 93 GATAAGGCCCAAGCTGAAG 110

RESULT 14

ABK54988
ID ABK54988 standard; cDNA; 438 BP.

XX AC ABK54988;

XX DT 18-JUN-2002 (first entry)

XX DE Human colon cancer-associated cDNA, SEQ ID No 458.

XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200212280-A2.

XX PD 14-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23826.

XX PR 03-AUG-2000; 2000US-223265P.

XX PR 02-OCT-2000; 2000US-237406P.

XX PR 20-MAR-2001; 2001US-277495P.

XX PR 03-JUL-2001; 2001US-302702P.

XX PA (CORI-) CORIXA CORP.

XX PI Pyle RA, Xu J, Secretist H;

XX DR WPI; 2002-257462/30.

XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers -

XX PS Claim 1; Page 280-281; 425pp; English.

XX CC The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.

XX SQ Sequence 438 BP; 126 A; 118 C; 117 G; 77 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 438;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

|||||

DB 99 GATAAGGCCAAGCTGAAG 116

RESULT 15

ABK55113

ID ABK55113 standard; cDNA; 438 BP.

XX AC ABK55113;

XX DT 18-JUN-2002 (first entry)

XX DE Human colon cancer-associated cDNA, SEQ ID No 583.

XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200212280-A2.

XX PD 14-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23826.

XX PR 03-AUG-2000; 2000US-223265P.

XX PR 02-OCT-2000; 2000US-237406P.

XX PR 20-MAR-2001; 2001US-277495P.

XX PR 03-JUL-2001; 2001US-302702P.

XX PA (CORI-) CORIXA CORP.

XX PI Pyle RA, Xu J, Secretist H;

XX DR WPI; 2002-257462/30.

XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers -

XX PS Claim 1; Page 315-316; 425pp; English.

XX CC The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.

XX SQ Sequence 438 BP; 126 A; 118 C; 117 G; 77 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 438;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

|||||

DB 99 GATAAGGCCAAGCTGAAG 116

RESULT 16

ABK55440

ID ABK55440 standard; cDNA; 439 BP.

XX AC ABK55440;

XX DT 18-JUN-2002 (first entry)

XX DE Human colon cancer-associated cDNA, SEQ ID No 910.

XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200212280-A2.

XX PD 14-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23826.

XX PR 03-AUG-2000; 2000US-223265P.

XX PR 02-OCT-2000; 2000US-237406P.

XX PR 20-MAR-2001; 2001US-277495P.

XX PR 03-JUL-2001; 2001US-302702P.

us-09-915-178-1.oli10.rng

Wed Jun 4 11:04:53 2003

CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

XX SQ Sequence 443 BP; 128 A; 119 C; 119 G; 77 T; 0 other;
 Query Match 13.6%; Score 18; DB 24; Length 443;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
 |||||
 Db 104 GATAAGGCCAAGCTGAAG 121

RESULT 18
 ABK55257
 ID ABK55257 standard; cDNA; 445 BP.

XX AC ABK55257;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human colon cancer-associated cDNA, SEQ ID No 727.
 XX DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
 XX KW Homo sapiens.
 XX OS WO200212280-A2.
 XX PN 14-FEB-2002.
 XX PD 30-JUL-2001; 2001WO-US23826.
 XX PF 03-AUG-2000; 2000US-223265P.
 XX PR 02-OCT-2000; 2000US-237406P.
 XX PR 20-MAR-2001; 2001US-277495P.
 XX PR 03-JUL-2001; 2001US-302702P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Pyle RA, Xu J, Secrist H;
 XX XX WPI; 2002-257462/30.
 XX DR Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX PT vaccines for treating colon cancers
 XX PS Claim 1; Page 355; 425pp; English.
 XX XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

PA (CORI-) CORIXA CORP.
 XX PI Pyle RA, Xu J, Secrist H;
 XX XX WPI; 2002-257462/30.
 XX DR Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX PT vaccines for treating colon cancers
 XX PS Claim 1; Page 415; 425pp; English.
 XX XX The invention relates to isolated polynucleotides (I) encoding colon
 CC tumour polypeptides (II). (I) is useful for stimulating an immune
 CC response in a patient and treating colon cancer in a patient.
 CC Oligonucleotides derived from (I) are useful for determining the presence
 CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
 CC compositions, e.g. vaccines, and other compositions for the diagnosis
 CC and treatment of colon cancer. A composition comprising a first component
 CC selected from physiologically acceptable carriers and immunostimulants,
 CC and an antigen-presenting cell expressing (II) is useful for inhibiting
 CC development of cancer in a patient. (I) is useful in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
 CC sequences of the invention.

XX SQ Sequence 439 BP; 127 A; 116 C; 115 G; 78 T; 3 other;
 Query Match 13.6%; Score 18; DB 24; Length 439;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
 |||||
 Db 94 GATAAGGCCAAGCTGAAG 111

RESULT 17
 ABK55189
 ID ABK55189 standard; cDNA; 443 BP.

XX AC ABK55189;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human colon cancer-associated cDNA, SEQ ID No 659.
 XX DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
 XX KW Homo sapiens.
 XX OS WO200212280-A2.
 XX PN 14-FEB-2002.
 XX PD 30-JUL-2001; 2001WO-US23826.
 XX PF 03-AUG-2000; 2000US-223265P.
 XX PR 02-OCT-2000; 2000US-237406P.
 XX PR 20-MAR-2001; 2001US-277495P.
 XX PR 03-JUL-2001; 2001US-302702P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Pyle RA, Xu J, Secrist H;
 XX XX WPI; 2002-257462/30.
 XX DR Novel polynucleotide encoding colon tumour polypeptides, useful as
 XX PT vaccines for treating colon cancers
 XX PS Claim 1; Page 337; 425pp; English.
 XX XX The invention relates to isolated polynucleotides (I) encoding colon

```
XX SQ Sequence 445 BP; 130 A; 119 C; 119 G; 77 T; 0 other;
Query Match 13.6%; Score 18; DB 24; Length 445;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Dd 99 GATAAGGCCAAGCTGAAG 116

RESULT 19
ABN96661/c
ID ABN96661 standard; DNA; 446 BP.
XX AC ABN96661;
XX DT 13-AUG-2002 (first entry)
XX DE Gene #3159 used to diagnose liver cancer.
XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX KW metastatic liver tumour; cytostatic; expression profile; disease state;
XX KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX OS Homo sapiens.
XX PN WO200229103-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30589.
XX PR 02-OCT-2000; 2000US-237054P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX DR WPI; 2002-426119/45.
XX PT Diagnosing and detecting the progression of liver cancer,
XX PT hepatocellular carcinoma or metastatic liver tumor in a patient,
XX PT involves detecting the level of expression of two or more genes in a
XX PT liver tissue sample
XX PS Claim 1; SEQ ID NO 3159; 298pp; English.
XX CC The invention relates to a novel method for diagnosing and detecting the
XX CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX CC tumour in a patient, and differentiating metastatic liver cancer from
XX CC hepatocellular carcinoma in a patient, involving detecting the level of
XX CC expression of two or more genes represented in ABN93503-ABN97455 in a
XX CC tissue sample. The method of the invention has hepatotropic, and
XX CC cytosstatic activity. The method is useful for diagnosing and detecting
XX CC the progression of liver cancer, hepatocellular carcinoma and metastatic
XX CC liver carcinoma in a patient. The method is useful for identifying
XX CC expression profiles which serve as useful diagnostic markers as well as
XX CC markers that can be used to monitor disease states, disease progression,
XX CC drug toxicity, drug efficacy and drug metabolism.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 446 BP; 74 A; 120 C; 122 G; 120 T; 10 other;
Query Match 13.6%; Score 18; DB 24; Length 446;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
```

```
Dd 336 GATAAGGCCAAGCTGAAG 319

RESULT 20
ABK55421
ID ABK55421 standard; CDNA; 446 BP.
XX AC ABK55421;
XX DT 18-JUN-2002 (first entry)
XX DE Human colon cancer-associated CDNA, SEQ ID No 891.
XX DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX KW Homo sapiens.
XX PN WO200212280-A2.
XX PD 14-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US23826.
XX PR 03-AUG-2000; 2000US-223265P.
XX PR 02-OCT-2000; 2000US-237406P.
XX PR 20-MAR-2001; 2001US-277495P.
XX PR 03-JUL-2001; 2001US-302702P.
XX PA (CORI-) CORIXA CORP.
XX PI Pyle RA, Xu J, Secrlist H;
XX DR WPI; 2002-257462/30.
XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
XX PT vaccines for treating colon cancers
XX PS Claim 1; Page 408; 425pp; English.
XX CC The invention relates to isolated polynucleotides (I) encoding colon
XX CC tumour polypeptides (II). (I) is useful for stimulating an immune
XX CC response in a patient and treating colon cancer in a patient.
XX CC Oligonucleotides derived from (I) are useful for determining the presence
XX CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
XX CC and treatment of colon cancer. A composition comprising a first component
XX CC selected from physiologically acceptable carriers and immunostimulants,
XX CC and an antigen-presenting cell expressing (II) is useful for inhibiting
XX CC development of cancer in a patient. (I) is useful in the design and
XX CC preparation of ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer CDNA
XX CC sequences of the invention.
XX SQ Sequence 446 BP; 141 A; 113 C; 111 G; 79 T; 2 other;
Query Match 13.6%; Score 18; DB 24; Length 446;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Dd 83 GATAAGGCCAAGCTGAAG 100

RESULT 21
ABK54652
ID ABK54652 standard; CDNA; 449 BP.
XX AC ABK54652;
XX DT 18-JUN-2002 (first entry)
XX DE Human colon cancer-associated CDNA, SEQ ID No 122.
```

us-09-915-178-1.olilo.rng

Wed Jun 4 11:04:53 2003

XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

XX 02-OCT-2000; 2000US-237406P.

XX 20-MAR-2001; 2001US-277495P.

XX 03-JUL-2001; 2001US-302702P.

XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secrlist H;

XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as

XX vaccines for treating colon cancers

XX Claim 1; Page 185; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

XX tumour polypeptides (II). (I) is useful for stimulating an immune

XX response in a patient and treating colon cancer in a patient.

XX Oligonucleotides derived from (I) are useful for determining the presence

XX of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX compositions, e.g. vaccines, and other compositions comprising a first component

XX and treatment of colon cancer. A composition comprising a first component

XX selected from physiologically acceptable carriers and immunostimulants,

XX and an antigen-presenting cell expressing (II) is useful for inhibiting

XX development of cancer in a patient. (I) is useful in the design and

XX preparation of ribozyme molecules for inhibiting expression of tumour

XX polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA

XX sequences of the invention.

XX Sequence 449 BP; 127 A; 120 C; 124 G; 78 T; 0 other;

XX Query Match 13.6%; Score 18; DB 24; Length 449;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 40 GATAAGGCCCAAGCTGAAG 57

XX 112 GATAAGGCCCAAGCTGAAG 129

XX DB

XX RESULT 22

XX ABK54720

XX ID ABK54720 standard; cDNA; 451 BP.

XX AC ABK54720;

XX 18-JUN-2002 (first entry)

XX Human colon cancer-associated cDNA, SEQ ID No 190.

XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as

XX vaccines for treating colon cancers

XX Claim 1; Page 185; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

XX tumour polypeptides (II). (I) is useful for stimulating an immune

XX response in a patient and treating colon cancer in a patient.

XX Oligonucleotides derived from (I) are useful for determining the presence

XX of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX compositions, e.g. vaccines, and other compositions comprising a first component

XX and treatment of colon cancer. A composition comprising a first component

XX selected from physiologically acceptable carriers and immunostimulants,

XX and an antigen-presenting cell expressing (II) is useful for inhibiting

XX development of cancer in a patient. (I) is useful in the design and

XX preparation of ribozyme molecules for inhibiting expression of tumour

XX polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA

XX sequences of the invention.

PR 02-OCT-2000; 2000US-237406P.

PR 20-MAR-2001; 2001US-277495P.

PR 03-JUL-2001; 2001US-302702P.

XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secrlist H;

XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as

XX vaccines for treating colon cancers

XX Claim 1; Page 205; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

XX tumour polypeptides (II). (I) is useful for stimulating an immune

XX response in a patient and treating colon cancer in a patient.

XX Oligonucleotides derived from (I) are useful for determining the presence

XX of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX compositions, e.g. vaccines, and other compositions comprising a first component

XX and treatment of colon cancer. A composition comprising a first component

XX selected from physiologically acceptable carriers and immunostimulants,

XX and an antigen-presenting cell expressing (II) is useful for inhibiting

XX development of cancer in a patient. (I) is useful in the design and

XX preparation of ribozyme molecules for inhibiting expression of tumour

XX polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA

XX sequences of the invention.

XX Sequence 451 BP; 127 A; 120 C; 126 G; 78 T; 0 other;

XX Query Match 13.6%; Score 18; DB 24; Length 451;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 40 GATAAGGCCCAAGCTGAAG 57

XX 112 GATAAGGCCCAAGCTGAAG 129

XX DB

XX RESULT 23

XX ABK55083

XX ID ABK55083 standard; cDNA; 451 BP.

XX AC ABK55083;

XX 18-JUN-2002 (first entry)

XX Human colon cancer-associated cDNA, SEQ ID No 553.

XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

XX 02-OCT-2000; 2000US-237406P.

XX 20-MAR-2001; 2001US-277495P.

XX 03-JUL-2001; 2001US-302702P.

XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secrlist H;

XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as

XX vaccines for treating colon cancers

XX Claim 1; Page 205; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

XX tumour polypeptides (II). (I) is useful for stimulating an immune

XX response in a patient and treating colon cancer in a patient.

XX Oligonucleotides derived from (I) are useful for determining the presence

XX of cancer in a patient. (I) and (II) are useful in pharmaceutical

XX compositions, e.g. vaccines, and other compositions comprising a first component

XX and treatment of colon cancer. A composition comprising a first component

XX selected from physiologically acceptable carriers and immunostimulants,

XX and an antigen-presenting cell expressing (II) is useful for inhibiting

XX development of cancer in a patient. (I) is useful in the design and

XX preparation of ribozyme molecules for inhibiting expression of tumour

XX polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA

XX sequences of the invention.

XX Sequence 451 BP; 127 A; 120 C; 126 G; 78 T; 0 other;

XX Claim 1; Page 308; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

CC tumour polypeptides (II). (I) is useful for stimulating an immune

CC response in a patient and treating colon cancer in a patient.

CC Oligonucleotides derived from (I) are useful for determining the presence

CC of cancer in a patient. (I) and (II) are useful in pharmaceutical

CC compositions, e.g. vaccines, and other compositions for the diagnosis

CC and treatment of colon cancer. A composition comprising a first component

CC selected from physiologically acceptable carriers and immunostimulants,

CC and an antigen-presenting cell expressing (II) is useful for inhibiting

CC development of cancer in a patient. (I) is useful for inhibiting

CC preparation of ribozyme molecules for inhibiting expression of tumour

CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA

CC sequences of the invention.

XX Sequence 451 BP; 129 A; 120 C; 124 G; 78 T; 0 other;

SQ

Query Match 13.6%; Score 18; DB 24; Length 451;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

|||||

Db 112 GATAGGCCCAAGCTGAAG 129

|||||

RESULT 24

ABK54878

ID ABK54878 standard; cDNA; 452 BP.

XX AC ABK54878;

XX 18-JUN-2002 (first entry)

XX Human colon cancer-associated cDNA, SEQ ID No 348..

DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.

XX Homo sapiens.

XX WO200212280-A2.

XX 14-FEB-2002.

XX 30-JUL-2001; 2001WO-US23826.

XX 03-AUG-2000; 2000US-223265P.

PR 02-OCT-2000; 2000US-237406P.

PR 20-MAR-2001; 2001US-277495P.

PR 03-JUL-2001; 2001US-302702P.

XX (CORI-) CORIXA CORP.

XX Pyle RA, Xu J, Secretist H;

XX WPI; 2002-257462/30.

XX Novel polynucleotide encoding colon tumour polypeptides, useful as

PT vaccines for treating colon cancers

XX Claim 1; Page 249; 425pp; English.

XX The invention relates to isolated polynucleotides (I) encoding colon

CC tumour polypeptides (II). (I) is useful for stimulating an immune

CC response in a patient and treating colon cancer in a patient.

CC Oligonucleotides derived from (I) are useful for determining the presence

CC of cancer in a patient. (I) and (II) are useful in pharmaceutical

CC compositions, e.g. vaccines, and other compositions for the diagnosis

CC and treatment of colon cancer. A composition comprising a first component

CC selected from physiologically acceptable carriers and immunostimulants,

CC and an antigen-presenting cell expressing (II) is useful for inhibiting

CC

CC development of cancer in a patient. (I) is useful in the design and

CC preparation of ribozyme molecules for inhibiting expression of tumour

CC sequences of the invention.

XX Sequence 452 BP; 129 A; 121 C; 124 G; 78 T; 0 other;

SQ

Query Match 13.6%; Score 18; DB 24; Length 452;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

|||||

Db 113 GATAGGCCCAAGCTGAAG 130

|||||

RESULT 25

AAC10525

ID AAC10525 standard; cDNA; 453 BP.

XX AC AAC10525;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 14600.

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

PS Claim 1; SEQ ID 14600; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included.

CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be

CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used

CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors.

XX Sequence 453 BP; 111 A; 132 C; 130 G; 78 T; 2 other;

SQ

Query Match 13.6%; Score 18; DB 21; Length 453;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

us-09-915-178-1.0110.rng

Wed Jun 4 11:04:53 2003

```

XX DT 18-JUN-2002 (first entry)
XX DE Human colon cancer-associated cDNA, SEQ ID NO 274.
XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200212280-A2.
XX PD 14-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US23826.
XX PR 03-AUG-2000; 2000US-223265P.
XX PR 02-OCT-2000; 2000US-237406P.
XX PR 20-MAR-2001; 2001US-277495P.
XX PR 03-JUL-2001; 2001US-302702P.
XX PA (CORI-) CORIXA CORP.
XX PI Pyle RA, Xu J, Secretist H;
XX DR WPI; 2002-257462/30.
XX PT Novel polynucleotide encoding colon tumour polypeptides, useful as
XX PT vaccines for treating colon cancers
XX PS Claim 1; Page 228; 425pp; English.
XX CC The invention relates to isolated polynucleotides (I) encoding colon
XX CC tumour polypeptides (II). (I) is useful for stimulating an immune
XX CC response in a patient and treating colon cancer in a patient.
XX CC Oligonucleotides derived from (I) are useful for determining the presence
XX CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
XX CC compositions, e.g. vaccines, and other compositions for the diagnosis
XX CC and treatment of colon cancer. A composition comprising a first component
XX CC selected from physiologically acceptable carriers and immunostimulants,
XX CC and an antigen-presenting cell expressing (II) is useful for inhibiting
XX CC development of cancer in a patient. (I) is useful in the design and
XX CC preparation of ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
XX CC sequences of the invention.
XX SQ Sequence 453 BP; 130 A; 121 C; 124 G; 78 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 453;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
Db 114 GATAAGGCCAAGCTGAAG 131

RESULT 28
ABK54803
ID ABK54803 standard; cDNA; 455 BP.
XX AC ABK54803;
XX DT 18-JUN-2002 (first entry)
XX DE Human colon cancer-associated cDNA, SEQ ID NO 273.
XX KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200212280-A2.
XX PD 14-FEB-2002.

117 GATAAGGCCAAGCTGAAG 164

RESULT 26
ABN96522
ID ABN96522 standard; DNA; 453 BP.
XX AC ABN96522;
XX DT 13-AUG-2002 (first entry)
XX DE Gene #3020 used to diagnose liver cancer.
XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX KW metastatic liver tumour; cytostatic; expression profile; disease state;
XX KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX OS Homo sapiens.
XX PN WO200229103-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30589.
XX PR 02-OCT-2000; 2000US-237054P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX DR WPI; 2002-426119/45.
XX PT Diagnosing and detecting the progression of liver cancer,
XX PT hepatocellular carcinoma or metastatic liver tumor in a patient,
XX PT involves detecting the level of expression of two or more genes in a
XX PT liver tissue sample
XX PS Claim 1; SEQ ID NO 3020; 298pp; English.
XX CC The invention relates to a novel method for diagnosing and detecting the
XX CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX CC tumour in a patient, and differentiating metastatic liver cancer from
XX CC hepatocellular carcinoma in a patient, involving detecting the level of
XX CC expression of two or more genes represented in ABN93503-ABN97455 in a
XX CC tissue sample. The method of the invention has hepatotropic, and
XX CC cytostatic activity. The method is useful for diagnosing and detecting
XX CC the progression of liver cancer, hepatocellular carcinoma and metastatic
XX CC liver carcinoma in a patient. The method is useful for identifying
XX CC expression profiles which serve as useful diagnostic markers as well as
XX CC markers that can be used to monitor disease states, disease progression,
XX CC drug toxicity, drug efficacy and drug metabolism.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 453 BP; 132 A; 119 C; 124 G; 78 T; 0 other;

Query Match 13.6%; Score 18; DB 24; Length 453;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57
Db 105 GATAAGGCCAAGCTGAAG 122

RESULT 27
ABK54804
ID ABK54804 standard; cDNA; 453 BP.
XX AC ABK54804;
```


CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (ii) is useful for inhibiting
CC development of cancer in a patient. (i) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (i). ABK54531-ABK5464 represent human colon cancer cDNA
CC sequences of the invention.

XX Sequence 465 BP; 130 A; 124 C; 124 G; 84 T; 3 other;

Query Match 13.6%; Score 18; DB 24; Length 465;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57

Db 101 GATAAGGCCCAAGCTGAAG 118

RESULT 31

AAC10524

ID AAC10524 standard; cDNA; 488 BP.

XX AAC10524;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 14599.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GBST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 14599; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.

XX Sequence 488 BP; 135 A; 127 C; 136 G; 90 T; 0 other;

Query Match 13.6%; Score 18; DB 21; Length 488;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57

Db 147 GATAAGGCCCAAGCTGAAG 164

RESULT 32

AAD03640

ID AAD03640 standard; DNA; 491 BP.

XX AAD03640;

XX 19-JUN-2001 (first entry)

XX Human thymosin b-10 gene from clone NL_33.

XX Human; natural antisense mRNA enrichment; antisense-based therapy;
KW thymosin b-10; clone NL_33; ds.

XX Homo sapiens.

XX WO200125488-A2.

XX 12-APR-2001.

XX 06-OCT-2000; 2000WO-US27557.

XX 06-OCT-1999; 99US-0157843.

XX (QUAR-) QUARK BIOTECH INC.

XX Gilad S, Einat P, Grossman A;

XX WPI; 2001-266326/27.

XX Enrichment and detection of natural antisense mRNA comprises generating
XX double stranded hybrid cDNA using a polymerase with an exonuclease
XX activity, amplifying using a DT primer and cloning -

XX Disclosure; Page 30; 37pp; English.

XX The invention relates to a method for enrichment of natural
XX antisense messenger RNA. This method involves generating a
XX population of cDNA from mRNA, incubating the generated cDNA
XX to produce double stranded hybrid DNA molecules consisting
XX of sense and antisense cDNA, treating the hybrid molecules
XX using DNA polymerase with an exonuclease activity, amplifying
XX the double stranded molecule using a deoxythymidine (dT)
XX primer and cloning the amplified double stranded molecule.
XX This method is useful for enrichment of natural antisense
XX mRNA from any natural source of RNA. It is used to detect
XX whether mRNAs have a natural anti-sense counterpart. The
XX method provides a basis for finding new genes with important
XX cellular regulatory roles or new regulatory information for
XX known genes and provides a starting material for development
XX of an antisense-based therapeutic to treat a disease in which
XX down regulation or inhibition of the sense gene or transcript
XX is involved.

XX The present sequence is human thymosin b-10 gene from clone
XX NL_33. This clone is obtained from the antisense enriched
XX library and is individually confirmed for the presence of
XX matching antisense mRNA.

XX Sequence 491 BP; 150 A; 120 C; 123 G; 98 T; 0 other;

Query Match 13.6%; Score 18; DB 22; Length 491;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCCAAGCTGAAG 57

|||||

Db 131. GATAAGGCCAAGCTGAAG 148

RESULT 33
ABK55404
ID ABK55404 standard; cDNA; 517 BP.
XX AC
XX ABK55404;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human colon cancer-associated cDNA, SEQ ID No 874.
DE
XX Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX KW
XX Homo sapiens.
OS
XX WO200212280-A2.
PN
XX 14-FEB-2002.
PD
XX 30-JUL-2001; 2001WO-US23826.
XX PF
XX 03-AUG-2000; 2000US-223265P.
XX PR
XX 02-OCT-2000; 2000US-237406P.
XX PR
XX 20-MAR-2001; 2001US-277495P.
XX PR
XX 03-JUL-2001; 2001US-302702P.
XX PR
XX (CORI-) CORIXA CORP.
PA
XX Pyle RA, Xu J, Secrlist H;
XX
XX WPI; 2002-257462/30.
XX
XX Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers
PT
XX
XX Claim 1; Page 402; 425pp; English.
PS
XX The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.
XX
SQ Sequence 517 BP; 190 A; 119 C; 128 G; 77 T; 3 other;
Query Match 13.6%; Score 18; DB 24; Length 517;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 103 GATAAGGCCAAGCTGAAG 120
RESULT 34
ABV33875
ID ABV33875 standard; cDNA; 534 BP.
XX AC
XX ABV33875;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 33866.
DE

XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
XX WO200160860-A2.
PN
XX 23-AUG-2001.
PD
XX 20-FEB-2001; 2001WO-US05171.
XX PF
XX 17-FEB-2000; 2000US-183319P.
XX PR
XX 16-MAR-2000; 2000US-189862P.
XX PR
XX 25-MAY-2000; 2000US-207454P.
XX PR
XX 09-JUN-2000; 2000US-211314P.
XX PR
XX 18-JUL-2000; 2000US-219007P.
XX PR
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 7146; 11750pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 534 BP; 137 A; 131 C; 113 G; 153 T; 0 other;
SQ
Query Match 13.6%; Score 18; DB 23; Length 534;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
|||||
Db 377 GATAAGGCCAAGCTGAAG 394
RESULT 35
ABV42758
ID ABV42758 standard; cDNA; 534 BP.
XX
XX AC
XX ABV42758;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 42749.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS

us-09-915-178-1.0110.rng

Wed Jun 4 11:04:53 2003

```

PR WO200160860-A2.
PR 23-AUG-2001.
PR 20-FEB-2001; 2001WO-US05171.
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
PR (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PR Schlegel R, Endege WO, Monahan JE;
PR WPI; 2001-662795/76.
PR Novel isolated nucleic acid molecule associated with cancerous state of
PR prostate cells and correlating with presence of prostate cancer, useful
PR for detecting presence of prostate cancer, stage of prostate cancer
PR
PR Claim 1; Page 8549; 11750pp; English.
PR The invention relates to an isolated nucleic acid molecule (I) comprising
PR a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
PR specification or its complement. (I) is useful for:
PR (a) assessing whether a patient is afflicted with prostate cancer;
PR (b) monitoring the progression of prostate cancer in a patient;
PR (c) assessing the efficacy of a test compound to inhibit prostate
PR cancer in a patient;
PR (d) assessing the efficacy of a therapy for inhibiting prostate cancer
PR in a patient;
PR (e) selecting a composition for inhibiting prostate cancer in a patient;
PR (f) assessing the prostate cell carcinogenic potential of a compound;
PR (g) determining whether prostate cancer has metastasized in a patient;
PR (h) assessing the aggressiveness or indolence of prostate cancer in a
PR patient;
PR (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
PR
PR Sequence 534 BP; 137 A; 131 C; 113 G; 153 T; 0 other;
PR
PR Query Match 13.6%; Score 18; DB 23; Length 534;
PR Best Local Similarity 100.0%; Pred. No. 23;
PR Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR
PR QY 40 GATAAGGCCCAAGCTGAAG 57
PR DB 377 GATAAGGCCCAAGCTGAAG 394
PR
PR RESULT 36
PR ABK54689
PR ID ABK54689 standard; cDNA; 559 BP.
PR AC ABK54689;
PR AC ABK54689;
PR DT 18-JUN-2002 (first entry)
PR DE Human colon cancer-associated cDNA, SEQ ID NO 159.
PR DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
PR OS Homo sapiens.
PR PN WO200212280-A2.
PR PD 14-FEB-2002.
PR PF 30-JUL-2001; 2001WO-US23826.
PR PR 03-AUG-2000; 2000US-223265P.
PR PR 02-OCT-2000; 2000US-237406P.
PR PR 20-MAR-2001; 2001US-277495P.
PR PR 03-JUL-2001; 2001US-302702P.
PR PR (CORI-) CORIXA CORP.
PR PR Pyle RA, Xu J, Secrist H;
PR PR WPI; 2002-257462/30.
PR PR Novel polynucleotide encoding colon tumour polypeptides, useful as
PR PT vaccines for treating colon cancers
PR
PR Claim 1; Page 196; 425pp; English.
PR The invention relates to isolated polynucleotides (I) encoding colon
PR tumour polypeptides (II). (I) is useful for stimulating an immune
PR response in a patient and treating colon cancer in a patient.
PR Oligonucleotides derived from (I) are useful for determining the presence
PR of cancer in a patient. (I) and (II) are useful in pharmaceutical
PR compositions, e.g. vaccines, and other compositions for the diagnosis
PR and treatment of colon cancer. A composition comprising a first component
PR selected from physiologically acceptable carriers and immunostimulants,
PR and an antigen-presenting cell expressing (II) is useful for inhibiting
PR development of cancer in a patient. (I) is useful in the design and
PR preparation of ribozyme molecules for inhibiting expression of tumour
PR polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
PR sequences of the invention.
PR
PR Sequence 559 BP; 118 A; 196 C; 144 G; 99 T; 2 other;
PR
PR Query Match 13.6%; Score 18; DB 24; Length 559;
PR Best Local Similarity 100.0%; Pred. No. 23;
PR Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR
PR QY 40 GATAAGGCCCAAGCTGAAG 57
PR DB 90 GATAAGGCCCAAGCTGAAG 107
PR
PR RESULT 37
PR ABK55328
PR ID ABK55328 standard; cDNA; 693 BP.
PR AC ABK55328;
PR AC ABK55328;
PR DT 18-JUN-2002 (first entry)
PR DE Human colon cancer-associated cDNA, SEQ ID NO 798.
PR DE Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
PR OS Homo sapiens.
PR PN WO200212280-A2.
PR PD 14-FEB-2002.
PR PF 30-JUL-2001; 2001WO-US23826.
PR PR 03-AUG-2000; 2000US-223265P.
PR PR 02-OCT-2000; 2000US-237406P.
PR PR 20-MAR-2001; 2001US-277495P.
PR PR 03-JUL-2001; 2001US-302702P.
PR PR (CORI-) CORIXA CORP.
PR PR Pyle RA, Xu J, Secrist H;
PR PR WPI; 2002-257462/30.
PR PR Novel polynucleotide encoding colon tumour polypeptides, useful as
PR PT vaccines for treating colon cancers

```

XX Claim 1; Page 376; 425pp; English.
PS The invention relates to isolated polynucleotides (I) encoding colon
CC tumour polypeptides (II). (I) is useful for stimulating an immune
CC response in a patient and treating colon cancer in a patient.
CC Oligonucleotides derived from (I) are useful for determining the presence
CC of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis
CC and treatment of colon cancer. A composition comprising a first component
CC selected from physiologically acceptable carriers and immunostimulants,
CC and an antigen-presenting cell expressing (II) is useful for inhibiting
CC development of cancer in a patient. (I) is useful in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
CC sequences of the invention.
XX
SQ Sequence 693 BP; 203 A; 168 C; 172 G; 130 T; 20 other;
Query Match 13.6%; Score 18; DB 24; Length 693;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
Db 80 GATAAGGCCAAGCTGAAG 97
RESULT 38
ABV25565
ID ABV25565 standard; cDNA; 736 BP.
XX AC ABV25565;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 25556.
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KW Homo sapiens.
OS
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US05171.
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 5098; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
XX
XX Claim 1; Page 5098; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 736 BP; 165 A; 245 C; 188 G; 138 T; 0 other;
Query Match 13.6%; Score 18; DB 23; Length 736;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 GATAAGGCCAAGCTGAAG 57
Db 127 GATAAGGCCAAGCTGAAG 144
RESULT 39
ABV03577
ID ABV03577 standard; cDNA; 792 BP.
XX AC ABV03577;
XX 13-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 3568.
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KW Homo sapiens.
OS
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US05171.
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 645; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;

us-09-915-178-1.olilo.rng

Wed Jun 4 11:04:53 2003

CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 792 BP; 207 A; 187 C; 154 G; 190 T; 54 other;
 SQ Query Match 13.6%; Score 18; DB 23; Length 792;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 GATAGGCCCAAGCTGAAG 57
 DB 381 GATAGGCCCAAGCTGAAG 398
 RESULT 40
 ABV12746
 ID ABV12746 standard; cDNA; 836 BP.
 AC ABV12746;
 XX 13-SEP-2002 (first entry)
 DT Human prostate expression marker cDNA 12737.
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 XX 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 XX for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 2099; 11750pp; English.
 PS The invention relates to an isolated nucleic acid molecule (I) comprising
 XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 836 BP; 226 A; 201 C; 178 G; 221 T; 10 other;
 SQ

Query Match 13.6%; Score 18; DB 23; Length 836;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 GATAGGCCCAAGCTGAAG 57
 DB 402 GATAGGCCCAAGCTGAAG 419
 RESULT 41
 ABV21155
 ID ABV21155 standard; cDNA; 1201 BP.
 AC ABV21155;
 XX 13-SEP-2002 (first entry)
 DT Human prostate expression marker cDNA 21146.
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 XX 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 XX for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 3506; 11750pp; English.
 PS The invention relates to an isolated nucleic acid molecule (I) comprising
 XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 1201 BP; 355 A; 291 C; 289 G; 265 T; 1 other;
 SQ Query Match 13.6%; Score 18; DB 23; Length 1201;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 GATAGGCCCAAGCTGAAG 57

|||||
401 GATAAGGCCAAGCTGAAG 418

RESULT 42

ABV22339

ID ABV22339 standard; cDNA; 1201 BP.

XX AC

XX ABV22339;

XX DT

XX 13-SEP-2002 (first entry)

XX DE

XX Human prostate expression marker cDNA 22330.

XX KW

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW

XX pharmacogenomic marker; gene; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200160860-A2.

XX PD

XX 23-AUG-2001.

XX PF

XX 20-FEB-2001; 2001WO-US05171.

XX XX

XX 17-FEB-2000; 2000US-183319P.

XX PR

XX 16-MAR-2000; 2000US-189862P.

XX PR

XX 25-MAY-2000; 2000US-207454P.

XX PR

XX 09-JUN-2000; 2000US-211314P.

XX PR

XX 18-JUL-2000; 2000US-219007P.

XX PR

XX 13-DEC-2000; 2000US-255281P.

XX XX

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PA

XX Schlegel R, Endege WO, Monahan JE;

XX PI

XX WPI; 2001-662795/76.

XX DR

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX PT

XX prostate cells and correlating with presence of prostate cancer, useful

XX PT

XX for detecting presence of prostate cancer, stage of prostate cancer -

XX PS

XX Claim 1; Page 3869; 11750pp; English.

XX XX

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX CC

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX CC

XX specification or its complement. (I) is useful for:

XX CC

XX (a) assessing whether a patient is afflicted with prostate cancer;

XX CC

XX (b) monitoring the progression of prostate cancer in a patient;

XX CC

XX (c) assessing the efficacy of a test compound to inhibit prostate

XX CC

XX cancer in a patient;

XX CC

XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer

XX CC

XX in a patient;

XX CC

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX CC

XX (f) assessing the prostate cell carcinogenic potential of a compound;

XX CC

XX (g) determining whether prostate cancer has metastasized in a patient;

XX CC

XX (h) assessing the aggressiveness or indolence of prostate cancer in a

XX CC

XX patient;

XX CC

XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX XX

SQ Sequence 1201 BP; 355 A; 291 C; 289 G; 265 T; 1 other;

Query Match 13.6%; Score 18; DB 23; Length 1201;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

|||||

Db 401 GATAAGGCCAAGCTGAAG 418

RESULT 43

ABV28163

ID ABV28163 standard; cDNA; 1201 BP.

XX AC

XX ABV28163;

XX DT

XX 16-SEP-2002 (first entry)

XX XX

XX Human prostate expression marker cDNA 28154.

XX KW

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW

XX pharmacogenomic marker; gene; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200160860-A2.

XX PD

XX 23-AUG-2001.

XX PF

XX 20-FEB-2001; 2001WO-US05171.

XX XX

XX 17-FEB-2000; 2000US-183319P.

XX PR

XX 16-MAR-2000; 2000US-189862P.

XX PR

XX 25-MAY-2000; 2000US-207454P.

XX PR

XX 09-JUN-2000; 2000US-211314P.

XX PR

XX 18-JUL-2000; 2000US-219007P.

XX PR

XX 13-DEC-2000; 2000US-255281P.

XX XX

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PA

XX Schlegel R, Endege WO, Monahan JE;

XX PI

XX WPI; 2001-662795/76.

XX DR

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX PT

XX prostate cells and correlating with presence of prostate cancer, useful

XX PT

XX for detecting presence of prostate cancer, stage of prostate cancer -

XX PS

XX Claim 1; Page 5839-5840; 11750pp; English.

XX XX

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX CC

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX CC

XX specification or its complement. (I) is useful for:

XX CC

XX (a) assessing whether a patient is afflicted with prostate cancer;

XX CC

XX (b) monitoring the progression of prostate cancer in a patient;

XX CC

XX (c) assessing the efficacy of a test compound to inhibit prostate

XX CC

XX cancer in a patient;

XX CC

XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer

XX CC

XX in a patient;

XX CC

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX CC

XX (f) assessing the prostate cell carcinogenic potential of a compound;

XX CC

XX (g) determining whether prostate cancer has metastasized in a patient;

XX CC

XX (h) assessing the aggressiveness or indolence of prostate cancer in a

XX CC

XX patient;

XX CC

XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX XX

SQ Sequence 1201 BP; 355 A; 291 C; 289 G; 265 T; 1 other;

Query Match 13.6%; Score 18; DB 23; Length 1201;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAAGGCCAAGCTGAAG 57

|||||

Db 401 GATAAGGCCAAGCTGAAG 418

RESULT 44

ABK84119

ID ABK84119 standard; cDNA; 1262 BP.

XX AC

XX ABK84119;

XX XX

XX 14-AUG-2002 (first entry)

XX XX

Query Match 13.6%; Score 18; DB 24; Length 1262;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GATAGGCCCAAGCTGAAG 57

Db 603 GATAGGCCCAAGCTGAAG 620

RESULT 45

AAS02039

ID AAS02039 standard; cDNA; 1517 BP.

XX AAS02039;

XX 16-JUL-2001 (first entry)

XX DNA encoding molecule for disease detection and treatment, mddt4.

XX Human; mddt4; zinc finger; gene therapy; adenosine deaminase deficiency;

XX ADA; severe combined immunodeficiency syndrome; cystic fibrosis;

XX thalassaemia; familial hypercholesterolaemia; haemophilia; factor VIII;

XX factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;

XX hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;

XX Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.

XX Homo sapiens.

XX WO200123538-A2.

XX 05-APR-2001.

XX 22-SEP-2000; 2000WO-US26085.

XX 28-SEP-1999; 99US-0156565.

XX 30-NOV-1999; 99US-0168197.

XX (INCY-) INCYTE GENOMICS INC.

XX Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;

XX Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Chalup MS;

XX Hillman JL, Jones AL, Yu JY, Greenwalt LB, Panzer SR;

XX Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;

XX Anshey S, Fong WT;

XX WPI; 2001-258131/26.

XX Purified disease treatment and detection molecule polynucleotides and

XX polypeptides, useful for providing diagnostic assays and gene therapy -

XX Claim 1; Page 97-98; 113pp; English.

XX The sequence represents the coding sequence of molecule for disease
XX detection and treatment, mddt4, shown by computer analysis to be similar
XX to zinc finger C2H2 type family of proteins. The sequence may be used for
XX somatic or germline gene therapy. Gene therapy may be performed to: (i)
XX correct genetic deficiency such as in severe immunodeficiency syndrome
XX associated with adenosine deaminase (ADA) deficiency, cystic fibrosis,
XX thalassaemias, familial hypercholesterolaemia and haemophilia caused by
XX factor VIII or factor IX deficiencies; (ii) express a conditional lethal
XX gene product (such as in the case of cancers which result from
XX unregulated cell proliferation); (iii) express a protein which affords
XX protection against intracellular parasites (for example, human
XX retroviruses such as HIV, hepatitis B or C, fungal parasites such as
XX Candida albicans and Paracoccidioides brasiliensis, and protozoal
XX parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.

XX Sequence 1517 BP; 289 A; 544 C; 447 G; 233 T; 4 other;

XX Query Match 13.6%; Score 18; DB 22; Length 1517;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Human cDNA differentially expressed in granulocytic cells #690.

Human; ss; granulocytic cell; DNA chip; bacterial infection;

viral infection; parasitic infection; protozoal infection;

fungal infection; sterile inflammatory disease; psoriasis;

rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

cardiac reperfusion injury; renal reperfusion injury; ARDS;

adult respiratory distress syndrome; inflammatory bowel disease;

Crohn's disease; ulcerative colitis; periodontal disease;

granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression

XX of genes associated with granulocyte activation, which serves as

XX diagnostic markers that is useful for monitoring disease states and

XX drug toxicity -

XX Claim 1; SEQ ID NO 690; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation

XX (GCA); by detecting the level of expression of gene(s) (Gs) identified by

XX DNA chip analysis as given in the specification, and comparing

XX the expression level to an expression level in an unactivated

XX GC, where differential expression of Gs is indicative of GCA.

XX Also included are modulation of at least one gene in Gs; (2) screening (M3)

XX that alters the expression of GCA or an inflammation (especially

XX chronic) in a tissue, an allergic response in a subject, exposure of a

XX subject to a pathogen or sterile inflammatory disease using the

XX gene expression profile; (3) detecting (M4) an inflammation (especially

XX chronic) in a tissue, an allergic response in a subject, exposure of a

XX subject to a pathogen or sterile inflammatory disease, by detecting the

XX level of expression in a sample of the tissue of gene(s) from Gs, where

XX the level of expression of the gene is indicative of inflammation;

XX (4) treating (M5) an inflammation (especially chronic) or in a tissue,

XX an allergic response in a subject, exposure of a subject to a pathogen

XX or sterile inflammatory disease, by contacting a tissue having

XX inflammation with an agent that modulates the expression of gene(s)

XX from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for

XX modulating GCA; M3 is useful for screening an agent capable of modulating

XX GCA preferably in an inflammation (especially chronic) in a tissue, an allergic

XX response in a subject, exposure of a subject to a pathogen or sterile

XX inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal

XX glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal

XX reperfusion injury, ARDS, adult respiratory distress syndrome,

XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,

XX parasitic infection, protozoal infection, fungal infection, and M5 is

XX useful for treating one of the above conditions. The present

XX sequence represents a gene differentially expressed in granulocytes.

XX Note: The sequence data for this patent did not form part

XX of the printed specification, but was obtained in electronic

XX format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1262 BP; 240 A; 404 C; 400 G; 215 T; 3 other;

QY 43 AAGCCCAAGCTGAAGGCC 60
Db 50 AAGCCCAAGCTGAAGGCC 67

RESULT 46
ABL06285
ID ABL06285 standard; cDNA; 2606 BP.
XX AC ABL06285;
XX XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13337.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PS New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 13337; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
PS Sequence 2606 BP; 711 A; 567 C; 633 G; 595 T; 0 other;
XX
CC Query Match 13.6%; Score 18; DB 23; Length 2606;
CC Best Local Similarity 100.0%; Pred. No. 23;
CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 44 AGGCCCAAGCTGAAGGCCA 61
Db 1712 AGGCCCAAGCTGAAGGCCA 1729

RESULT 47
ABL21125
ID ABL21125 standard; DNA; 2609 BP.
XX AC ABL21125;
XX
DT 26-MAR-2002 (first entry)
XX

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14848.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PS New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 14848; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
PS Sequence 2609 BP; 681 A; 670 C; 656 G; 602 T; 0 other;
XX
CC Query Match 13.6%; Score 18; DB 23; Length 2609;
CC Best Local Similarity 100.0%; Pred. No. 23;
CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 44 AGGCCCAAGCTGAAGGCCA 61
Db 1715 AGGCCCAAGCTGAAGGCCA 1732

RESULT 48
AAK52974
ID AAK52974 standard; cDNA; 3291 BP.
XX AC AAK52974;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2503.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.

us-09-915-178-1.olil0.rng

Wed Jun 4 11:04:53 2003

```
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI: 2001-476283/51.
DR P-PSDB; AAM79841.
XX Nucleic acids encoding polypeptides with cytokine-like activities,
DR useful in diagnosis and gene therapy -
XX Claim 1; Page 4781-4782; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX Sequence 3291 BP; 620 A; 1131 C; 989 G; 551 T; 0 other;
XX Query Match 13.6%; Score 18; DB 22; Length 3291;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 AGGCCAAGCTGAAGGCCA 61
DB 2929 AGGCCAAGCTGAAGGCCA 2946
RESULT 49
AAK51990
ID AAK51990 standard; CDNA; 3754 BP.
XX AC AAK51990;
XX DE 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 535.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX Homo sapiens.
XX OS
XX PN WO200157190-A2.
XX PD
XX PF 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US04098.
XX PF
XX XX
```

```
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI: 2001-476283/51.
DR P-PSDB; AAM78857.
XX Nucleic acids encoding polypeptides with cytokine-like activities,
DR useful in diagnosis and gene therapy -
XX Claim 1; Page 1931-1934; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX Sequence 3754 BP; 811 A; 1165 C; 1035 G; 743 T; 0 other;
XX Query Match 13.6%; Score 18; DB 22; Length 3754;
XX Best Local Similarity 100.0%; Pred. No. 23;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 AGGCCAAGCTGAAGGCCA 61
DB 3392 AGGCCAAGCTGAAGGCCA 3409
RESULT 50
ABL25848
ID ABL25848 standard; DNA; 4229 BP.
XX AC ABL25848;
XX DE 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29017.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX OS
XX PN WO200171042-A2.
XX PD
XX PF 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PF 23-MAR-2000; 2000US-191637P.
XX PF 11-JUL-2000; 2000US-0614150.
XX PF
XX XX
```


PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li PWD, Myers EW;
XX	
DR	WPI; 2001-656860/75.
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions -
XX	
PS	Claim 1; SEQ ID NO 29017; Zipp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (ABLL16176-ABL30511), expressed DNA
CC	sequences (ABL01840-ABL116175) and the encoded proteins
CC	(ABB57737-ABB72072).
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences .
xx	
SQ	Sequence 4229 BP; 1287 A; 1022 C; 928 G; 992 T; 0 other;
	Query Match 13.6%; Score 18; DB 23; Length 4229;
	Best Local Similarity 100.0%; Pred. No. 23;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	29 TTGCCAGCTTGGATAAGG 46
Db	2080 TTGCCAGCTTGGATAAGG 2097

Search completed: June 2, 2003, 15:56:08
Job time : 250 secs

THIS PAGE BLANK (USPTO)